

C 107	42	4.2	51	1	AA177521	Human silent SNP c	180	36.2	3.7	41	1	ABZ46915	Human ATP-binding
C 108	42	4.2	51	1	AA179584	Human silent SNP c	C 181	36.2	3.7	41	1	ABZ49741	Human cerebroside
C 109	42	4.2	51	1	AA178039	Human silent SNP c	C 182	35.8	3.6	40	1	AAH91207	Human inflammatory
C 110	42	4.2	51	1	AA178300	Human silent SNP c	C 183	35.8	3.6	41	1	ABZ50133	Human NDUF51 gene
C 111	42	4.2	51	1	AA173860	Human silent SNP c	C 184	35.8	3.6	41	1	ABZ44123	Human NDUF51 gene
C 112	42	4.2	51	1	AA173760	Human silent SNP c	C 185	35.2	3.6	40	1	ABT97407	Synthetic oligomer
C 113	42	4.2	51	1	AA177806	Human silent SNP c	C 186	35.2	3.6	40	1	AAV19045	Alu PCR primer 2.
C 114	42	4.2	51	1	AA173533	Human silent SNP c	C 187	35.2	3.6	40	1	ABL51901	Nucleotide sequenc
C 115	42	4.2	51	1	ABL00195	Human silent nonco	C 188	35.2	3.6	41	1	AAH49727	Human DNA mismatch
C 116	42	4.2	48	1	AD112525	Human BRCA1 DNA ju	C 189	35.2	3.6	41	1	ABL40963	Transcription regu
C 117	42	4.2	51	1	AA175849	Human silent SNP c	C 190	35.2	3.6	41	1	ABL40964	Transcription regu
C 118	42	4.2	51	1	ABL00141	Human silent nonco	C 191	35.2	3.6	41	1	ABZ20666	Human G protein su
C 119	42	4.2	51	1	AA177442	Human Alubfamily	C 192	35.2	3.6	41	1	ABQ77547	Human red blood ce
C 120	42	4.2	51	1	AA176988	Human clone c94292	C 193	35.2	3.6	41	1	ABV77328	Human protein 10.0
C 121	42	4.2	51	1	AA177021	Human clone c94308	C 194	35.2	3.6	41	1	ACC00156	Probe #1 for guano
C 122	42	4.2	51	1	AD016930	Human single nucle	C 195	35	3.5	35	1	AAO27391	Inter-Alu specific
C 123	42	4.2	51	1	AA176193	Human silent SNP c	C 196	34.6	3.5	41	1	ABQ83633	Human mper3-10.01
C 124	42	4.2	51	1	AA173061	Human silent SNP c	C 197	34.6	3.5	41	1	ABQ83634	Human mper3-10.01
C 125	42	4.2	51	1	AA174775	Human silent SNP c	C 198	34.6	3.5	41	1	ABL52955	Serine proteinase
C 126	42	4.2	51	1	AA173736	Human silent SNP c	C 199	34.6	3.5	41	1	ABZ49715	Human sulphotransf
C 127	42	4.2	51	1	AA176185	Human silent SNP c	C 200	34.6	3.5	41	1	ABZ43958	Human glutathione-
C 128	42	4.2	51	1	AA174502	Human silent SNP c	C 201	34.6	3.5	41	1	ABZ49550	Human glutathione-
C 129	42	4.2	51	1	AA176499	Human silent SNP c	C 202	34.6	3.5	41	1	ABZ49230	Human aldehyde deh
C 130	42	4.2	51	1	AA179533	Human silent SNP c	C 203	34.6	3.5	41	1	ABZ45236	Human aldehyde deh
C 131	42	4.2	51	1	AA179539	Human silent SNP c	C 204	34.6	3.5	41	1	ABZ43562	Human sulphotransf
C 132	42	4.2	51	1	AA176814	Human silent SNP c	C 205	34.6	3.5	41	1	ADP75520	Human ADAM19 gene,
C 133	42	4.2	51	1	AA176092	Human silent SNP c	C 206	34.6	3.5	41	1	ADL64137	Human single nucle
C 134	42	4.2	51	1	AA179838	Human nonconservat	C 207	34.6	3.5	41	1	ADL64139	Human single nucle
C 135	42	4.2	51	1	AA176541	Human silent SNP c	C 208	34.6	3.5	41	1	ADL64284	Human single nucle
C 136	42	4.2	51	1	AA179697	Human conservative	C 209	34.6	3.4	40	1	AA197406	Synthetic oligomer
C 137	42	4.2	51	1	AA174778	Human silent SNP c	C 210	33.6	3.4	41	1	ADK41334	Human chromosome 1
C 138	42	4.2	51	1	AA173250	Human silent SNP c	C 211	33.6	3.4	41	1	AAH49728	Human DNA mismatch
C 139	42	4.2	51	1	AA179700	Human conservative	C 212	33.6	3.4	41	1	ABL49776	Human tyrosinase 1
C 140	42	4.2	51	1	AA178366	Human silent SNP c	C 213	33.6	3.4	41	1	ABL49775	Human tyrosinase 1
C 141	42	4.2	51	1	AA173862	Human silent SNP c	C 214	33.6	3.4	41	1	ABZ20657	Human G protein su
C 142	42	4.2	51	1	AA179783	Human nonconservat	C 215	33.6	3.4	41	1	ABZ49091	Human tumour suppr
C 143	42	4.2	51	1	AAH90585	Human clone c94308	C 216	33.6	3.4	41	1	AA143826	Human oncogene pro
C 144	42	4.2	51	1	AAH89405	Human coding seque	C 217	33.6	3.4	41	1	AA143827	Human oncogene pro
C 145	42	4.2	51	1	AAH89485	Human coding seque	C 218	33.6	3.4	41	1	ABZ44551	Human glycosyltran
C 146	42	4.2	51	1	AAH89519	Human coding seque	C 219	33.6	3.4	41	1	ABZ50761	Human glycosyltran
C 147	42	4.2	51	1	AAH89519	Human coding seque	C 220	33.6	3.4	41	1	ABV77329	Human protein 10.0
C 148	42	4.2	51	1	AAH89467	Human coding seque	C 221	33.6	3.4	41	1	ACC00157	Probe #2 for guano
C 149	42	4.2	51	1	AAH89553	Human coding seque	C 222	33.6	3.4	41	1	ABZ57114	Human KIA0608 pro
C 150	42	4.2	51	1	AAH89472	Human coding seque	C 223	33.6	3.4	41	1	ADL64136	Human single nucle
C 151	42	4.2	51	1	ADK19818	Human mannosyl tra	C 224	33.2	3.4	41	1	ABZ45510	Human ATP-binding
C 152	42	4.2	51	1	AA179589	Human silent SNP c	C 225	33.2	3.4	41	1	ABZ46916	Human ATP-binding
C 153	42	4.2	49	1	AD112532	Mutant human BRCA1	C 226	33	3.3	33	1	ACC84461	NTP peptide encodi
C 154	42	4.2	51	1	AA176816	Human silent SNP c	C 227	33	3.3	41	1	AA197976	Human eukaryotic a
C 155	42	4.2	51	1	AA179093	Human silent SNP c	C 228	33	3.3	41	1	ABL52956	Serine proteinase
C 156	42	4.2	51	1	AA173524	Human silent SNP c	C 229	33	3.3	41	1	ABZ44124	Human NDUF51 gene
C 157	42	4.2	51	1	AAH89516	Human coding seque	C 230	33	3.3	41	1	ABZ45508	Human ATP-binding
C 158	42	4.2	51	1	AAH38408	Human SNP flanking	C 231	33	3.3	41	1	ABZ49572	Human glutathione-
C 159	42	4.2	51	1	AAH40504	Human SNP flanking	C 232	33	3.3	41	1	ABZ49713	Human sulphotransf
C 160	42	4.2	51	1	ABL00045	Human silent nonco	C 233	33	3.3	41	1	ABZ50134	Human NDUF51 gene
C 161	42	4.2	49	1	AAZ68649	Human map-related	C 234	33	3.3	41	1	ABZ43960	Human sulphotransf
C 162	42	4.2	47	1	ADZ77198	KALPA SNP CV51660	C 235	33	3.3	41	1	ABZ43980	Human glutathione-
C 163	42	4.2	42	1	AD112523	Human BRCA1 DNA ju	C 236	33	3.3	41	1	ABZ46914	Human ATP-binding
C 164	42	4.2	50	1	ABZ07627	Human leukocyte ge	C 237	33	3.3	41	1	ABZ47296	Human ATP-binding
C 165	42	4.2	40	1	AAV19044	Alu PCR primer 1.	C 238	33	3.3	41	1	ABA94080	Human multi-copper
C 166	42	4.2	40	1	ABL59100	Nucleotide sequenc	C 239	33	3.3	41	1	AA15590	Human DNA mismatch
C 167	42	4.2	40	1	ABZ49631	Human sulphotransf	C 240	33	3.3	41	1	ADL64285	Human single nucle
C 168	42	4.2	40	1	ABZ43598	Human sulphotransf	C 241	33	3.3	41	1	ADL64286	Human single nucle
C 169	42	4.2	50	1	AAH89819	Human coding seque	C 242	32	3.2	40	1	ABZ48532	Human oligopeptide
C 170	42	4.2	39	1	ACC84472	NTP peptide encodi	C 243	31.8	3.2	35	1	AAO45257	Alu primer PDJ34 t
C 171	42	4.2	39	1	ACC84471	NTP peptide encodi	C 244	31.8	3.2	35	1	ABA93847	Human GAS1 PCR pr
C 172	42	4.2	39	1	ABA96813	Human uteroglobin	C 245	31.8	3.2	35	1	AAO27392	Inter-Alu specific
C 173	42	4.2	41	1	ABA96812	Human uteroglobin	C 246	30.4	3.1	32	1	ADE14248	Optineurin promote
C 174	42	4.2	41	1	ABZ44526	Human neuropathy t	C 247	30.2	3.1	36	1	AAH91142	Human inflammatory
C 175	42	4.2	41	1	ABZ50785	Human neuropathy t	C 248	30	3.0	32	1	ACC84462	NTP peptide encodi
C 176	42	4.2	42	1	AD112521	Human BRCA1 DNA ju	C 249	29.4	3.0	32	1	ADE14029	Optineurin promote
C 177	42	4.2	47	1	AAZ68806	Human map-related	C 250	29	2.9	31	1	AAO73572	Enhancer element e
C 178	42	4.2	41	1	ABZ43589	Human cerebroside	C 251	27.6	2.8	29	1	AAO4659	Polymorphic fragme
C 179	42	4.2	41	1	ABZ45509	Human ATP-binding	C 252	27.4	2.8	29	1	AAH37977	SNP specific upper

253	27.4	2.8	31	1	AAK06467	Human biallelic po	C 326	23.4	2.4	25	1	ABK70489	In-situ analysis s
254	27.4	2.8	32	1	AAQ27389	Inter-Alu specific	327	23.4	2.4	25	1	ABD27391	PCR primer #1, use
C 255	27.4	2.8	32	1	ADRI4206	Optineurin promote	328	23.4	2.4	25	1	ABD04743	Human MD27 scannin
C 256	27.2	2.7	33	1	AD162688	Human breast or ov	329	23.4	2.4	25	1	ADN48682	Human interleukin-
C 257	27.2	2.7	33	1	AA106807	Human reproductive	C 330	23.4	2.4	27	1	AA237279	PCR primer for SGR
258	27.2	2.7	33	1	ABLA0976	HOMO glandulae mam	C 331	23.4	2.4	27	1	AAH38611	SNP specific SNPE
259	27	2.7	37	1	ACC84460	NTP peptide encodi	C 332	23.4	2.4	28	1	AA227185	Reverse primer ilu
260	27	2.7	29	1	AAA04371	Polyomphic fragme	333	23.4	2.4	28	1	ACC84463	RT-PCR primer 2 re
261	27	2.7	29	1	AAA04506	Polyomphic fragme	C 334	23.4	2.4	28	1	ADP70455	Polyomphic fragme
262	27	2.7	29	1	AAA04303	Polyomphic fragme	C 335	23.4	2.4	29	1	AAA04010	Human inflammatory
263	27	2.7	29	1	AAA04500	Polyomphic fragme	C 336	23.2	2.3	29	1	AAH91536	PCR primer F1209 u
264	27	2.7	29	1	AAA03996	Polyomphic fragme	C 337	23.2	2.3	29	1	ADA74797	Human inflammatory
265	27	2.7	32	1	AAQ03570	Enhancer element e	C 338	23	2.3	23	1	AAH91561	X-T-D oligonucleot
266	27	2.7	32	1	AAQ04505	Enhancer element e	C 339	23	2.3	24	1	AAH91572	Inter-Alu region p
267	27	2.7	32	1	AAK31040	Human digestive by	C 340	22.8	2.3	26	1	AAQ71189	Human NOV-associat
268	26.8	2.7	32	1	AAK32075	Human liver associ	C 341	22.8	2.3	26	1	ABX97392	Human NOV20a RTQ-P
269	26.8	2.7	32	1	ABN90430	Human liver antige	C 342	22.8	2.3	26	1	ADN62195	SNP specific SNPE
C 270	26.8	2.7	32	1	ADU15343	Human liver-relate	C 343	22.8	2.3	27	1	AAH38083	SNP specific SNPE
C 271	26.4	2.7	30	1	AAQ77890	Neural thread prot	C 344	22.8	2.3	27	1	AAH40487	SNP specific SNPE
C 272	26.4	2.7	30	1	AAQ77890	Neural thread prot	C 345	22.8	2.3	27	1	AAH40803	Human inflammatory
C 273	26.2	2.6	32	1	AAH91474	Human inflammatory	C 346	22.8	2.3	27	1	AAH91322	Human ABC1 transcr
C 274	26	2.6	29	1	AAA04663	Polyomphic fragme	C 347	22.4	2.3	24	1	AAE92843	Human transglutami
C 275	26	2.6	29	1	AAA03961	Polyomphic fragme	C 348	22.4	2.3	24	1	AA169885	PCR primer #2, use
C 276	26	2.6	29	1	AAA03993	Polyomphic fragme	C 349	22.4	2.3	24	1	AA500333	Zinc finger protei
C 277	25.8	2.6	30	1	AAQ77889	Neural thread prot	C 350	22.4	2.3	24	1	ABZ21100	Human argininas 9
C 278	25.8	2.6	30	1	AAI27743	Neural thread prot	C 351	22.4	2.3	24	1	ABA69912	Human breast suace
C 279	25.8	2.6	31	1	AAQ73573	Enhancer element e	C 352	22.4	2.3	24	1	ABQ83933	Human PSF promoter
C 280	25.8	2.6	31	1	AAI78748	Human genomic DNA	C 353	22.4	2.3	24	1	ABT08420	Human genomic DNA
C 281	25.6	2.6	32	1	AAAD3091	Human tandem tag D	C 354	22.4	2.3	24	1	ACF05122	Human TGN promote
C 282	25.4	2.6	29	1	AAA04017	Polyomphic fragme	C 355	22.4	2.3	24	1	ADG28972	PCR primer SEQ ID
C 283	25.4	2.6	29	1	AAA04065	Polyomphic fragme	C 356	22.4	2.3	24	1	ABX15537	Human VII exon 1d
C 284	25.4	2.6	29	1	AAA04512	Polyomphic fragme	C 357	22.4	2.3	25	1	ADQ30417	Human II-1 genotyp
C 285	25.4	2.6	29	1	AAA04499	Polyomphic fragme	C 358	22.4	2.3	25	1	AAH38447	SNP specific SNPE
C 286	25.4	2.6	29	1	AAA03984	Polyomphic fragme	C 359	22.4	2.3	25	1	ADH04744	Human MD27 scannin
C 287	25.4	2.6	29	1	AAA04645	Polyomphic fragme	C 360	22.4	2.3	25	1	ADB04742	Human MD27 scannin
C 288	25.4	2.6	29	1	AAH38989	SNP specific upper	C 361	22.4	2.3	25	1	ADOI2082	Single multiplex p
C 289	25.4	2.6	30	1	AAH40734	SNP specific lower	C 362	22.2	2.2	27	1	ADOI2035	Nucleotide sequenc
C 290	25.2	2.5	30	1	AAH40734	SNP specific lower	C 363	22.2	2.2	27	1	AAV29285	Human ALU sequence
C 291	25	2.5	25	1	AAH40799	SNP specific SNPE	C 364	22.2	2.2	22	1	AAZ07500	Human thyroid mal
C 292	25	2.5	25	1	AAH40799	SNP specific SNPE	C 365	22	2.2	22	1	AAZ07500	Human thyroid mal
C 293	25	2.5	25	1	AAH40799	SNP specific SNPE	C 366	22	2.2	22	1	AAZ07500	Human thyroid mal
C 294	25	2.5	25	1	AAH40799	SNP specific SNPE	C 367	22	2.2	22	1	AAZ07500	Human thyroid mal
C 295	24.8	2.5	29	1	AAH91598	Human Med-6 gene p	C 368	22	2.2	22	1	AAZ07500	Human thyroid mal
C 296	24.6	2.5	29	1	AAA03985	Polyomphic fragme	C 369	22	2.2	22	1	AAZ07500	Human thyroid mal
C 297	24.4	2.5	26	1	ABK65978	Human gene specific	C 370	22	2.2	22	1	AAZ07500	Human thyroid mal
C 298	24.4	2.5	26	1	ABK65984	Human gene specific	C 371	22	2.2	22	1	AAZ07500	Human thyroid mal
C 299	24.4	2.5	28	1	AAH91530	Human inflammatory	C 372	21.8	2.2	25	1	AAH38404	SNP specific SNPE
C 300	24.4	2.5	29	1	AAA04000	Polyomphic fragme	C 373	21.8	2.2	25	1	ADB04745	Human MD27 scannin
C 301	24.4	2.5	29	1	AAA04507	Polyomphic fragme	C 374	21.8	2.2	25	1	ADB04741	Human MD27 scannin
C 302	24.4	2.5	29	1	AAA04369	Polyomphic fragme	C 375	21.8	2.2	25	1	ADJ33167	Primer sequence R2
C 303	24.4	2.5	29	1	AAA03994	Polyomphic fragme	C 376	21.8	2.2	26	1	AAH91005	Human inflammatory
C 304	24.4	2.5	29	1	AAA04389	Polyomphic fragme	C 377	21.8	2.2	26	1	AAH91096	Human inflammatory
C 305	24.4	2.5	29	1	AAA04314	Polyomphic fragme	C 378	21.8	2.2	27	1	AAH38507	SNP specific SNPE
C 306	24.4	2.5	30	1	AD182609	Prostate-specific	C 379	21.8	2.2	27	1	AAH37975	SNP specific SNPE
C 307	24.2	2.4	30	1	AAH91549	Alu family consens	C 380	21.8	2.2	27	1	AAH31552	Human inflammatory
C 308	24.2	2.4	30	1	AAH91549	Alu family consens	C 381	21.4	2.2	23	1	AAH3037	Primer B2C to isol
C 309	24.2	2.4	30	1	AAH91549	Alu family consens	C 382	21.4	2.2	23	1	AAH3037	Primer B2C to isol
C 310	24	2.4	24	1	AAH45830	Human inflammatory	C 383	21.4	2.2	24	1	AA165098	Human zinc finger
C 311	24	2.4	24	1	AAH45828	Telomere size dete	C 384	21.4	2.2	24	1	ABSS58183	RT-PCR primer #1 f
C 312	24	2.4	24	1	ADL07545	Telomere size dete	C 385	21.4	2.2	24	1	ABSS58184	RT-PCR primer #2 f
C 313	23.8	2.4	28	1	AAH91303	Human inflammatory	C 386	21.4	2.2	24	1	ABA04737	Human alkylation D
C 314	23.8	2.4	29	1	AAA03956	Polyomphic fragme	C 387	21.4	2.2	24	1	AAH45771	Human acid phospha
C 315	23.8	2.4	29	1	AAA04662	Polyomphic fragme	C 388	21.4	2.2	24	1	AAH45771	PCR primer #1 used
C 316	23.8	2.4	29	1	AAA04486	Polyomphic fragme	C 389	21.4	2.2	25	1	AAH38231	RT-PCR primer #1 f
C 317	23.8	2.4	29	1	AAA03878	Polyomphic fragme	C 390	21.4	2.2	25	1	AAH38231	SNP specific SNPE
C 318	23.8	2.4	29	1	AAA04600	Polyomphic fragme	C 391	21.2	2.1	26	1	AAZ45143	Oligonucleotide us
C 319	23.8	2.4	29	1	AAA04502	Polyomphic fragme	C 392	21.2	2.1	26	1	ABK61474	Human gene specific
C 320	23.8	2.4	29	1	AAA04661	Polyomphic fragme	C 393	21.2	2.1	26	1	ABK61474	Human gene specific
C 321	23.8	2.4	29	1	AAA04307	Polyomphic fragme	C 394	21.2	2.1	26	1	ABZ22656	Human gene specific
C 322	23.4	2.4	25	1	AAZ09548	Human Apo E oligon	C 395	21.2	2.1	26	1	AD125447	Human gene specific
C 323	23.4	2.4	25	1	AAH16609	Human Apo E oligon	C 396	21	2.1	21	1	AAH16609	Human gene specific
C 324	23.4	2.4	25	1	AAH16609	Human Apo E oligon	C 397	21	2.1	21	1	AAH16609	Human gene specific
C 325	23.4	2.4	25	1	AAH16609	Human Apo E oligon	C 398	21	2.1	21	1	AAH16609	Human gene specific

399	21	2.1	21	1	ABSG8163	Human multidrug re	472	20	2.0	20	1	AAZ35378	Interspersed repea
C 400	21	2.1	21	1	ADFG8789	Human TNF-alpha in	C 473	20	2.0	20	1	AAAI1945	PCR primer SRI use
C 401	21	2.1	21	1	ADDS5495	HIV gene expressio	C 474	20	2.0	20	1	AAAD14808	Human glycogen syn
C 402	21	2.1	23	1	ADH13395	Human malignant ne	C 475	20	2.0	20	1	AAK95176	Human cDNA clone-s
C 403	20.8	2.1	24	1	AAV19046	Alu PCR primer 3.	C 476	20	2.0	20	1	AAFB80866	Human mdm2 phospho
C 404	20.8	2.1	24	1	AAAZ7181	Reverse primer p2	C 477	20	2.0	20	1	AAFB80891	Human mdm2 phospho
C 405	20.8	2.1	24	1	AAI65251	Human dihydroorota	C 478	20	2.0	20	1	AAFB80890	Human mdm2 phospho
C 406	20.8	2.1	24	1	AAAF24627	Primer for a polym	C 479	20	2.0	20	1	AAH38246	SNP specific lower
C 407	20.8	2.1	24	1	AAAF24635	Primer for polymer	C 480	20	2.0	20	1	AAAS29506	Human mdm2 antisen
C 408	20.8	2.1	24	1	AAH758670	Human reverse tran	C 481	20	2.0	20	1	AAAS29505	Human mdm2 antisen
C 409	20.8	2.1	24	1	AAAI2447	Ribosome size prot	C 482	20	2.0	20	1	AAAS29481	Human mdm2 antisen
C 410	20.8	2.1	24	1	AAI65532	Human pterin-molyb	C 483	20	2.0	20	1	AAK96932	Human Beta-globin
C 411	20.8	2.1	24	1	AAI71673	Human myosin heavy	C 484	20	2.0	20	1	AAAS59253	Human CAS gene ant
C 412	20.8	2.1	24	1	AAAF69722	Human Ikaralpa ge	C 485	20	2.0	20	1	ABSG67840	Human casein kinase
C 413	20.8	2.1	24	1	AAI68386	Human ATP-dependen	C 486	20	2.0	20	1	AAI40355	Human caspase 6 an
C 414	20.8	2.1	24	1	ABAB2841	Human protective D	C 487	20	2.0	20	1	AAI40351	Human caspase 6 an
C 415	20.8	2.1	24	1	ABIS59102	PCR primer used to	C 488	20	2.0	20	1	AAI40354	Human caspase 6 an
C 416	20.8	2.1	24	1	ABKI4186	Human splicing fac	C 489	20	2.0	20	1	ABL44512	Human chromosome 1
C 417	20.8	2.1	24	1	ABKI2860	Human topoisomeras	C 490	20	2.0	20	1	ABLA44004	Human chromosome 1
C 418	20.8	2.1	24	1	ABZ25248	Human peroxidase 9	C 491	20	2.0	20	1	ABAG2187	Polymorphisim 506B1
C 419	20.8	2.1	24	1	ABAO2134	Human zinc ion tra	C 492	20	2.0	20	1	ABAG2208	Reverse PCR primer
C 420	20.8	2.1	24	1	ABSI6055	Human microtubulin	C 493	20	2.0	20	1	AAAG6659	Telomerase reverse
C 421	20.8	2.1	24	1	ABBS7470	Human plasminogen	C 494	20	2.0	20	1	ABK91100	PCR primer Alu3. f
C 422	20.8	2.1	24	1	ABZ21093	Starch precursor p	C 495	20	2.0	20	1	ACC40946	Human superoxide d
C 423	20.8	2.1	24	1	ACA90126	Human kinesin gene	C 496	20	2.0	20	1	ABZ79385	Acetyl-Coenzyme A-
C 424	20.8	2.1	24	1	ACCA90127	Human kinesin gene	C 497	20	2.0	20	1	AAI60008	Human GH-1 gene am
C 425	20.8	2.1	24	1	ACCS7313	Zinc finger protei	C 498	20	2.0	20	1	ADD21702	Human mdm2 antisen
C 426	20.8	2.1	24	1	ADG83872	Human SLG6A14 forw	C 499	20	2.0	20	1	ADD21701	Human mdm2 antisen
C 427	20.8	2.1	25	1	AAZ24391	Chemokine receptor	C 500	20	2.0	20	1	ABD21677	Human mdm2 antisen
C 428	20.8	2.1	25	1	ABD04739	Human MD27 scannin	C 501	20	2.0	20	1	ABZ97911	Human RANTES oligo
C 429	20.8	2.1	25	1	ABD04618	Human MD27 scannin	C 502	20	2.0	20	1	ABZ99076	Human PDE4C oligon
C 430	20.8	2.1	25	1	ABD04738	Human MD27 scannin	C 503	20	2.0	20	1	ABZ98014	Human RANTES oligo
C 431	20.8	2.1	25	1	ABD04740	Human MD27 scannin	C 504	20	2.0	20	1	ABZ99055	Human PDE4C oligon
C 432	20.8	2.1	25	1	ABD04617	Human MD27 scannin	C 505	20	2.0	20	1	ABZ99075	Human PDE4C oligon
C 433	20.8	2.1	25	1	ABD04578	Human MD27 scannin	C 506	20	2.0	20	1	ABZ92715	Human oligonucleot
C 434	20.8	2.1	25	1	ABD04746	Human MD27 scannin	C 507	20	2.0	20	1	ABZ92716	Human oligonucleot
C 435	20.8	2.1	25	1	ABD04580	Human MD27 scannin	C 508	20	2.0	20	1	ABZ99068	Human PDE4C oligon
C 436	20.8	2.1	25	1	AD011741	Single multiplex P	C 509	20	2.0	20	1	ABX94882	Human MBH1K recep
C 437	20.4	2.1	22	1	AAZ25152	Human short inters	C 510	20	2.0	20	1	ADL25066	Intestinal epithel
C 438	20.4	2.1	22	1	AAZ25149	Human short inters	C 511	20	2.0	20	1	ADM65742	Human Y chromosome
C 439	20.4	2.1	22	1	AAZ25146	Human short inters	C 512	20	2.0	20	1	ADM65739	Human Y chromosome
C 440	20.4	2.1	22	1	AAZ25146	Human short inters	C 513	20	2.0	20	1	ADM65575	NK1 polymorphisim d
C 441	20.4	2.1	22	1	AAZ25146	Human ABC1 BAC con	C 514	20	2.0	20	1	ADM65575	Human Y chromosome
C 442	20.4	2.1	22	1	AAZ25146	Human ABC1 BAC con	C 515	20	2.0	20	1	ADM65575	NK1 polymorphisim d
C 443	20.4	2.1	22	1	ADL66997	Primer #66. Homo	C 516	20	2.0	20	1	ADM65578	Human cryopyrin cd
C 444	20.4	2.1	22	1	ADL66997	Human novel GPCR p	C 517	20	2.0	20	1	ADM34330	Human PDE4C-deriv
C 445	20.4	2.1	23	1	AAZ25146	Human IL4ralpha ge	C 518	20	2.0	20	1	ABD31045	Human RANTES-deriv
C 446	20.4	2.1	24	1	ABBS6869	Human uncoiling en	C 519	20	2.0	20	1	ABD30942	Human RANTES-deriv
C 447	20.4	2.1	24	1	AAH40563	Human receptor tel	C 520	20	2.0	20	1	ABD32107	Human PDE4C-deriv
C 448	20.2	2.0	25	1	AAH38991	SNP specific SNPE	C 521	20	2.0	20	1	ABD28946	NS473-derived oli
C 449	20.2	2.0	25	1	AAH40899	SNP specific SNPE	C 522	20	2.0	20	1	ABD32106	Human PDE4C-deriv
C 450	20.2	2.0	25	1	AAH37979	SNP specific SNPE	C 523	20	2.0	20	1	ABD32086	Human PDE4C-deriv
C 451	20.2	2.0	25	1	AAH37611	SNP specific SNPE	C 524	20	2.0	20	1	ABD28945	NS473-derived oli
C 452	20.2	2.0	25	1	AAH39587	SNP specific SNPE	C 525	20	2.0	20	1	ADI80086	Human transforming
C 453	20.2	2.0	25	1	AAH39123	SNP specific SNPE	C 526	20	2.0	20	1	ADI80087	Human transforming
C 454	20.2	2.0	25	1	AAH40067	SNP specific SNPE	C 527	20	2.0	20	1	ADI80022	Human transforming
C 455	20.2	2.0	25	1	AAH40295	SNP specific SNPE	C 528	20	2.0	20	1	ADI80221	Human transforming
C 456	20.2	2.0	25	1	ABD04682	Human MD27 scannin	C 529	20	2.0	20	1	ADJ53542	Human PPI3CB DNA a
C 457	20.2	2.0	25	1	ABD04614	Human MD27 scannin	C 530	20	2.0	20	1	ADJ53600	Human PPI3CB DNA a
C 458	20.2	2.0	25	1	ABD04577	Human MD27 scannin	C 531	20	2.0	20	1	ADJ60953	Oligonucleotide as
C 459	20.2	2.0	25	1	ABD04684	Human MD27 scannin	C 532	20	2.0	20	1	ADJ60960	Oligonucleotide as
C 460	20.2	2.0	25	1	ABD04683	Human MD27 scannin	C 533	20	2.0	20	1	ADJ59879	Oligonucleotide as
C 461	20.2	2.0	25	1	ABD04576	Human MD27 scannin	C 534	20	2.0	20	1	ADJ60940	Oligonucleotide as
C 462	20.2	2.0	25	1	ABD04681	Human MD27 scannin	C 535	20	2.0	20	1	ADJ60961	Oligonucleotide as
C 463	20.2	2.0	25	1	ADJ70378	Human MD27 scannin	C 536	20	2.0	20	1	ADJ59776	Oligonucleotide as
C 464	20.2	2.0	20	1	AAZ73704	Primer used to anly	C 537	20	2.0	20	1	ADL23339	Primer #1 for ampl
C 465	20.2	2.0	20	1	AAZ73703	PCR primer used to	C 538	20	2.0	20	1	ADL32388	Clone specific PCR
C 466	20.2	2.0	20	1	AAZ73703	PCR primer SRI use	C 539	20	2.0	20	1	ADL61592	Human protein tyro
C 467	20.2	2.0	20	1	AAZ69963	Human c-fos protei	C 540	20	2.0	20	1	ADM14394	Human mPGES-1 chim
C 468	20.2	2.0	20	1	AAZ37736	Human mdm2 phospho	C 541	20	2.0	20	1	ADM14746	Human mPGES-1 chim
C 469	20.2	2.0	20	1	AAZ37712	Human mdm2 phospho	C 542	20	2.0	20	1	ADM14277	Human mPGES-1 chim
C 470	20.2	2.0	20	1	AAZ37737	Human mdm2 phospho	C 543	20	2.0	20	1	ADM14482	Human mPGES-1 chim
C 471	20.2	2.0	20	1	AAA96410	Primer used to amp	C 544	20	2.0	20	1	ADM15309	Human mPGES-1 chim

C 545	20	2.0	20	1	ADM15160	Human mPGEs-1 chim	C 618	19.4	2.0	22	1	AAF93028	Polymorphic sequen
C 546	20	2.0	20	1	ADM14957	Human mPGEs-1 chim	C 619	19.4	2.0	22	1	ADC24360	PCR primer for amp
C 547	20	2.0	20	1	ADM15553	Human mPGEs-1 chim	C 620	19.4	2.0	24	1	AAQ73576	Enhancer element e
C 548	20	2.0	20	1	ADM15081	Human mPGEs-1 chim	C 621	19.4	2.0	24	1	AAQ73577	Enhancer element e
C 549	20	2.0	20	1	ADM15268	Human mPGEs-1 chim	C 622	19.2	1.9	20	1	AAAT63214	Primer Alu 5' used
C 550	20	2.0	20	1	ADM14958	Human oligonucleot	C 623	19.2	1.9	24	1	AAA35956	Human genomic SNP
C 551	20	2.0	20	1	ADO45369	Human oligonucleot	C 624	19.2	1.9	24	1	AAA27180	Forward primer P2
C 552	20	2.0	20	1	ADO46449	Human oligonucleot	C 625	19.2	1.9	24	1	AAH45660	PCR primer specifici
C 553	20	2.0	20	1	ADO46442	Human oligonucleot	C 626	19.2	1.9	24	1	AAH46154	Cysteine protease
C 554	20	2.0	20	1	ADO45266	Human oligonucleot	C 627	19.2	1.9	24	1	AAH75665	Human Pax protein
C 555	20	2.0	20	1	ADO46449	Human oligonucleot	C 628	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 556	20	2.0	20	1	ADO46449	Human oligonucleot	C 629	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 557	20	2.0	20	1	ADO46449	Human oligonucleot	C 630	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 558	20	2.0	20	1	ADO46449	Human oligonucleot	C 631	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 559	20	2.0	20	1	ADO52273	Human inhibitor of	C 632	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 560	20	2.0	20	1	AAV27991	Human inhibitor of	C 633	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 561	20	2.0	20	1	AAZ25145	Human short inters	C 634	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 562	20	2.0	20	1	AAZ25143	Human short inters	C 635	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 563	20	2.0	20	1	AAZ25144	Human short inters	C 636	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 564	20	2.0	20	1	AAZ25144	Human short inters	C 637	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 565	20	2.0	20	1	ADG70428	REN-34 SNP binding	C 638	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 566	20	2.0	20	1	ADG70427	REN-34 SNP binding	C 639	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 567	20	2.0	20	1	ADG70427	REN-34 SNP binding	C 640	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 568	20	2.0	20	1	ADG70427	REN-34 SNP binding	C 641	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 569	20	2.0	20	1	ADG70427	REN-34 SNP binding	C 642	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 570	20	2.0	20	1	AAZ25151	Human short inters	C 643	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 571	20	2.0	20	1	AAZ25147	Human short inters	C 644	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 572	20	2.0	20	1	AAZ25147	Human short inters	C 645	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 573	20	2.0	20	1	ABLS55369	Human leucine zip	C 646	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 574	20	2.0	20	1	ADG56863	Human dihydroxypro	C 647	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 575	20	2.0	20	1	AAH75599	Human dihydroxypro	C 648	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 576	20	2.0	20	1	AAH75599	Human dihydroxypro	C 649	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 577	20	2.0	20	1	AAH75599	Human dihydroxypro	C 650	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 578	20	2.0	20	1	AAH75599	Human dihydroxypro	C 651	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 579	20	2.0	20	1	AAH75599	Human dihydroxypro	C 652	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 580	20	2.0	20	1	AAH75599	Human dihydroxypro	C 653	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 581	20	2.0	20	1	AAH75599	Human dihydroxypro	C 654	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 582	20	2.0	20	1	AAH75599	Human dihydroxypro	C 655	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 583	20	2.0	20	1	AAH75599	Human dihydroxypro	C 656	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 584	20	2.0	20	1	AAH75599	Human dihydroxypro	C 657	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 585	20	2.0	20	1	AAH75599	Human dihydroxypro	C 658	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 586	20	2.0	20	1	AAH75599	Human dihydroxypro	C 659	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 587	20	2.0	20	1	AAH75599	Human dihydroxypro	C 660	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 588	20	2.0	20	1	AAH75599	Human dihydroxypro	C 661	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 589	20	2.0	20	1	AAH75599	Human dihydroxypro	C 662	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 590	20	2.0	20	1	AAH75599	Human dihydroxypro	C 663	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 591	20	2.0	20	1	AAH75599	Human dihydroxypro	C 664	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 592	20	2.0	20	1	AAH75599	Human dihydroxypro	C 665	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 593	20	2.0	20	1	AAH75599	Human dihydroxypro	C 666	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 594	20	2.0	20	1	AAH75599	Human dihydroxypro	C 667	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 595	20	2.0	20	1	AAH75599	Human dihydroxypro	C 668	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 596	20	2.0	20	1	AAH75599	Human dihydroxypro	C 669	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 597	20	2.0	20	1	AAH75599	Human dihydroxypro	C 670	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 598	20	2.0	20	1	AAH75599	Human dihydroxypro	C 671	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 599	20	2.0	20	1	AAH75599	Human dihydroxypro	C 672	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 600	20	2.0	20	1	AAH75599	Human dihydroxypro	C 673	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 601	20	2.0	20	1	AAH75599	Human dihydroxypro	C 674	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 602	20	2.0	20	1	AAH75599	Human dihydroxypro	C 675	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 603	20	2.0	20	1	AAH75599	Human dihydroxypro	C 676	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 604	20	2.0	20	1	AAH75599	Human dihydroxypro	C 677	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 605	20	2.0	20	1	AAH75599	Human dihydroxypro	C 678	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 606	20	2.0	20	1	AAH75599	Human dihydroxypro	C 679	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 607	20	2.0	20	1	AAH75599	Human dihydroxypro	C 680	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 608	20	2.0	20	1	AAH75599	Human dihydroxypro	C 681	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 609	20	2.0	20	1	AAH75599	Human dihydroxypro	C 682	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 610	20	2.0	20	1	AAH75599	Human dihydroxypro	C 683	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 611	20	2.0	20	1	AAH75599	Human dihydroxypro	C 684	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 612	20	2.0	20	1	AAH75599	Human dihydroxypro	C 685	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 613	20	2.0	20	1	AAH75599	Human dihydroxypro	C 686	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 614	20	2.0	20	1	AAH75599	Human dihydroxypro	C 687	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 615	20	2.0	20	1	AAH75599	Human dihydroxypro	C 688	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 616	20	2.0	20	1	AAH75599	Human dihydroxypro	C 689	19.2	1.9	24	1	AAH75665	Human ABC1 transcr
C 617	20	2.0	20	1	AAH75599	Human dihydroxypro	C 690	19.2	1.9	24	1	AAH75665	Human ABC1 transcr

C 691	19	1.9	20	1	ADN15184	Human mPGES-1 chim	C 764	18.4	1.9	20	1	ABZ71056	Human HKR1 phospho
C 692	19	1.9	20	1	ADN45265	Human oligonucleot	C 765	18.4	1.9	20	1	ADA20921	Human BAX chimeric
C 693	19	1.9	20	1	ADN45357	Human oligonucleot	C 766	18.4	1.9	20	1	ACF39682	MHC class II trans
C 694	19	1.9	20	1	ADP08716	Extend primer 53 u	C 767	18.4	1.9	20	1	ABT44432	Chimeric antisense
C 695	19	1.9	21	1	ADG30202	PKR-targeted siNA	C 768	18.4	1.9	20	1	ADD21681	Human mdm2 antisen
C 696	19	1.9	21	1	ADL25534	Intestinal epithel	C 769	18.4	1.9	20	1	ADD21703	Human mdm2 antisen
C 697	19	1.9	22	1	AAZ25166	Human short inters	C 770	18.4	1.9	20	1	ADE43606	Human KNSL1 sequen
C 698	19	1.9	22	1	AAZ25157	Human short inters	C 771	18.4	1.9	20	1	ADE86781	GATA primer #1. H
C 699	19	1.9	22	1	AAZ25158	Human short inters	C 772	18.4	1.9	20	1	ADI61628	Human SAP-1 gene t
C 700	19	1.9	22	1	AAZ25170	Human short inters	C 773	18.4	1.9	20	1	ABZ97965	Human RANTES oligo
C 701	19	1.9	22	1	AAZ25172	Human short inters	C 774	18.4	1.9	20	1	ABZ89864	Human oligonucleot
C 702	19	1.9	22	1	AAZ25159	Human short inters	C 775	18.4	1.9	20	1	ABZ97964	Human RANTES oligo
C 703	19	1.9	22	1	AAZ25163	Human short inters	C 776	18.4	1.9	20	1	ABZ97909	Human RANTES oligo
C 704	19	1.9	22	1	AAZ25169	Human short inters	C 777	18.4	1.9	20	1	ABZ89861	Human oligonucleot
C 705	19	1.9	22	1	AAZ25171	Human short inters	C 778	18.4	1.9	20	1	ABZ97902	Human RANTES oligo
C 706	19	1.9	22	1	AAZ25160	Human short inters	C 779	18.4	1.9	20	1	ABZ98012	Human oligonucleot
C 707	19	1.9	22	1	AAZ25164	Human short inters	C 780	18.4	1.9	20	1	ABZ98012	Human RANTES oligo
C 708	19	1.9	22	1	AAZ25165	Human short inters	C 781	18.4	1.9	20	1	ABZ98015	Human RANTES oligo
C 709	19	1.9	22	1	ADG30198	PKR-targeted siNA	C 782	18.4	1.9	20	1	ABZ97908	Human RANTES oligo
C 710	18.8	1.9	22	1	AAZ39493	Steroidogenesis ac	C 783	18.4	1.9	20	1	ABZ98003	Human RANTES oligo
C 711	18.8	1.9	22	1	AAZ83018	Primer K to isolat	C 784	18.4	1.9	20	1	ABZ97903	Human RANTES oligo
C 712	18.8	1.9	22	1	AAZ69375	Human ABC1 BAC con	C 785	18.4	1.9	20	1	ABZ99062	Human PDE4C oligon
C 713	18.8	1.9	22	1	AAZ32938	Sequence tagged si	C 786	18.4	1.9	20	1	ABZ99105	Human PDE4C oligon
C 714	18.8	1.9	22	1	AAZ84349	Human CYP2C181 PCR	C 787	18.4	1.9	20	1	ABZ98013	Human RANTES oligo
C 715	18.8	1.9	22	1	AAZ29797	Preseniline-1 gene	C 788	18.4	1.9	20	1	ABZ99071	Human PDE4C oligon
C 716	18.8	1.9	22	1	ADN31453	Human chromosome 1	C 789	18.4	1.9	20	1	ABZ89844	Human oligonucleot
C 717	18.8	1.9	22	1	ADN31457	Human chromosome 1	C 790	18.4	1.9	20	1	ABZ92736	Human oligonucleot
C 718	18.8	1.9	22	1	ADL66998	Human chromosome 1	C 791	18.4	1.9	20	1	ABZ99077	Human PDE4C oligon
C 719	18.8	1.9	23	1	AAZ37708	Multiplex PCR prim	C 792	18.4	1.9	20	1	ACA88928	Human PDE4C oligon
C 720	18.8	1.9	23	1	AAZ37708	Human Rad51 antis	C 793	18.4	1.9	20	1	ADA26875	Human PDE4C oligon
C 721	18.8	1.9	23	1	AAZ37708	Human Rad51 antis	C 794	18.4	1.9	20	1	ADL24948	Human PDE4C oligon
C 722	18.8	1.9	23	1	ADN43247	Antisense oligonuc	C 795	18.4	1.9	20	1	ADL25083	Human oligonucleot
C 723	18.4	1.9	20	1	ADH26585	Human hunc93b1 pool	C 796	18.4	1.9	20	1	ABD30939	Human RANTES-deriv
C 724	18.4	1.9	20	1	AAZ10907	Human cytochrome P	C 797	18.4	1.9	20	1	ABD31043	Human RANTES-deriv
C 725	18.4	1.9	20	1	AAZ66010	Primer #1 to ampli	C 798	18.4	1.9	20	1	ABD32136	Human PDE4C-deriv
C 726	18.4	1.9	20	1	AAZ66017	Primer #2 to ampli	C 799	18.4	1.9	20	1	ABD31044	Human RANTES-deriv
C 727	18.4	1.9	20	1	AAZ85762	Human DPC4 sequenc	C 800	18.4	1.9	20	1	ABD28966	Human RANTES-deriv
C 728	18.4	1.9	20	1	AAZ85840	LRPS exon primer 5	C 801	18.4	1.9	20	1	ABD30933	Human RANTES-deriv
C 729	18.4	1.9	20	1	AAZ85801	LRPS exon primer 5	C 802	18.4	1.9	20	1	ABD26091	Human RANTES-deriv
C 730	18.4	1.9	20	1	AAZ85879	LRPS SNP primer 58	C 803	18.4	1.9	20	1	ABD26094	Human RANTES-deriv
C 731	18.4	1.9	20	1	AAZ90795	Human 7SL RNA spec	C 804	18.4	1.9	20	1	ABD30934	Human RANTES-deriv
C 732	18.4	1.9	20	1	AAZ86546	Primer r6617 used	C 805	18.4	1.9	20	1	ABD31046	Human RANTES-deriv
C 733	18.4	1.9	20	1	AAZ37738	Human mdm2 phospho	C 806	18.4	1.9	20	1	ABD32108	Human PDE4C-deriv
C 734	18.4	1.9	20	1	AAZ37716	Human mdm2 phospho	C 807	18.4	1.9	20	1	ABD32093	Human PDE4C-deriv
C 735	18.4	1.9	20	1	AAA28013	Uncoupling protein	C 808	18.4	1.9	20	1	ABD26074	Human PDE4C-deriv
C 736	18.4	1.9	20	1	AAA11943	Human MDX antisen	C 809	18.4	1.9	20	1	ABD30995	Human RANTES-deriv
C 737	18.4	1.9	20	1	AAZ52253	Primer ZC12502 for	C 810	18.4	1.9	20	1	ABD31034	Human RANTES-deriv
C 738	18.4	1.9	20	1	AAZ31822	Human RANK antisen	C 811	18.4	1.9	20	1	ABD30940	Human RANTES-deriv
C 739	18.4	1.9	20	1	AAZ31823	Human RANK antisen	C 812	18.4	1.9	20	1	ABD30946	Human RANTES-deriv
C 740	18.4	1.9	20	1	AAZ14819	Human glycogen syn	C 813	18.4	1.9	20	1	ABD28954	Human RANTES-deriv
C 741	18.4	1.9	20	1	AAZ14817	Human glycogen syn	C 814	18.4	1.9	20	1	ABD32102	Human PDE4C-deriv
C 742	18.4	1.9	20	1	AAZ95122	Human CDNA clone-s	C 815	18.4	1.9	20	1	ADH70951	Human Vbeta PCR pr
C 743	18.4	1.9	20	1	AAH02356	Human AKAP10 codin	C 816	18.4	1.9	20	1	ADH54084	Human neurodegener
C 744	18.4	1.9	20	1	AAZ92892	Human ABC1 transcr	C 817	18.4	1.9	20	1	ADL25029	Human ZNF9 exon 1
C 745	18.4	1.9	20	1	AAZ8044	PCR primer for a m	C 818	18.4	1.9	20	1	ADH76733	MCIR1 genomic sequ
C 746	18.4	1.9	20	1	AAZ80892	Human mdm2 phospho	C 819	18.4	1.9	20	1	ADH76678	MCIR1 locus SNP pr
C 747	18.4	1.9	20	1	AAZ80870	Human mdm2 phospho	C 820	18.4	1.9	20	1	ADH76813	MCIR1 locus SNP pr
C 748	18.4	1.9	20	1	AAZ38602	SNP specific lower	C 821	18.4	1.9	20	1	ADJ46556	Human reguim targ
C 749	18.4	1.9	20	1	AAZ37610	SNP specific lower	C 822	18.4	1.9	20	1	ADJ46607	Human reguim anti
C 750	18.4	1.9	20	1	AAZ40090	SNP specific lower	C 823	18.4	1.9	20	1	ADJ59878	Oligonucleotide as
C 751	18.4	1.9	20	1	AAZ28586	Epo-R PCR primer #	C 824	18.4	1.9	20	1	ADJ59868	Oligonucleotide as
C 752	18.4	1.9	20	1	AAZ86126	Primer JNF14 to is	C 825	18.4	1.9	20	1	ADJ59877	Oligonucleotide as
C 753	18.4	1.9	20	1	AAZ20704	Human telomeric re	C 826	18.4	1.9	20	1	ADJ60947	Oligonucleotide as
C 754	18.4	1.9	20	1	AAZ20699	Human telomeric re	C 827	18.4	1.9	20	1	ADJ59768	Oligonucleotide as
C 755	18.4	1.9	20	1	AAZ29507	Human mdm2 antisen	C 828	18.4	1.9	20	1	ADJ60990	Oligonucleotide as
C 756	18.4	1.9	20	1	AAZ29485	Human mdm2 antisen	C 829	18.4	1.9	20	1	ADJ59767	Oligonucleotide as
C 757	18.4	1.9	20	1	AAZ28754	Target specific PC	C 830	18.4	1.9	20	1	ADJ59830	Oligonucleotide as
C 758	18.4	1.9	20	1	AAZ40357	Human caspase 6 an	C 831	18.4	1.9	20	1	ADJ59829	Oligonucleotide as
C 759	18.4	1.9	20	1	AAZ68939	Human phosphorylas	C 832	18.4	1.9	20	1	ADJ60962	Oligonucleotide as
C 760	18.4	1.9	20	1	AAZ38181	Human BH3 interact	C 833	18.4	1.9	20	1	ADJ59773	Oligonucleotide as
C 761	18.4	1.9	20	1	AAZ38190	Human BH3 interact	C 834	18.4	1.9	20	1	ADJ59774	Oligonucleotide as
C 762	18.4	1.9	20	1	ABQ74794	Human TNFR2 antis	C 835	18.4	1.9	20	1	ADJ59880	Oligonucleotide as
C 763	18.4	1.9	20	1	ACC55324	Human ADAMTS13 SPS	C 836	18.4	1.9	20	1	ADJ60956	Oligonucleotide as

837	18.4	1.9	20	1	ADJ96297	Human breast cance	C 910	18.2	1.8	19	1	AAQ48683	Human Alu segment
C 838	18.4	1.9	20	1	ADJ96333	Human breast cance	C 911	18.2	1.8	19	1	AAQ85677	PCR primer alu 2 f
839	18.4	1.9	20	1	ADJ96393	Human breast cance	C 912	18.2	1.8	19	1	AAQ85676	PCR primer alu 1 f
C 840	18.4	1.9	20	1	ADJ96457	Human breast cance	C 913	18.2	1.8	19	1	AAQ76249	Generic Alu consen
C 841	18.4	1.9	20	1	ADJ32334	Clonore specific PCR	C 914	18.2	1.8	19	1	AAQ76247	Generic primer fro
C 842	18.4	1.9	20	1	ADJ10332	Phosphorothioate a	C 915	18.2	1.8	19	1	AAV83937	PCR primer used to
C 843	18.4	1.9	20	1	ADJ17893	Primer of the inve	C 916	18	1.8	18	1	AAV09336	Human biallelic po
C 844	18.4	1.9	20	1	ADJ18178	Human mPGEs-1 chim	C 917	18	1.8	18	1	AAV74139	Human FLAME-1 PCR
C 845	18.4	1.9	20	1	ADJ14163	Human mPGEs-1 chim	C 918	18	1.8	18	1	AAV74141	Human CREL mRNA in
C 846	18.4	1.9	20	1	ADJ15069	Human mPGEs-1 chim	C 919	18	1.8	18	1	AAZ39610	SNP specific lower
C 847	18.4	1.9	20	1	ADJ14236	Human mPGEs-1 chim	C 920	18	1.8	18	1	AAH38730	SNP specific lower
C 848	18.4	1.9	20	1	ADJ14395	Human mPGEs-1 chim	C 921	18	1.8	18	1	AAH38990	Human FLAME-1 spec
C 849	18.4	1.9	20	1	ADJ15353	Human mPGEs-1 chim	C 922	18	1.8	18	1	AAH38990	Human FLAME-1 spec
C 850	18.4	1.9	20	1	ADJ15261	Human mPGEs-1 chim	C 923	18	1.8	18	1	AAH38990	Murine TRPV trans
C 851	18.4	1.9	20	1	ADJ15038	Human mPGEs-1 chim	C 924	18	1.8	18	1	ADH532591	Non-nucleotide pro
C 852	18.4	1.9	20	1	ADJ15183	Human mPGEs-1 chim	C 925	18	1.8	18	1	ADH59598	Non-nucleotide pro
C 853	18.4	1.9	20	1	ADJ15204	Human mPGEs-1 chim	C 926	18	1.8	18	1	ADH59610	NTP peptide encodi
C 854	18.4	1.9	20	1	ADJ15265	Human mPGEs-1 chim	C 927	18	1.8	18	1	ACC84469	NTP peptide encodi
C 855	18.4	1.9	20	1	ADJ13950	Human mPGEs-1 chim	C 928	18	1.8	18	1	ACC84468	SNP specific lower
C 856	18.4	1.9	20	1	ADJ14044	Human mPGEs-1 chim	C 929	18	1.8	18	1	AAH37310	Human inflammatory
C 857	18.4	1.9	20	1	ADJ14120	Human mPGEs-1 chim	C 930	18	1.8	18	1	AAH91092	Human inflammatory
C 858	18.4	1.9	20	1	ADJ14121	Human mPGEs-1 chim	C 931	18	1.8	18	1	AAH91352	Forward PCR primer
C 859	18.4	1.9	20	1	ADJ15337	Human mPGEs-1 chim	C 932	18	1.8	18	1	AAH91352	Human familial bip
C 860	18.4	1.9	20	1	ADJ15330	Human mPGEs-1 chim	C 933	18	1.8	18	1	ACA58212	Human cancer supp
C 861	18.4	1.9	20	1	ADJ13895	Human mPGEs-1 chim	C 934	18	1.8	18	1	ADH89039	Human POLYX PCR pr
C 862	18.4	1.9	20	1	ADJ14082	Human mPGEs-1 chim	C 935	18	1.8	18	1	ADH89039	Human interleukin-
C 863	18.4	1.9	20	1	ADJ14445	Human mPGEs-1 chim	C 936	18	1.8	18	1	ADP09291	Extend primer 86 u
C 864	18.4	1.9	20	1	ADJ14651	Human mPGEs-1 chim	C 937	18	1.8	18	1	AAH38402	SNP specific lower
C 865	18.4	1.9	20	1	ADJ15095	Human mPGEs-1 chim	C 938	18	1.8	18	1	AAH20695	Human telomeric re
C 866	18.4	1.9	20	1	ADJ15230	Human mPGEs-1 chim	C 939	18	1.8	18	1	ABK70676	Human hepatocellula
C 867	18.4	1.9	20	1	ADJ15230	Human mPGEs-1 chim	C 940	18	1.8	18	1	ABK70676	Human RANRES oligo
C 868	18.4	1.9	20	1	ADJ15203	Human mPGEs-1 chim	C 941	18	1.8	18	1	ABE298008	Human oligonucleot
C 869	18.4	1.9	20	1	ADJ15442	Human mPGEs-1 chim	C 942	18	1.8	18	1	ABE292737	Human oligonucleot
C 870	18.4	1.9	20	1	ADJ14079	Human mPGEs-1 chim	C 943	18	1.8	18	1	ABD31039	NS473-derived oli
C 871	18.4	1.9	20	1	ADJ15245	Human mPGEs-1 chim	C 944	18	1.8	18	1	ABD31039	Human RANRES-deriv
C 872	18.4	1.9	20	1	ADJ15422	Human mPGEs-1 chim	C 945	18	1.8	18	1	ADH77439	Human PTPN12 antis
C 873	18.4	1.9	20	1	ADJ14686	Human mPGEs-1 chim	C 946	18	1.8	18	1	ADJ59873	Oligonucleotide as
C 874	18.4	1.9	20	1	ADJ15137	Human mPGEs-1 chim	C 947	18	1.8	18	1	ADJ15386	Human mPGEs-1 chim
C 875	18.4	1.9	20	1	ADJ15251	Human mPGEs-1 chim	C 948	18	1.8	18	1	ADJ15386	Human oligonucleot
C 876	18.4	1.9	20	1	ADJ13907	Human mPGEs-1 chim	C 949	18	1.8	18	1	AAZ18411	Polyomphic fragme
C 877	18.4	1.9	20	1	ADJ13925	Human mPGEs-1 chim	C 950	18	1.8	18	1	AAH80033	Human ASTHJ 5' re
C 878	18.4	1.9	20	1	ADJ14074	Human mPGEs-1 chim	C 951	18	1.8	18	1	AAH40033	SNP specific upper
C 879	18.4	1.9	20	1	ADJ15368	Human oligonucleot	C 952	18	1.8	18	1	ABA91975	Single nucleotide
C 880	18.4	1.9	20	1	ADJ15368	Human oligonucleot	C 953	18	1.8	18	1	AAZ87585	Primer specific fo
C 881	18.4	1.9	20	1	ADJ15368	Human oligonucleot	C 954	18	1.8	18	1	AAZ87585	Primer specific fo
C 882	18.4	1.9	20	1	ADJ15370	Human oligonucleot	C 955	18	1.8	18	1	AAZ87585	Primer specific fo
C 883	18.4	1.9	20	1	ADJ15257	Human oligonucleot	C 956	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 884	18.4	1.9	20	1	ADJ15258	Human oligonucleot	C 957	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 885	18.4	1.9	20	1	ADJ15258	Human oligonucleot	C 958	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 886	18.4	1.9	20	1	ADJ15258	Human oligonucleot	C 959	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 887	18.4	1.9	20	1	ADJ15258	Human oligonucleot	C 960	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 888	18.4	1.9	20	1	ADJ15258	Human oligonucleot	C 961	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 889	18.4	1.9	20	1	ADJ15258	Human oligonucleot	C 962	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 890	18.4	1.9	20	1	ADJ15258	Human oligonucleot	C 963	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 891	18.4	1.9	20	1	ADJ15258	Human oligonucleot	C 964	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 892	18.4	1.9	20	1	ADJ15258	Human oligonucleot	C 965	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 893	18.4	1.9	20	1	ADJ15258	Human oligonucleot	C 966	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 894	18.4	1.9	20	1	ADJ15258	Human oligonucleot	C 967	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 895	18.4	1.9	20	1	ADJ15258	Human oligonucleot	C 968	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 896	18.4	1.9	20	1	ADJ15258	Human oligonucleot	C 969	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 897	18.4	1.9	20	1	ADJ15258	Human oligonucleot	C 970	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 898	18.4	1.9	20	1	ADJ15258	Human oligonucleot	C 971	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 899	18.4	1.9	20	1	ADJ15258	Human oligonucleot	C 972	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 900	18.4	1.9	20	1	ADJ15258	Human oligonucleot	C 973	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 901	18.4	1.9	20	1	ADJ15258	Human oligonucleot	C 974	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 902	18.4	1.9	20	1	ADJ15258	Human oligonucleot	C 975	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 903	18.4	1.9	20	1	ADJ15258	Human oligonucleot	C 976	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 904	18.4	1.9	20	1	ADJ15258	Human oligonucleot	C 977	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 905	18.4	1.9	20	1	ADJ15258	Human oligonucleot	C 978	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 906	18.4	1.9	20	1	ADJ15258	Human oligonucleot	C 979	17.8	1.8	19	1	ABX95026	Human chromosome 1
C 907	18.2	1.8	19	1	AAQ25869	5' Alu primer. SY	C 980	17.8	1.8	21	1	ADH47846	Human tumour-associ
C 908	18.2	1.8	19	1	AAQ25868	5' Alu primer. SY	C 981	17.8	1.8	21	1	ADH47846	Human tumour-associ
C 909	18.2	1.8	19	1	AAQ48682	Human Alu segment	C 982	17.8	1.8	21	1	ABX97680	Novel human protei

c 983	17.8	1.8	21	1	AC564055	IFNARI forward PCR	1056	17.4	1.8	19	1	ADO80022	CENPC1 extend pri
c 984	17.8	1.8	21	1	AC564053	IFNARI forward PCR	c1057	17.4	1.8	20	1	AAZ07267	Human telomerase R
c 985	17.8	1.8	21	1	AD561633	Alternate human SR	c1058	17.4	1.8	20	1	AAZ37719	Human mdm2 phospho
c 986	17.8	1.8	21	1	AD561652	Human sclerostin g	c1059	17.4	1.8	20	1	AAZ37727	Human mdm2 phospho
c 987	17.8	1.8	21	1	AD5612370	L1 retrotransposon	c1060	17.4	1.8	20	1	AAZ37726	Human mdm2 phospho
c 988	17.8	1.8	21	1	AD5612525	Chromosome 8p21.3-	c1061	17.4	1.8	20	1	AAZ21805	Exemplary oligonuc
c 989	17.8	1.8	21	1	AD565601	Non-nucleotide pro	c1062	17.4	1.8	20	1	AAAF1821	Human RANK antisen
c 990	17.8	1.8	21	1	AD5659613	Non-nucleotide pro	c1063	17.4	1.8	20	1	AAAF80881	Human mdm2 phospho
c 991	17.8	1.8	21	1	AD5659339	Novel NOVX gene se	c1064	17.4	1.8	20	1	AAAF80873	Human mdm2 phospho
c 992	17.8	1.8	21	1	AD5652832	Rat DNA microarray	c1065	17.4	1.8	20	1	AAAF80880	Human mdm2 phospho
c 993	17.8	1.8	21	1	AD56501329	Rat DNA microarray	c1066	17.4	1.8	20	1	AAAF40109	SNP specific upper
c 994	17.8	1.8	21	1	AD5668377	DNA probe used to	c1067	17.4	1.8	20	1	AAAF66127	Primer JNPF15 to is
c 995	17.8	1.8	21	1	AD566416	VLA4 antagonist-re	c1068	17.4	1.8	20	1	AAAF01235	Reverse PCR primer
c 996	17.8	1.8	21	1	AD5641377	Human chromosome 1	c1069	17.4	1.8	20	1	AAAF74118	Primer #52. Homo
c 997	17.8	1.8	21	1	AD5641251	Human chromosome 1	c1070	17.4	1.8	20	1	AAAF20696	Human telomeric re
c 998	17.8	1.8	21	1	AD5632266	Human interleukin-1	c1071	17.4	1.8	20	1	AAAF29495	Human mdm2 antisen
c 999	17.8	1.8	21	1	AD5625728	Human NOVX gene, p	c1072	17.4	1.8	20	1	AAAF29488	Human mdm2 antisen
c1000	17.8	1.8	21	1	AD5694155	BCU-2 gene related	c1073	17.4	1.8	20	1	AAAF29496	Human mdm2 antisen
c1001	17.8	1.8	22	1	AA571928	Primer detects mar	c1074	17.4	1.8	20	1	AAAF67842	Human casein kinas
c1002	17.8	1.8	22	1	AA571942	Primer detects mar	c1075	17.4	1.8	20	1	AAAF40350	Human casein kinas
c1003	17.8	1.8	22	1	AA571925	Primer detects mar	c1076	17.4	1.8	20	1	AAAF40285	Human caspase 6 an
c1004	17.8	1.8	22	1	AA572000	Primer detects mar	c1077	17.4	1.8	20	1	AAAF38206	Human BH3 interact
c1005	17.8	1.8	22	1	AA571997	Primer detects mar	c1078	17.4	1.8	20	1	AAAF38189	Human BH3 interact
c1006	17.8	1.8	22	1	AA572014	Primer detects mar	c1079	17.4	1.8	20	1	AAAF42949	Human PLA2, group
c1007	17.8	1.8	22	1	AA5699910	Human biallelic po	c1080	17.4	1.8	20	1	AAAF96658	Telomerase reverse
c1008	17.8	1.8	22	1	AA569933	Human MACK gene-sp	c1081	17.4	1.8	20	1	AAAF65070	Human casein kinas
c1009	17.8	1.8	22	1	AA5640206	SNP specific lower	c1082	17.4	1.8	20	1	AAAF40949	Human superoxide d
c1010	17.8	1.8	22	1	AA5631451	Human chromosome 1	c1083	17.4	1.8	20	1	AAAF61497	Human ATRP3 antisen
c1011	17.8	1.8	22	1	AA5659597	Human gene specific	c1084	17.4	1.8	20	1	AAAF47544	Human Artemis exon
c1012	17.8	1.8	22	1	AA5643557	Human CD2000 DNA	c1085	17.4	1.8	20	1	AAAF20977	Mouse BAX chimeric
c1013	17.8	1.8	22	1	AA5633370	Human CD2000 PCR	c1086	17.4	1.8	20	1	AAAF61525	Human inhibitor-ka
c1014	17.8	1.8	22	1	AA5623730	Human LpDLR PCR pr	c1087	17.4	1.8	20	1	AAAF21684	Human mdm2 antisen
c1015	17.6	1.8	41	1	AB577329	Human protein 10.0	c1088	17.4	1.8	20	1	ADD21691	Human mdm2 antisen
c1016	17.4	1.8	19	1	AA566003	Primer #2 to ampli	c1089	17.4	1.8	20	1	ADD21692	Human mdm2 antisen
c1017	17.4	1.8	19	1	AA5635373	Interspersed repa	c1090	17.4	1.8	20	1	ADD713343	GFAT 1 gene intron
c1018	17.4	1.8	19	1	AA5600279	Human HPC2 cDNA ex	c1091	17.4	1.8	20	1	AB299106	Human PDB4C oligon
c1019	17.4	1.8	19	1	AA5648211	Reverse PCR primer	c1092	17.4	1.8	20	1	AB297916	Human RANTES oligo
c1020	17.4	1.8	19	1	AA5659729	Human protease-act	c1093	17.4	1.8	20	1	AB2968007	Human RANTES oligo
c1021	17.4	1.8	19	1	AA5638445	SNP specific upper	c1094	17.4	1.8	20	1	AB2923731	Human oligonucleot
c1022	17.4	1.8	19	1	AA5638669	SNP specific upper	c1095	17.4	1.8	20	1	AB572400	PCR primer used to
c1023	17.4	1.8	19	1	AA5638226	SNP specific lower	c1096	17.4	1.8	20	1	AB5614992	Human delta opioid
c1024	17.4	1.8	19	1	AA5638229	SNP specific upper	c1097	17.4	1.8	20	1	ACA88946	Selection and ampl
c1025	17.4	1.8	19	1	AA5638627	SNP specific upper	c1098	17.4	1.8	20	1	AB234284	Opoid receptor D1
c1026	17.4	1.8	19	1	AA5638221	SNP specific upper	c1099	17.4	1.8	20	1	ABD28961	NS8473-derived ol
c1027	17.4	1.8	19	1	AA5631576	Reverse PCR primer	c1100	17.4	1.8	20	1	ABD31038	Human RANTES-deriv
c1028	17.4	1.8	19	1	AA5631569	Forward PCR primer	c1101	17.4	1.8	20	1	ABD30947	Human RANTES-deriv
c1029	17.4	1.8	19	1	AA5624568	Human Alu sequence	c1102	17.4	1.8	20	1	ABD32137	Human PDB4C-deriv
c1030	17.4	1.8	19	1	AB5682157	Zmaki gene region	c1103	17.4	1.8	20	1	AD5647745	Human 5-HT7 recept
c1031	17.4	1.8	19	1	AA5699014	Human prostate can	c1104	17.4	1.8	20	1	AD5689041	Human FOLYX PCR pr
c1032	17.4	1.8	19	1	AB5643899	Human chromosome 1	c1105	17.4	1.8	20	1	AD5659781	Oligonucleotide as
c1033	17.4	1.8	19	1	AB5644463	Human chromosome 1	c1106	17.4	1.8	20	1	AD5660991	Oligonucleotide as
c1034	17.4	1.8	19	1	AB5644464	Human chromosome 1	c1107	17.4	1.8	20	1	AD5659872	Oligonucleotide as
c1035	17.4	1.8	19	1	AB5645272	Human chromosome 1	c1108	17.4	1.8	20	1	AD5643371	Human PTPRA DNA ta
c1036	17.4	1.8	19	1	AB5659043	Nucleotide sequenc	c1109	17.4	1.8	20	1	AD5643253	Antisense 2'-MOE g
c1037	17.4	1.8	19	1	AB5622994	Human Zmaki CDNA r	c1110	17.4	1.8	20	1	AD5610489	Phosphorothioate a
c1038	17.4	1.8	19	1	AB5681231	Human NOV4 PCR prim	c1111	17.4	1.8	20	1	AD5610565	Target DNA oligo f
c1039	17.4	1.8	19	1	AD567845	Human HBM STS mark	c1112	17.4	1.8	20	1	AD5613970	Human mpegS-1 chim
c1040	17.4	1.8	19	1	AD5645577	Sequence tagged si	c1113	17.4	1.8	20	1	AD5614037	Human mpegS-1 chim
c1041	17.4	1.8	19	1	AD5698275	Intestinal epithel	c1114	17.4	1.8	20	1	AD5615339	Human mpegS-1 chim
c1042	17.4	1.8	19	1	AD5625097	Human interleukin-1	c1115	17.4	1.8	20	1	AD5614714	Human mpegS-1 chim
c1043	17.4	1.8	19	1	AD5614391	Human interleukin-1	c1116	17.4	1.8	20	1	AD5614492	Human mpegS-1 chim
c1044	17.4	1.8	19	1	AD5614519	Human interleukin-1	c1117	17.4	1.8	20	1	AD5614961	Human mpegS-1 chim
c1045	17.4	1.8	19	1	AD5614515	Human interleukin-1	c1118	17.4	1.8	20	1	AD5614962	Human mpegS-1 chim
c1046	17.4	1.8	19	1	AD5614387	Human interleukin-1	c1119	17.4	1.8	20	1	AD5615080	Human mpegS-1 chim
c1047	17.4	1.8	19	1	AD5668376	PCR primer used to	c1120	17.4	1.8	20	1	AD5615324	Human mpegS-1 chim
c1048	17.4	1.8	19	1	AD5636283	Human purinergic r	c1121	17.4	1.8	20	1	AD5614687	Human mpegS-1 chim
c1049	17.4	1.8	19	1	AD5636287	Human purinergic r	c1122	17.4	1.8	20	1	AD5615431	Human mpegS-1 chim
c1050	17.4	1.8	19	1	AD5676756	MCHN1 genomic sequ	c1123	17.4	1.8	20	1	AD5615427	Human mpegS-1 chim
c1051	17.4	1.8	19	1	AD5676751	MCHN1 genomic sequ	c1124	17.4	1.8	20	1	AD5614038	Human mpegS-1 chim
c1052	17.4	1.8	19	1	AD5632301	Human interleukin-1	c1125	17.4	1.8	20	1	AD5646480	Human oligonucleot
c1053	17.4	1.8	19	1	AD5625727	Human NOVX gene, f	c1126	17.4	1.8	20	1	AD5645362	Human oligonucleot
c1054	17.4	1.8	19	1	AD5608706	Extend primer 43 u	c1127	17.4	1.8	20	1	AD5645271	Human oligonucleot
c1055	17.4	1.8	19	1	AD5609402	Extend primer 24 u	c1128	17.4	1.8	20	1	AD5652269	Human inhibitor of

1139	17.4	1.8	20	1	AD052207	Human inhibitor of	1202	17	1.7	17	1	ADL49971	Human PKR substrat
c1130	17.4	1.8	20	1	AD052271	Human inhibitor of	1203	17	1.7	17	1	ADL49955	Human PKR substrat
1131	17.4	1.8	20	1	AD052203	Human inhibitor of	1204	17	1.7	17	1	ADL50733	Human PKR substrat
1132	17.4	1.8	20	1	ADP45826	Extend primer 18 u	1205	17	1.7	17	1	ADL50752	Human PKR substrat
1133	17.4	1.8	21	1	AAQ10789	Probe for identify	1206	17	1.7	17	1	ADL49954	Human PKR substrat
c1134	17.4	1.8	21	1	AAH37857	SNP specific upper	1207	17	1.7	17	1	ADL49970	Human PKR substrat
c1135	17.4	1.8	21	1	AAH38405	SNP specific upper	1208	17	1.7	17	1	ADL49455	Human PKR substrat
1136	17.4	1.8	21	1	AAFA24290	Complementary nucl	1209	17	1.7	17	1	ADL49667	Human PKR substrat
c1137	17.4	1.8	21	1	ABK86837	Human cholecyctoki	1210	17	1.7	17	1	ADL50753	Human PKR substrat
c1138	17.4	1.8	21	1	ABK60598	Human polymorphis	1211	17	1.7	17	1	ADL31231	Human glioma endot
c1139	17.4	1.8	21	1	ABK60817	Human polymorphis	1212	17	1.7	17	1	ADL82338	Human ER+ breast c
c1140	17.4	1.8	21	1	ABK60599	Human polymorphis	1213	17	1.7	17	1	ADP08723	Extend primer 60 u
c1141	17.4	1.8	21	1	ABK60816	Human polymorphis	1214	17	1.7	17	1	ADP08674	Extend primer 120
1142	17.4	1.8	21	1	ABK79794	EST polymorphic DN	1215	17	1.7	17	1	ADP08783	Extend primer 124
1143	17.4	1.8	21	1	ADG79161	Caldineurin A cata	1216	17	1.7	17	1	ADP08264	Extend primer 59 u
c1144	17.4	1.8	21	1	ABZ58851	PCR primer MR for	1217	17	1.7	17	1	ADP09266	SNP specific upper
c1145	17.4	1.8	21	1	ADP08769	Extend primer 106	1218	17	1.7	17	1	AAH38113	Human inflammatory
1146	17.2	1.7	18	1	AD056549	Human cyclin-depen	1219	17	1.7	17	1	AAH91237	Human neutropilin 1
c1147	17.2	1.7	18	1	AD056979	Human GAK/FPET pr	1220	17	1.7	17	1	AD048752	Human cyclin-depen
c1148	17.2	1.7	18	1	AD056537	Human cyclin-depen	1221	17	1.7	17	1	AD056532	Human cyclin-depen
c1149	17.2	1.7	19	1	AAQ76248	Generic primer frc	1222	17	1.7	17	1	AD056536	Human cyclin-depen
1150	17.2	1.7	19	1	ABX93649	Human Alu-specific	1223	17	1.7	17	1	AD056532	Human cyclin-depen
c1151	17.2	1.7	20	1	ABX95025	Human Alu specific	1224	17	1.7	17	1	AAH58817	5' end fragment of
c1152	17.2	1.7	20	1	AAV29284	Nucleotide sequenc	1225	17	1.7	17	1	AAH48298	5' end fragment of
1153	17	1.7	17	1	AAA22861	Integrin subunit b	1226	17	1.7	17	1	AAH74905	5' end fragment of
1154	17	1.7	17	1	AAA22747	Integrin subunit b	1227	17	1.7	17	1	AAH74721	Capped RNA influen
1155	17	1.7	17	1	AAA22744	Integrin subunit b	1228	17	1.7	17	1	AAH74726	Capped RNA influen
1156	17	1.7	17	1	AAA22759	Integrin subunit b	1229	17	1.7	17	1	AAH74726	Capped RNA influen
1157	17	1.7	17	1	AAA22860	Integrin subunit b	1230	17	1.7	17	1	AAH74729	Capped RNA influen
1158	17	1.7	17	1	AAA22741	Integrin subunit b	1231	17	1.7	17	1	AAH74727	Capped RNA influen
1159	17	1.7	17	1	AAA22722	Integrin subunit b	1232	17	1.7	17	1	AAH74723	Capped RNA influen
c1160	17	1.7	17	1	AAA22959	Integrin subunit b	1233	17	1.7	17	1	AAH74726	5' fragment of Alf
c1161	17	1.7	17	1	AAA22958	Integrin subunit b	1234	17	1.7	17	1	AAH74728	Capped RNA influen
1162	17	1.7	17	1	AAA22746	Integrin subunit b	1235	17	1.7	17	1	AAH74727	Capped RNA influen
1163	17	1.7	17	1	AAA22745	Integrin subunit b	1236	17	1.7	17	1	AAH747267	Capped RNA influen
c1164	17	1.7	17	1	AAA22831	Integrin subunit b	1237	17	1.7	17	1	AAH747267	Capped RNA influen
c1165	17	1.7	17	1	AAAC87597	Human Alu sequence	1238	17	1.7	17	1	AAH63215	Primer Alu 3' used
1166	17	1.7	17	1	ADB044439	Human MD27 scannin	1239	17	1.7	17	1	AAH91329	Alu PCR primer 8C
1167	17	1.7	17	1	ADB04442	Human MD27 scannin	1240	17	1.7	17	1	AAH91329	Human inflammatory
1168	17	1.7	17	1	ADB044282	Human MD27 scannin	1241	17	1.7	17	1	ABK93751	Human inhibitor of
1169	17	1.7	17	1	ADB04440	Human MD27 scannin	1242	17	1.7	17	1	ABZ75622	STR marker 21-32S
1170	17	1.7	17	1	ADB04314	Human MD27 scannin	1243	17	1.7	17	1	AAH747265	5' fragment #2 of
1171	17	1.7	17	1	ADB04283	Human MD27 scannin	1244	17	1.7	17	1	AAZ37711	Human mdm2 phospho
1172	17	1.7	17	1	ADB04441	Human MD27 scannin	1245	17	1.7	17	1	AAH96372	Primer used to amp
1173	17	1.7	17	1	ABZ60587	Human K-Ras DNAzym	1246	17	1.7	17	1	AAK59889	Oligonucleotide pr
1174	17	1.7	17	1	ABZ60584	Human K-Ras DNAzym	1247	17	1.7	17	1	AAK94972	Human CDNA clone-s
1175	17	1.7	17	1	ABZ60583	Tumour suppression	1248	17	1.7	17	1	AAK94972	Human mdm2 phospho
c1176	17	1.7	17	1	ADBL4243	Optineurin promote	1249	17	1.7	17	1	AAK29980	Human mdm2 antisen
c1177	17	1.7	17	1	ADBL4243	Non-nucleotide pro	1250	17	1.7	17	1	ABK68204	Human HYPLIP1 locu
c1178	17	1.7	17	1	ADHS9604	Non-nucleotide pro	1251	17	1.7	17	1	ABK68204	Human chromosome 1
1179	17	1.7	17	1	ADHS9616	Non-nucleotide pro	1252	17	1.7	17	1	ABK71108	Mouse HYPLIP1 locu
1180	17	1.7	17	1	ADHS9618	Non-nucleotide pro	1253	17	1.7	17	1	ADHS52338	Mouse IFNGR2 antis
c1181	17	1.7	17	1	ADHS9618	Non-nucleotide pro	1254	17	1.7	17	1	ADHS52338	Mouse HYPLIP1 locu
1182	17	1.7	17	1	ADHS9618	Non-nucleotide pro	1255	17	1.7	17	1	ADHS52338	Mouse HYPLIP1 PCR
1183	17	1.7	17	1	ADHS9618	Non-nucleotide pro	1256	17	1.7	17	1	ADHS52338	Mouse HYPLIP1 PCR
1184	17	1.7	17	1	ADHS9618	Non-nucleotide pro	1257	17	1.7	17	1	ADHS52338	Mouse HYPLIP1 PCR
1185	17	1.7	17	1	ADHS9618	Non-nucleotide pro	1258	17	1.7	17	1	ADHS52338	Mouse HYPLIP1 PCR
1186	17	1.7	17	1	ADHS9618	Non-nucleotide pro	1259	17	1.7	17	1	ADHS52338	Mouse HYPLIP1 PCR
1187	17	1.7	17	1	ADHS9618	Non-nucleotide pro	1260	17	1.7	17	1	ADHS52338	Mouse HYPLIP1 PCR
1188	17	1.7	17	1	ADHS9618	Non-nucleotide pro	1261	17	1.7	17	1	ADHS52338	Mouse HYPLIP1 PCR
1189	17	1.7	17	1	ADHS9618	Non-nucleotide pro	1262	17	1.7	17	1	ADHS52338	Mouse HYPLIP1 PCR
1190	17	1.7	17	1	ADHS9618	Non-nucleotide pro	1263	17	1.7	17	1	ADHS52338	Mouse HYPLIP1 PCR
1191	17	1.7	17	1	ADHS9618	Non-nucleotide pro	1264	17	1.7	17	1	ADHS52338	Mouse HYPLIP1 PCR
1192	17	1.7	17	1	ADHS9618	Non-nucleotide pro	1265	17	1.7	17	1	ADHS52338	Mouse HYPLIP1 PCR
1193	17	1.7	17	1	ADHS9618	Non-nucleotide pro	1266	17	1.7	17	1	ADHS52338	Mouse HYPLIP1 PCR
1194	17	1.7	17	1	ADHS9618	Non-nucleotide pro	1267	17	1.7	17	1	ADHS52338	Mouse HYPLIP1 PCR
1195	17	1.7	17	1	ADHS9618	Non-nucleotide pro	1268	17	1.7	17	1	ADHS52338	Mouse HYPLIP1 PCR
1196	17	1.7	17	1	ADHS9618	Non-nucleotide pro	1269	17	1.7	17	1	ADHS52338	Mouse HYPLIP1 PCR
1197	17	1.7	17	1	ADHS9618	Non-nucleotide pro	1270	17	1.7	17	1	ADHS52338	Mouse HYPLIP1 PCR
1198	17	1.7	17	1	ADHS9618	Non-nucleotide pro	1271	17	1.7	17	1	ADHS52338	Mouse HYPLIP1 PCR
1199	17	1.7	17	1	ADHS9618	Non-nucleotide pro	1272	17	1.7	17	1	ADHS52338	Mouse HYPLIP1 PCR
1200	17	1.7	17	1	ADHS9618	Non-nucleotide pro	1273	17	1.7	17	1	ADHS52338	Mouse HYPLIP1 PCR
1201	17	1.7	17	1	ADHS9618	Non-nucleotide pro	1274	17	1.7	17	1	ADHS52338	Mouse HYPLIP1 PCR

1275	16.8	1.7	20	1	AA053171	Familial dysautono	1348	16.8	1.7	20	1	ABX75089	Human gene 216 pol
1276	16.8	1.7	20	1	AA047775	Antisense oligonuc	1349	16.8	1.7	20	1	ACB86680	Human VEGFR-1 chim
1277	16.8	1.7	20	1	AA063001	Hypertension/ACE 1	1350	16.8	1.7	20	1	ABE71057	Human HKR1 phospho
1278	16.8	1.7	20	1	AA075579	Reverse transcript	1351	16.8	1.7	20	1	ABE71059	Human HKR1 phospho
1279	16.8	1.7	20	1	AA075581	Reverse transcript	1352	16.8	1.7	20	1	ADA20923	Human BAX chimeric
1280	16.8	1.7	20	1	AA075581	Reverse transcript	1353	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1281	16.8	1.7	20	1	AA075581	Reverse transcript	1354	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1282	16.8	1.7	20	1	AA075581	Reverse transcript	1355	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1283	16.8	1.7	20	1	AA075581	Reverse transcript	1356	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1284	16.8	1.7	20	1	AA075581	Reverse transcript	1357	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1285	16.8	1.7	20	1	AA075581	Reverse transcript	1358	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1286	16.8	1.7	20	1	AA075581	Reverse transcript	1359	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1287	16.8	1.7	20	1	AA075581	Reverse transcript	1360	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1288	16.8	1.7	20	1	AA075581	Reverse transcript	1361	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1289	16.8	1.7	20	1	AA075581	Reverse transcript	1362	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1290	16.8	1.7	20	1	AA075581	Reverse transcript	1363	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1291	16.8	1.7	20	1	AA075581	Reverse transcript	1364	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1292	16.8	1.7	20	1	AA075581	Reverse transcript	1365	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1293	16.8	1.7	20	1	AA075581	Reverse transcript	1366	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1294	16.8	1.7	20	1	AA075581	Reverse transcript	1367	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1295	16.8	1.7	20	1	AA075581	Reverse transcript	1368	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1296	16.8	1.7	20	1	AA075581	Reverse transcript	1369	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1297	16.8	1.7	20	1	AA075581	Reverse transcript	1370	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1298	16.8	1.7	20	1	AA075581	Reverse transcript	1371	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1299	16.8	1.7	20	1	AA075581	Reverse transcript	1372	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1300	16.8	1.7	20	1	AA075581	Reverse transcript	1373	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1301	16.8	1.7	20	1	AA075581	Reverse transcript	1374	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1302	16.8	1.7	20	1	AA075581	Reverse transcript	1375	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1303	16.8	1.7	20	1	AA075581	Reverse transcript	1376	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1304	16.8	1.7	20	1	AA075581	Reverse transcript	1377	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1305	16.8	1.7	20	1	AA075581	Reverse transcript	1378	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1306	16.8	1.7	20	1	AA075581	Reverse transcript	1379	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1307	16.8	1.7	20	1	AA075581	Reverse transcript	1380	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1308	16.8	1.7	20	1	AA075581	Reverse transcript	1381	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1309	16.8	1.7	20	1	AA075581	Reverse transcript	1382	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1310	16.8	1.7	20	1	AA075581	Reverse transcript	1383	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1311	16.8	1.7	20	1	AA075581	Reverse transcript	1384	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1312	16.8	1.7	20	1	AA075581	Reverse transcript	1385	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1313	16.8	1.7	20	1	AA075581	Reverse transcript	1386	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1314	16.8	1.7	20	1	AA075581	Reverse transcript	1387	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1315	16.8	1.7	20	1	AA075581	Reverse transcript	1388	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1316	16.8	1.7	20	1	AA075581	Reverse transcript	1389	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1317	16.8	1.7	20	1	AA075581	Reverse transcript	1390	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1318	16.8	1.7	20	1	AA075581	Reverse transcript	1391	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1319	16.8	1.7	20	1	AA075581	Reverse transcript	1392	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1320	16.8	1.7	20	1	AA075581	Reverse transcript	1393	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1321	16.8	1.7	20	1	AA075581	Reverse transcript	1394	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1322	16.8	1.7	20	1	AA075581	Reverse transcript	1395	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1323	16.8	1.7	20	1	AA075581	Reverse transcript	1396	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1324	16.8	1.7	20	1	AA075581	Reverse transcript	1397	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1325	16.8	1.7	20	1	AA075581	Reverse transcript	1398	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1326	16.8	1.7	20	1	AA075581	Reverse transcript	1399	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1327	16.8	1.7	20	1	AA075581	Reverse transcript	1400	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1328	16.8	1.7	20	1	AA075581	Reverse transcript	1401	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1329	16.8	1.7	20	1	AA075581	Reverse transcript	1402	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1330	16.8	1.7	20	1	AA075581	Reverse transcript	1403	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1331	16.8	1.7	20	1	AA075581	Reverse transcript	1404	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1332	16.8	1.7	20	1	AA075581	Reverse transcript	1405	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1333	16.8	1.7	20	1	AA075581	Reverse transcript	1406	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1334	16.8	1.7	20	1	AA075581	Reverse transcript	1407	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1335	16.8	1.7	20	1	AA075581	Reverse transcript	1408	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1336	16.8	1.7	20	1	AA075581	Reverse transcript	1409	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1337	16.8	1.7	20	1	AA075581	Reverse transcript	1410	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1338	16.8	1.7	20	1	AA075581	Reverse transcript	1411	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1339	16.8	1.7	20	1	AA075581	Reverse transcript	1412	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1340	16.8	1.7	20	1	AA075581	Reverse transcript	1413	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1341	16.8	1.7	20	1	AA075581	Reverse transcript	1414	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1342	16.8	1.7	20	1	AA075581	Reverse transcript	1415	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1343	16.8	1.7	20	1	AA075581	Reverse transcript	1416	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1344	16.8	1.7	20	1	AA075581	Reverse transcript	1417	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1345	16.8	1.7	20	1	AA075581	Reverse transcript	1418	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1346	16.8	1.7	20	1	AA075581	Reverse transcript	1419	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1347	16.8	1.7	20	1	AA075581	Reverse transcript	1420	16.8	1.7	20	1	ADA20924	Human BAX chimeric

C1567	16.8	1.7	21	1	AB560534	Human polymorphism	1640	16.4	1.7	20	1	ADP56753	Antisense 2'-MOE g
C1568	16.8	1.7	21	1	AB560764	Human polymorphism	C1641	16.4	1.7	20	1	ADP56830	Human AMACR DNA ta
C1569	16.8	1.7	21	1	AB560765	Human polymorphism	C1642	16	1.6	16	1	AAF88161	Human thymoid malif
C1570	16.8	1.7	21	1	AB560535	Human polymorphism	1643	16	1.6	16	1	AB597400	Human cyclooxigena
C1571	16.8	1.7	21	1	AB093617	Human DISC1/DISC2	C1644	16	1.6	16	1	AB598039	Human multidrug re
C1572	16.8	1.7	21	1	AB158478	HPT probe generat	C1645	16	1.6	16	1	ACA62885	Repeated nucleic a
C1573	16.8	1.7	21	1	AB566754	Human MRP-1 polyom	1646	16	1.6	16	1	ACA62878	Repeated nucleic a
C1574	16.8	1.7	21	1	AB566755	Human MRP-1 polyom	1647	16	1.6	16	1	ACA62880	Repeated nucleic a
C1575	16.8	1.7	21	1	ADC42667	Human FANCD2 PCR p	1648	16	1.6	16	1	ACA62882	Repeated nucleic a
C1576	16.8	1.7	21	1	ADC42666	Hypoxanthine phosp	1649	16	1.6	16	1	ACA62879	Repeated nucleic a
C1577	16.8	1.7	21	1	ADK01281	Rat DNA microarray	C1650	16	1.6	16	1	AD63080	Human tandem tag D
C1578	16.8	1.7	21	1	ADK01281	Rat DNA microarray	C1651	16	1.6	16	1	AD63081	Human tandem tag D
C1579	16.8	1.7	21	1	ADK01341	Rat DNA microarray	C1652	16	1.6	16	1	AD63078	Human tandem tag D
C1580	16.8	1.7	21	1	ADK01283	Rat DNA microarray	C1653	16	1.6	16	1	AD63084	Human tandem tag D
C1581	16.8	1.7	21	1	ADK01331	Rat DNA microarray	C1654	16	1.6	16	1	AD63086	Human tandem tag D
C1582	16.8	1.7	21	1	ADK01330	Rat DNA microarray	1655	16	1.6	17	1	AAA23740	Integrin subunit b
C1583	16.8	1.7	21	1	ADK01332	Rat DNA microarray	1656	16	1.6	17	1	AAA23748	Integrin subunit b
C1584	16.8	1.7	21	1	AD123739	Human LPDIR PCR pr	1657	16	1.6	17	1	AAA22736	Integrin subunit b
C1585	16.6	1.7	19	1	AAV83938	PCR primer used to	1658	16	1.6	17	1	AAA22742	Integrin subunit b
C1586	16.4	1.7	18	1	AAZ89776	Human RIP-1 antis	1659	16	1.6	17	1	AAA22957	Integrin subunit b
C1587	16.4	1.7	18	1	AAZ89747	Human RIP-1 antis	C1660	16	1.6	17	1	AAAF64147	Primer #89. Homo
C1588	16.4	1.7	18	1	AAZ39625	Human CREL mRNA in	C1661	16	1.6	17	1	AAE83022	Ataxia telangiecta
C1589	16.4	1.7	18	1	AAH40733	SNP specific upper	C1662	16	1.6	17	1	ABT38108	Tumour suppression
C1590	16.4	1.7	18	1	AAH38918	SNP specific lower	1663	16	1.6	17	1	ABT35067	Tumour suppression
C1591	16.4	1.7	18	1	AAH39265	SNP specific upper	1664	16	1.6	17	1	ADB04313	Human MD27 scanlin
C1592	16.4	1.7	18	1	AAH47615	Human Her-3 mRNA i	1665	16	1.6	17	1	ADB04443	Human MD27 scanlin
C1593	16.4	1.7	18	1	ABAB82413	Zmax1 gene region	1666	16	1.6	17	1	ADB04438	Human MD27 scanlin
C1594	16.4	1.7	18	1	ABAB82195	Zmax1 gene region	1667	16	1.6	17	1	ADB04281	Human MD27 scanlin
C1595	16.4	1.7	18	1	ABAB82195	Human multidrug re	1668	16	1.6	17	1	ADB04315	Human MD27 scanlin
C1596	16.4	1.7	18	1	ABR22992	Human Zmax1 CDNA r	1669	16	1.6	17	1	ADB04284	Human MD27 scanlin
C1597	16.4	1.7	18	1	ABR23210	Human Zmax1 CDNA r	1670	16	1.6	17	1	ABE26065	Human K-Ras DNazym
C1598	16.4	1.7	18	1	ACC49483	Human GAPDH revers	1671	16	1.6	17	1	ACC63031	Murine oligonucleo
C1599	16.4	1.7	18	1	ACC45793	Human HBM STS mark	C1672	16	1.6	17	1	ADB44260	Tumour suppression
C1600	16.4	1.7	18	1	ACC45575	Human HBM STS mark	1673	16	1.6	17	1	ACC54382	Human tumour supp
C1601	16.4	1.7	18	1	ACC45283	Human GAPDH PCR pr	C1675	16	1.6	17	1	ACC51495	Human tumour supp
C1602	16.4	1.7	18	1	ACA62881	Repeated nucleic a	1676	16	1.6	17	1	ADL50194	Human PKR substrat
C1603	16.4	1.7	18	1	ADB98491	Sequence tagged si	1677	16	1.6	17	1	ADL50204	Human PKR substrat
C1604	16.4	1.7	18	1	ADB98491	Sequence tagged si	1678	16	1.6	17	1	ADL49433	Human PKR substrat
C1605	16.4	1.7	18	1	ADH59603	Non-nucleotide pro	1679	16	1.6	17	1	ADL49459	Human PKR substrat
C1606	16.4	1.7	18	1	ADH59603	Non-nucleotide pro	1680	16	1.6	17	1	ADL50215	Human PKR substrat
C1607	16.4	1.7	18	1	ADH59615	Human Vbeta mltros	1681	16	1.6	17	1	ADL49914	Human PKR substrat
C1608	16.4	1.7	18	1	ADH71082	MCHRI genomic sequ	1682	16	1.6	17	1	ADL49909	Human PKR substrat
C1609	16.4	1.7	18	1	ADH76753	Extend primer 117	1683	16	1.6	17	1	ADL49932	Human PKR substrat
C1610	16.4	1.7	18	1	ADP08780	Extend primer 7 us	1684	16	1.6	17	1	ADL49915	Human PKR substrat
C1611	16.4	1.7	18	1	ADP46226	Human teratocarcin	1685	16	1.6	17	1	ADL49927	Human PKR substrat
C1612	16.4	1.7	19	1	AA923228	PCR primer 1 used	1686	16	1.6	17	1	ADL50427	Human PKR substrat
C1613	16.4	1.7	19	1	AA913553	Reverse primer use	1687	16	1.6	17	1	ADL49957	Human PKR substrat
C1614	16.4	1.7	19	1	AA91179	Human delta oloid	1688	16	1.6	17	1	ADP46267	Extend primer 48 u
C1615	16.4	1.7	19	1	ABX15007	Selection and ampl	C1689	16	1.6	18	1	AAAT36226	Oligonucleotide RT
C1616	16.4	1.7	19	1	ACA88919	Opioid receptor D1	C1690	16	1.6	18	1	AA903020	Haematopoietic cel
C1617	16.4	1.7	19	1	ADH70436	Human Vbeta gene r	1691	16	1.6	18	1	ABZ09942	Human cyclin-depen
C1618	16.4	1.7	19	1	ADH71084	Human Vbeta gene r	1692	16	1.6	18	1	AAV57826	Human chromosome 1
C1619	16.4	1.7	19	1	ADH70436	Human P-cadherin p	C1693	16	1.6	19	1	ADP68319	Human antisense Ap
C1620	16.4	1.7	19	1	ADP26951	Human P-cadherin p	C1694	16	1.6	19	1	ACA88916	Selection and ampl
C1621	16.4	1.7	19	1	AAQ95565	Primer A7 (Group 4	C1695	16	1.6	20	1	AAH48599	Human fascin assoc
C1622	16.4	1.7	20	1	AAQ95565	Primer B (Group 6,	C1696	16	1.6	20	1	AA521754	Mouse Survivin ant
C1623	16.4	1.7	20	1	AAH91108	Human inflammatory	C1697	16	1.6	20	1	AAAD25167	Human NOV7b gene e
C1624	16.4	1.7	20	1	ABL45527	Human chromosome 2	C1698	16	1.6	20	1	ADD71348	GFR1 1 gene intron
C1625	16.4	1.7	20	1	ABL45527	Human ADAMTS13 STS	C1699	16	1.6	20	1	ADL24993	Intestinal epithel
C1626	16.4	1.7	20	1	ABZ71060	Human HKR1 phospho	C1700	16	1.6	20	1	ADOB81026	Human piron protei
C1627	16.4	1.7	20	1	ABZ71060	Chimeric antisense	C1701	16	1.6	41	1	ABV77328	Human protein 10.0
C1628	16.4	1.7	20	1	ABZ71060	Human PKR exon 17	C1702	16	1.6	51	1	AAI73524	Human silent SNP c
C1629	16.4	1.7	20	1	ABZ71060	Human PDE4C oligon	C1703	16	1.6	19	1	AAO82623	Chromosome 11 (loc
C1630	16.4	1.7	20	1	ABZ71060	Human PDE4C-derive	C1704	16	1.6	19	1	AAQ75852	Reverse transcript
C1631	16.4	1.7	20	1	ADH56987	PCR primer used to	1705	16	1.6	19	1	AAQ95836	Primer B (Group 10
C1632	16.4	1.7	20	1	ADH56987	Human LIM domain k	1706	16	1.6	19	1	AAAT10757	Oligonucleotide pr
C1633	16.4	1.7	20	1	ADH56987	Human LIM domain k	1707	16	1.6	19	1	AAV66018	Primer #1 to ampl
C1634	16.4	1.7	20	1	ADH56987	Oligonucleotide as	C1708	15.8	1.6	19	1	AAV85747	LRP5 exon primer 5
C1635	16.4	1.7	20	1	ADH56987	Human mPGS-1 chim	C1709	15.8	1.6	19	1	AAV85825	LRP5 SNP primer 57
C1636	16.4	1.7	20	1	ADH56987	Human oligonucleot	C1710	15.8	1.6	19	1	AAV85862	LRP5 exon primer E
C1637	16.4	1.7	20	1	ADH56987	Extend primer 38 u	C1711	15.8	1.6	19	1	AAV07878	Aminoxy-modified
C1638	16.4	1.7	20	1	ADH56987		1712	15.8	1.6	19	1		

1713	15.8	1.6	19	1	AAV06820	Oligonucleotide co
1714	15.8	1.6	19	1	AAx81316	5' amino oligonuc
1715	15.8	1.6	19	1	AAx36671	PCR primer for mar
1716	15.8	1.6	19	1	AAx81977	Polynucleotide str
1717	15.8	1.6	19	1	AAZ01358	PCR primer for pci
1718	15.8	1.6	19	1	AAZ61390	Uniform phosphodi
1719	15.8	1.6	19	1	AAZ61404	2'-O-modified ribo
1720	15.8	1.6	19	1	AAZ62422	T19 diester for us
1721	15.8	1.6	19	1	AAZ95241	Modified oligonuc
1722	15.8	1.6	19	1	AAZ95240	Modified oligonuc
1723	15.8	1.6	19	1	AAAO6839	Modified T-contain
1724	15.8	1.6	19	1	AAAB8952	Oligonucleotide IS
1725	15.8	1.6	19	1	AAAB8965	2'-Modified chim
1726	15.8	1.6	19	1	AAAB8949	Oligonucleotide IS
1727	15.8	1.6	19	1	AAAB8950	Oligonucleotide IS
1728	15.8	1.6	19	1	AAAB8951	Oligonucleotide IS
1729	15.8	1.6	19	1	AAAB8947	Oligonucleotide IS
1730	15.8	1.6	19	1	AAAB8948	Phosphorothioate 2
1731	15.8	1.6	19	1	AAAB1630	Cleavage of nucle
1732	15.8	1.6	19	1	AAAC2454	Oligonucleotide IS
1733	15.8	1.6	19	1	AAAC1458	ISIS sequence 3232
1734	15.8	1.6	19	1	AAAC1564	S. aureus groE ope
1735	15.8	1.6	19	1	AAAC6776	SNP specific lower
1736	15.8	1.6	19	1	AAAB38442	SNP specific upper
1737	15.8	1.6	19	1	AAAB39785	SNP specific upper
1738	15.8	1.6	19	1	AAAB40317	Oligonucleotide #8
1739	15.8	1.6	19	1	AAAB46460	Human type II RNAs
1740	15.8	1.6	19	1	AAAB25737	Human type II RNAs
1741	15.8	1.6	19	1	AAAB25738	Human type II RNAs
1742	15.8	1.6	19	1	AAAC62165	PCR primer used to
1743	15.8	1.6	19	1	AAAC62165	PCR primer used to
1744	15.8	1.6	19	1	AAAC62165	Human multi drug r
1745	15.8	1.6	19	1	AAAC62165	Human multi drug r
1746	15.8	1.6	19	1	AAAC3664	2'-O-N-12-(dimethy
1747	15.8	1.6	19	1	AAAC3664	Nucleic acid quant
1748	15.8	1.6	19	1	AAAC3664	Human chromosome 1
1749	15.8	1.6	19	1	AAAD31455	Methyl thioethyl m
1750	15.8	1.6	19	1	AAAB91949	Dimethylaminopropyl
1751	15.8	1.6	19	1	ABAB91950	Methoxyethoxy mod
1752	15.8	1.6	19	1	ABAB94423	Human MTH1 DNA mis
1753	15.8	1.6	19	1	ABAB15520	Tailing reaction r
1754	15.8	1.6	19	1	ABAB15520	Single nucleotide
1755	15.8	1.6	19	1	AAAD2000	Oligonucleotide #3
1756	15.8	1.6	19	1	AAAD2002	Oligonucleotide #5
1757	15.8	1.6	19	1	AAAD2004	Oligonucleotide #7
1758	15.8	1.6	19	1	AAAD2010	Oligonucleotide #1
1759	15.8	1.6	19	1	AAAD2020	Oligonucleotide #2
1760	15.8	1.6	19	1	AAAD2001	Oligonucleotide #4
1761	15.8	1.6	19	1	AAAD2011	Oligonucleotide #1
1762	15.8	1.6	19	1	AAAD2005	Oligonucleotide #8
1763	15.8	1.6	19	1	AAAD2003	Oligonucleotide #6
1764	15.8	1.6	19	1	AAAD1998	Oligonucleotide #1
1765	15.8	1.6	19	1	AAAD1999	Oligonucleotide #2
1766	15.8	1.6	19	1	AAAD2009	Oligonucleotide #1
1767	15.8	1.6	19	1	ACF62693	Cancer based on CY
1768	15.8	1.6	19	1	ACF62692	Cancer based on CY
1769	15.8	1.6	19	1	ADB21364	MPPI based cancer
1770	15.8	1.6	19	1	ADB21363	MPPI based cancer
1771	15.8	1.6	19	1	ABZ58336	Oligonucleotide wi
1772	15.8	1.6	19	1	ACCE62369	Human NOV9 reverse
1773	15.8	1.6	19	1	ADB88452	Human UGT1A1 varia
1774	15.8	1.6	19	1	ADB88453	Human UGT1A1 varia
1775	15.8	1.6	19	1	ADB97435	Human MDRI variant
1776	15.8	1.6	19	1	ADB97436	Human MDRI variant
1777	15.8	1.6	19	1	ADB92627	Human MDRI variant
1778	15.8	1.6	19	1	ADB92626	Human MDRI variant
1779	15.8	1.6	19	1	ADBL14131	Optineurin promote
1780	15.8	1.6	19	1	ADBE92245	Modified oligomeri
1781	15.8	1.6	19	1	ADBE92265	Modified oligomeri
1782	15.8	1.6	19	1	ADH97218	Synthetically modi
1783	15.8	1.6	19	1	ADH97214	Synthetically modi
1784	15.8	1.6	19	1	ADH97224	Synthetically modi
1785	15.8	1.6	19	1	ABZ97252	Human nucleic acid
1786	15.8	1.6	19	1	ABZ97253	Human nucleic acid
1787	15.8	1.6	19	1	ABZ97333	Human IL4-R oligon
1788	15.8	1.6	19	1	ABZ97334	Human IL4-R oligon
1789	15.8	1.6	19	1	ACAB89302	Selection and ampl
1790	15.8	1.6	19	1	ACAB89302	Human familial btp
1791	15.8	1.6	19	1	ADW65614	NR1 polymorphism d
1792	15.8	1.6	19	1	ADW65614	Human interleukin-
1793	15.8	1.6	19	1	ADW65614	Human interleukin-
1794	15.8	1.6	19	1	ADW65614	Human interleukin-
1795	15.8	1.6	19	1	ADW65614	Human interleukin-
1796	15.8	1.6	19	1	ADW65614	Human interleukin-
1797	15.8	1.6	19	1	ADW65614	Human interleukin-
1798	15.8	1.6	19	1	ADW65614	Human interleukin-
1799	15.8	1.6	19	1	ADW65614	Human interleukin-
1800	15.8	1.6	19	1	ADW65614	Human interleukin-
1801	15.8	1.6	19	1	ADW65614	Human interleukin-
1802	15.8	1.6	19	1	ADW65614	Human interleukin-
1803	15.8	1.6	19	1	ADW65614	Human interleukin-
1804	15.8	1.6	19	1	ADW65614	Human interleukin-
1805	15.8	1.6	19	1	ADW65614	Human interleukin-
1806	15.8	1.6	19	1	ADW65614	Human interleukin-
1807	15.8	1.6	19	1	ADW65614	Human interleukin-
1808	15.8	1.6	19	1	ADW65614	Human interleukin-
1809	15.8	1.6	19	1	ADW65614	Human interleukin-
1810	15.8	1.6	19	1	ADW65614	Human interleukin-
1811	15.8	1.6	19	1	ADW65614	Human interleukin-
1812	15.8	1.6	19	1	ADW65614	Human interleukin-
1813	15.8	1.6	19	1	ADW65614	Human interleukin-
1814	15.8	1.6	19	1	ADW65614	Human interleukin-
1815	15.8	1.6	19	1	ADW65614	Human interleukin-
1816	15.8	1.6	19	1	ADW65614	Human interleukin-
1817	15.8	1.6	19	1	ADW65614	Human interleukin-
1818	15.8	1.6	19	1	ADW65614	Human interleukin-
1819	15.8	1.6	19	1	ADW65614	Human interleukin-
1820	15.8	1.6	19	1	ADW65614	Human interleukin-
1821	15.8	1.6	19	1	ADW65614	Human interleukin-
1822	15.8	1.6	19	1	ADW65614	Human interleukin-
1823	15.8	1.6	19	1	ADW65614	Human interleukin-
1824	15.8	1.6	19	1	ADW65614	Human interleukin-
1825	15.8	1.6	19	1	ADW65614	Human interleukin-
1826	15.8	1.6	19	1	ADW65614	Human interleukin-
1827	15.8	1.6	19	1	ADW65614	Human interleukin-
1828	15.8	1.6	19	1	ADW65614	Human interleukin-
1829	15.8	1.6	19	1	ADW65614	Human interleukin-
1830	15.8	1.6	19	1	ADW65614	Human interleukin-
1831	15.8	1.6	19	1	ADW65614	Human interleukin-
1832	15.8	1.6	19	1	ADW65614	Human interleukin-
1833	15.8	1.6	19	1	ADW65614	Human interleukin-
1834	15.8	1.6	19	1	ADW65614	Human interleukin-
1835	15.8	1.6	19	1	ADW65614	Human interleukin-
1836	15.8	1.6	19	1	ADW65614	Human interleukin-
1837	15.8	1.6	19	1	ADW65614	Human interleukin-
1838	15.8	1.6	19	1	ADW65614	Human interleukin-
1839	15.8	1.6	19	1	ADW65614	Human interleukin-
1840	15.8	1.6	19	1	ADW65614	Human interleukin-
1841	15.8	1.6	19	1	ADW65614	Human interleukin-
1842	15.8	1.6	19	1	ADW65614	Human interleukin-
1843	15.8	1.6	19	1	ADW65614	Human interleukin-
1844	15.8	1.6	19	1	ADW65614	Human interleukin-
1845	15.8	1.6	19	1	ADW65614	Human interleukin-
1846	15.8	1.6	19	1	ADW65614	Human interleukin-
1847	15.8	1.6	19	1	ADW65614	Human interleukin-
1848	15.8	1.6	19	1	ADW65614	Human interleukin-
1849	15.8	1.6	19	1	ADW65614	Human interleukin-
1850	15.8	1.6	19	1	ADW65614	Human interleukin-
1851	15.8	1.6	19	1	ADW65614	Human interleukin-
1852	15.8	1.6	19	1	ADW65614	Human interleukin-
1853	15.8	1.6	19	1	ADW65614	Human interleukin-
1854	15.8	1.6	19	1	ADW65614	Human interleukin-
1855	15.8	1.6	19	1	ADW65614	Human interleukin-
1856	15.8	1.6	19	1	ADW65614	Human interleukin-
1857	15.8	1.6	19	1	ADW65614	Human interleukin-
1858	15.8	1.6	19	1	ADW65614	Human interleukin-

C1859	15.4	1.6	17	1	ABT40194	Tumour suppression	1932	15.4	1.6	17	1	ADL49926	Human PKR substrat
1860	15.4	1.6	17	1	ABT35639	Tumour suppression	1933	15.4	1.6	17	1	ADL49965	Human PKR substrat
C1861	15.4	1.6	17	1	ABT40150	Tumour suppression	1934	15.4	1.6	17	1	ADL50214	Human PKR substrat
C1862	15.4	1.6	17	1	ABT35874	Tumour suppression	1935	15.4	1.6	17	1	ADL50747	Human PKR substrat
1863	15.4	1.6	17	1	ABT39264	Tumour suppression	1936	15.4	1.6	17	1	ADL49434	Human PKR substrat
C1864	15.4	1.6	17	1	ABT40140	Tumour suppression	1937	15.4	1.6	17	1	ADL50197	Human PKR substrat
1865	15.4	1.6	17	1	ADB04318	Human MD27 scanlin	1938	15.4	1.6	17	1	ADL50748	Human PKR substrat
1866	15.4	1.6	17	1	ADB04317	Human MD27 scanlin	1939	15.4	1.6	17	1	ADL49906	Human PKR substrat
1867	15.4	1.6	17	1	ADB04437	Human MD27 scanlin	1940	15.4	1.6	17	1	ADL49920	Human PKR substrat
1868	15.4	1.6	17	1	ADB04446	Human MD27 scanlin	1941	15.4	1.6	17	1	ADL49950	Human PKR substrat
1869	15.4	1.6	17	1	ADB04316	Human MD27 scanlin	1942	15.4	1.6	17	1	ADL49430	Human PKR substrat
1870	15.4	1.6	17	1	ADB04447	Human MD27 scanlin	1943	15.4	1.6	17	1	ADH54043	Human neurodegener
1871	15.4	1.6	17	1	ADB04444	Human MD27 scanlin	1944	15.4	1.6	17	1	ADK13186	Human glioma endot
1872	15.4	1.6	17	1	ADB04445	Human MD27 scanlin	1945	15.4	1.6	17	1	ADL82347	Human ER+ breast c
1873	15.4	1.6	17	1	ABZ60455	Human K-Ras DNazym	1946	15.4	1.6	17	1	ADL82349	Human ER+ breast c
1874	15.4	1.6	17	1	ABZ60585	Human K-Ras DNazym	1947	15.4	1.6	17	1	ADL82453	Human ER+ breast c
1875	15.4	1.6	17	1	ABZ60574	Human K-Ras DNazym	1948	15.4	1.6	17	1	ADP08740	Extend primer 77 u
1876	15.4	1.6	17	1	ABZ60568	Human K-Ras DNazym	1949	15.4	1.6	17	1	ADP09251	Extend primer 46 u
1877	15.4	1.6	17	1	ABZ60586	Human K-Ras DNazym	1950	15.4	1.6	17	1	ADP09278	Extend primer 73 u
1878	15.4	1.6	17	1	ABZ60606	Human K-Ras DNazym	1951	15.4	1.6	17	1	ADP08765	CENPC1 extend prim
1879	15.4	1.6	17	1	ABZ60606	Human K-Ras DNazym	1952	15.4	1.6	17	1	ADO80011	CEP1 extend prim
1880	15.4	1.6	17	1	ABZ60604	Human K-Ras DNazym	1953	15.4	1.6	17	1	ADO79480	CEP1 extend prim
1881	15.4	1.6	17	1	ABZ60597	Human K-Ras DNazym	1954	15.4	1.6	17	1	ADO80017	CEP1 extend prim
C1882	15.4	1.6	17	1	ABZ61843	Human H-Ras DNazym	1955	15.4	1.6	18	1	AAQ20109	Cross-linking olig
1883	15.4	1.6	17	1	ABZ60567	Human K-Ras DNazym	1956	15.4	1.6	18	1	AAQ30448	Oligomer TMR943 F
1884	15.4	1.6	17	1	ACC64751	Murine oligonucleo	1957	15.4	1.6	18	1	AAZ21792	Exemplary oligonuc
1885	15.4	1.6	17	1	ACC64751	Murine oligonucleo	1958	15.4	1.6	18	1	AAF76529	Human EFEMP1 codin
1886	15.4	1.6	17	1	ADB44008	Tumour suppression	1959	15.4	1.6	18	1	AAH40898	SNP specific lower
C1887	15.4	1.6	17	1	ADB41143	Tumour suppression	1960	15.4	1.6	18	1	AAH38514	SNP specific lower
1888	15.4	1.6	17	1	ADB43650	Tumour suppression	1961	15.4	1.6	18	1	AAH40802	SNP specific lower
1889	15.4	1.6	17	1	ADB44570	Tumour suppression	1962	15.4	1.6	18	1	ABK27429	Colo cancer assoc
1890	15.4	1.6	17	1	ADB44878	Tumour suppression	1963	15.4	1.6	18	1	ABS97649	Human glutathione-
1891	15.4	1.6	17	1	ADB44306	Tumour suppression	1964	15.4	1.6	18	1	ADG14613	Human IL-10 regula
C1892	15.4	1.6	17	1	ADB44574	Tumour suppression	1965	15.4	1.6	18	1	ABZ10660	Haematopoietic cel
1893	15.4	1.6	17	1	ADB44518	Tumour suppression	1966	15.4	1.6	18	1	ADM47300	NOX oligonucleoti
1894	15.4	1.6	17	1	ADB14015	Optineurin promote	1967	15.4	1.6	18	1	ADM02351	PCR primer 2 used
C1895	15.4	1.6	17	1	ADB14019	Optineurin promote	1968	15.4	1.6	18	1	ADM06374	Human FLAP related
C1896	15.4	1.6	17	1	ADB43565	Human IDE sequenci	1969	15.4	1.6	18	1	ADO43261	Bipolar and unipol
C1897	15.4	1.6	17	1	AD150915	Human tumour suppr	1970	15.4	1.6	18	1	ADO48762	Human neurotrophin
C1898	15.4	1.6	17	1	AD150723	Human tumour suppr	1971	15.4	1.6	18	1	ADO48745	Human neurotrophin
C1899	15.4	1.6	17	1	AD152180	Human tumour suppr	1972	15.4	1.6	18	1	ADO56946	Human CARK/FRGT pr
C1900	15.4	1.6	17	1	AD150051	Human tumour suppr	1973	15.4	1.6	18	1	ADO56480	Human cyclin-depen
C1901	15.4	1.6	17	1	AD151643	Human tumour suppr	1974	15.4	1.6	18	1	ADO57017	Human CARK/FRGT pr
C1902	15.4	1.6	17	1	ACC52610	Human tumour suppr	1975	15.4	1.6	18	1	ADO08750	Extend primer 87 u
C1903	15.4	1.6	17	1	ACC51497	Human tumour suppr	1976	15.4	1.6	18	1	ADO78196	PCR primer used to
1904	15.4	1.6	17	1	ACC54006	Human tumour suppr	1977	15.4	1.6	19	1	AAH39033	SNP specific upper
C1905	15.4	1.6	17	1	ACC53324	Human tumour suppr	1978	15.4	1.6	19	1	AAF91124	Human multi drug r
1906	15.4	1.6	17	1	ACC54016	Human tumour suppr	1979	15.4	1.6	19	1	AAF91126	Human multi drug r
C1907	15.4	1.6	17	1	ACC51566	Human tumour suppr	1980	15.4	1.6	19	1	ACF62694	Cancer based on Cy
1908	15.4	1.6	17	1	ACC52881	Human tumour suppr	1981	15.4	1.6	19	1	ACF62695	Cancer based on Cy
C1909	15.4	1.6	17	1	ACC53359	Human tumour suppr	1982	15.4	1.6	19	1	ADB21365	MRP1 based cancer
1910	15.4	1.6	17	1	ACC54020	Human tumour suppr	1983	15.4	1.6	19	1	ADB21366	MRP1 based cancer
1911	15.4	1.6	17	1	ADL49918	Human PKR substrat	1984	15.4	1.6	19	1	ADB88454	Human UGT1A1 varia
1912	15.4	1.6	17	1	ADL49916	Human PKR substrat	1985	15.4	1.6	19	1	ADB88455	Human UGT1A1 varia
1913	15.4	1.6	17	1	ADL49966	Human PKR substrat	1986	15.4	1.6	19	1	ADB97438	Human MDRI variant
1914	15.4	1.6	17	1	ADL50193	Human PKR substrat	1987	15.4	1.6	19	1	ADB97437	Human MDRI variant
1915	15.4	1.6	17	1	ADL50202	Human PKR substrat	1988	15.4	1.6	19	1	ADB92629	Human MDRI variant
1916	15.4	1.6	17	1	ADL50201	Human PKR substrat	1989	15.4	1.6	19	1	ADB92628	Human MDRI variant
1917	15.4	1.6	17	1	ADL49951	Human PKR substrat	1990	15.4	1.6	19	1	ADN02393	PCR primer 2 used
1918	15.4	1.6	17	1	ADL50417	Human PKR substrat	1991	15.4	1.6	51	1	AAI78387	Human silent SNP c
1919	15.4	1.6	17	1	ADL49931	Human PKR substrat	1992	15.2	1.5	18	1	ADO56498	Human cyclin-depen
1920	15.4	1.6	17	1	ADL50198	Human PKR substrat	1993	15.2	1.5	41	1	ABZ57114	Human KIAA0608 pro
1921	15.4	1.6	17	1	ADL50418	Human PKR substrat	1994	15.2	1.5	51	1	AAI79765	Human nonconservat
1922	15.4	1.6	17	1	ADL49930	Human PKR substrat	1995	15.2	1.5	51	1	AAI79764	Human nonconservat
1923	15.4	1.6	17	1	ADL50731	Human PKR substrat	1996	15.2	1.5	51	1	AAI27794	Human SNP oligonuc
1924	15.4	1.6	17	1	ADL49907	Human PKR substrat	1997	15.2	1.5	51	1	AAI77360	Human silent SNP c
1925	15.4	1.6	17	1	ADL50203	Human PKR substrat	1998	15.2	1.5	51	1	AAI79697	Human ICAM hammer
1926	15.4	1.6	17	1	ADL50749	Human PKR substrat	1999	15	1.5	15	1	AAI52114	Human conservative
1927	15.4	1.6	17	1	ADL49908	Human PKR substrat	2000	15	1.5	15	1	AAI30969	Tag sequence of a
1928	15.4	1.6	17	1	ADL50213	Human PKR substrat	2001	15	1.5	15	1	AAF98058	Human IGERA allele
1929	15.4	1.6	17	1	ADL50738	Human PKR substrat	2002	15	1.5	15	1	AAF97989	Human IGERA allele
1930	15.4	1.6	17	1	ADL50212	Human PKR substrat	2003	15	1.5	15	1	AAF98057	Human IGERA allele
1931	15.4	1.6	17	1	ADL49917	Human PKR substrat	2004	15	1.5	15	1	AAF69438	Human IL4Ra1pha ge

2005	15	1.5	15	1	ABK31922	Human colon cancer
C2006	15	1.5	15	1	ADBI4250	Optineurin promote
C2007	15	1.5	15	1	ADBI4031	Optineurin promote
2008	15	1.5	15	1	ACC84465	NTP peptide encodi
C2009	15	1.5	16	1	ADG63090	Human tandem tag D
C2010	15	1.5	16	1	ADH59602	Non-nucleotide pro
2011	15	1.5	16	1	ADH59614	Non-nucleotide pro
C2012	15	1.5	16	1	ADQ30388	Human VRI exon 1d
C2013	15	1.5	17	1	AAA22972	Integrin subunit b
C2014	15	1.5	17	1	AAA87041	Probe to Alu2 huma
2015	15	1.5	17	1	ADB04312	Human MDZ7 scannin
2016	15	1.5	17	1	ADB04280	Human MDZ7 scannin
C2017	15	1.5	17	1	ADB04285	Human MDZ7 scannin
2018	15	1.5	17	1	ADB260369	Human K-Ras DNAzym
2019	15	1.5	17	1	ABZ60598	Human K-Ras DNAzym
C2020	15	1.5	17	1	ACC65847	Murine oligonucleo
C2021	15	1.5	17	1	ACA62876	Repeated nucleic a
2022	15	1.5	17	1	ADBA3123	Tumour suppression
C2023	15	1.5	17	1	ADJ48985	Human tumour suppr
C2024	15	1.5	17	1	ADJ48613	Human tumour suppr
C2025	15	1.5	17	1	ADP45893	Extend primer 85 u
2026	15	1.5	18	1	AAV62683	Tango-63 primer t6
2027	15	1.5	18	1	AAH47613	Human Her-3 mRNA 1
2028	15	1.5	18	1	AAH33563	PCR primer 1 used
C2029	15	1.5	18	1	ADBE43701	Human KMSL1 PCR pr
2030	15	1.5	18	1	ADBE43701	Human Tango-63 map
2031	15	1.5	18	1	ADBI1281	Tango-63 chromosom
C2032	15	1.5	18	1	ADBI1281	Human neurodegener
C2033	15	1.5	18	1	ADH54179	Human neurodegener
2034	15	1.5	18	1	ADH54179	Human neurodegener
C2035	15	1.5	18	1	ADH54179	Human neurodegener
C2036	15	1.5	18	1	ADH54179	Human neurodegener
2037	15	1.5	18	1	ADH54179	Human neurodegener
2038	15	1.5	18	1	ADH54179	Human neurodegener
C2039	15	1.5	18	1	ADH54179	Human neurodegener
C2040	15	1.5	18	1	ADH54179	Human neurodegener
C2041	15	1.5	18	1	ADH54179	Human neurodegener
C2042	15	1.5	18	1	ADH54179	Human neurodegener
C2043	15	1.5	18	1	ADH54179	Human neurodegener
C2044	15	1.5	18	1	ADH54179	Human neurodegener
2045	15	1.5	18	1	ADH54179	Human neurodegener
C2046	15	1.5	18	1	ADH54179	Human neurodegener
C2047	15	1.5	18	1	ADH54179	Human neurodegener
C2048	15	1.5	18	1	ADH54179	Human neurodegener
2049	15	1.5	18	1	ADH54179	Human neurodegener
C2050	15	1.5	18	1	ADH54179	Human neurodegener
2051	15	1.5	18	1	ADH54179	Human neurodegener
C2052	15	1.5	18	1	ADH54179	Human neurodegener
C2053	15	1.5	18	1	ADH54179	Human neurodegener
2054	15	1.5	18	1	ADH54179	Human neurodegener
C2055	15	1.5	18	1	ADH54179	Human neurodegener
C2056	15	1.5	18	1	ADH54179	Human neurodegener
2057	15	1.5	18	1	ADH54179	Human neurodegener
C2058	15	1.5	18	1	ADH54179	Human neurodegener
C2059	15	1.5	18	1	ADH54179	Human neurodegener
C2060	15	1.5	18	1	ADH54179	Human neurodegener
C2061	15	1.5	18	1	ADH54179	Human neurodegener
2062	15	1.5	18	1	ADH54179	Human neurodegener
C2063	15	1.5	18	1	ADH54179	Human neurodegener
2064	15	1.5	18	1	ADH54179	Human neurodegener
C2065	15	1.5	18	1	ADH54179	Human neurodegener
2066	15	1.5	18	1	ADH54179	Human neurodegener
2067	15	1.5	18	1	ADH54179	Human neurodegener
2068	15	1.5	18	1	ADH54179	Human neurodegener
2069	15	1.5	18	1	ADH54179	Human neurodegener
C2070	15	1.5	18	1	ADH54179	Human neurodegener
2071	15	1.5	18	1	ADH54179	Human neurodegener
C2072	15	1.5	18	1	ADH54179	Human neurodegener
2073	15	1.5	18	1	ADH54179	Human neurodegener
C2074	15	1.5	18	1	ADH54179	Human neurodegener
2075	15	1.5	18	1	ADH54179	Human neurodegener
2076	15	1.5	18	1	ADH54179	Human neurodegener
2077	15	1.5	18	1	ADH54179	Human neurodegener

c2151	14.6	1.5	51	1	AAH89507	Human coding sequ	2224	14.4	1.5	17	1	ADB43380	Tumour suppression
2152	14.6	1.5	51	1	AAI76153	Human silent SNP c	2225	14.4	1.5	17	1	ADB40001	Tumour suppression
2153	14.4	1.5	16	1	AAQ95283	Simple tandem repe	c2226	14.4	1.5	17	1	ADB42612	Tumour suppression
c2154	14.4	1.5	16	1	AAJ122238	Human CYP450 2C19	2227	14.4	1.5	17	1	ADB42824	Tumour suppression
c2155	14.4	1.5	16	1	ADD28838	Escherichia coli 0	2228	14.4	1.5	17	1	ADB42825	Tumour suppression
2156	14.4	1.5	16	1	ADD28839	Escherichia coli 0	c2229	14.4	1.5	17	1	ADB42928	Tumour suppression
c2157	14.4	1.5	16	1	ADD28836	Escherichia coli 0	c2230	14.4	1.5	17	1	ADB44164	Tumour suppression
2158	14.4	1.5	16	1	ADD28837	Escherichia coli 0	2231	14.4	1.5	17	1	ADB41301	Tumour suppression
2159	14.4	1.5	16	1	ADD28837	Escherichia coli 0	2232	14.4	1.5	17	1	ADB40212	Tumour suppression
c2160	14.4	1.5	16	1	ADBI4208	Optineurin promote	2233	14.4	1.5	17	1	ADB44035	Tumour suppression
c2161	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2234	14.4	1.5	17	1	ADB456739	Tumour suppression
c2162	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2235	14.4	1.5	17	1	ADB456739	Tumour suppression
c2163	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2236	14.4	1.5	17	1	ADB456739	Tumour suppression
c2164	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2237	14.4	1.5	17	1	ADB456739	Tumour suppression
2165	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2238	14.4	1.5	17	1	ADB456739	Tumour suppression
c2166	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2239	14.4	1.5	17	1	ADB456739	Tumour suppression
c2167	14.4	1.5	16	1	ADBI4208	Optineurin promote	2240	14.4	1.5	17	1	ADB456739	Tumour suppression
c2168	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2241	14.4	1.5	17	1	ADB456739	Tumour suppression
c2169	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2242	14.4	1.5	17	1	ADB456739	Tumour suppression
2170	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2243	14.4	1.5	17	1	ADB456739	Tumour suppression
c2171	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2244	14.4	1.5	17	1	ADB456739	Tumour suppression
2172	14.4	1.5	16	1	ADBI4208	Optineurin promote	2245	14.4	1.5	17	1	ADB456739	Tumour suppression
2173	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2246	14.4	1.5	17	1	ADB456739	Tumour suppression
2174	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2247	14.4	1.5	17	1	ADB456739	Tumour suppression
2175	14.4	1.5	16	1	ADBI4208	Optineurin promote	2248	14.4	1.5	17	1	ADB456739	Tumour suppression
c2176	14.4	1.5	16	1	ADBI4208	Optineurin promote	2249	14.4	1.5	17	1	ADB456739	Tumour suppression
c2177	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2250	14.4	1.5	17	1	ADB456739	Tumour suppression
c2178	14.4	1.5	16	1	ADBI4208	Optineurin promote	2251	14.4	1.5	17	1	ADB456739	Tumour suppression
2179	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2252	14.4	1.5	17	1	ADB456739	Tumour suppression
2180	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2253	14.4	1.5	17	1	ADB456739	Tumour suppression
2181	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2254	14.4	1.5	17	1	ADB456739	Tumour suppression
2182	14.4	1.5	16	1	ADBI4208	Optineurin promote	2255	14.4	1.5	17	1	ADB456739	Tumour suppression
2183	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2256	14.4	1.5	17	1	ADB456739	Tumour suppression
2184	14.4	1.5	16	1	ADBI4208	Optineurin promote	2257	14.4	1.5	17	1	ADB456739	Tumour suppression
2185	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2258	14.4	1.5	17	1	ADB456739	Tumour suppression
2186	14.4	1.5	16	1	ADBI4208	Optineurin promote	2259	14.4	1.5	17	1	ADB456739	Tumour suppression
2187	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2260	14.4	1.5	17	1	ADB456739	Tumour suppression
c2188	14.4	1.5	16	1	ADBI4208	Optineurin promote	2261	14.4	1.5	17	1	ADB456739	Tumour suppression
2189	14.4	1.5	16	1	ADBI4208	Optineurin promote	2262	14.4	1.5	17	1	ADB456739	Tumour suppression
2190	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2263	14.4	1.5	17	1	ADB456739	Tumour suppression
c2191	14.4	1.5	16	1	ADBI4208	Optineurin promote	2264	14.4	1.5	17	1	ADB456739	Tumour suppression
c2192	14.4	1.5	16	1	ADBI4208	Optineurin promote	2265	14.4	1.5	17	1	ADB456739	Tumour suppression
2193	14.4	1.5	16	1	ADBI4208	Optineurin promote	2266	14.4	1.5	17	1	ADB456739	Tumour suppression
2194	14.4	1.5	16	1	ADBI4208	Optineurin promote	2267	14.4	1.5	17	1	ADB456739	Tumour suppression
2195	14.4	1.5	16	1	ADBI4208	Optineurin promote	2268	14.4	1.5	17	1	ADB456739	Tumour suppression
c2196	14.4	1.5	16	1	ADBI4208	Optineurin promote	2269	14.4	1.5	17	1	ADB456739	Tumour suppression
c2197	14.4	1.5	16	1	ADBI4208	Optineurin promote	2270	14.4	1.5	17	1	ADB456739	Tumour suppression
2198	14.4	1.5	16	1	ADBI4208	Optineurin promote	2271	14.4	1.5	17	1	ADB456739	Tumour suppression
2199	14.4	1.5	16	1	ADBI4208	Optineurin promote	2272	14.4	1.5	17	1	ADB456739	Tumour suppression
c2200	14.4	1.5	16	1	ADBI4208	Optineurin promote	2273	14.4	1.5	17	1	ADB456739	Tumour suppression
c2201	14.4	1.5	16	1	ADBI4208	Optineurin promote	2274	14.4	1.5	17	1	ADB456739	Tumour suppression
2202	14.4	1.5	16	1	ADBI4208	Optineurin promote	2275	14.4	1.5	17	1	ADB456739	Tumour suppression
2203	14.4	1.5	16	1	ADBI4208	Optineurin promote	2276	14.4	1.5	17	1	ADB456739	Tumour suppression
c2204	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2277	14.4	1.5	17	1	ADB456739	Tumour suppression
2205	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2278	14.4	1.5	17	1	ADB456739	Tumour suppression
2206	14.4	1.5	16	1	ADBI4208	Optineurin promote	2279	14.4	1.5	17	1	ADB456739	Tumour suppression
c2207	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2280	14.4	1.5	17	1	ADB456739	Tumour suppression
2208	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2281	14.4	1.5	17	1	ADB456739	Tumour suppression
2209	14.4	1.5	16	1	ADBI4208	Optineurin promote	2282	14.4	1.5	17	1	ADB456739	Tumour suppression
2210	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2283	14.4	1.5	17	1	ADB456739	Tumour suppression
2211	14.4	1.5	16	1	ADBI4208	Optineurin promote	2284	14.4	1.5	17	1	ADB456739	Tumour suppression
2212	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2285	14.4	1.5	17	1	ADB456739	Tumour suppression
2213	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2286	14.4	1.5	17	1	ADB456739	Tumour suppression
2214	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2287	14.4	1.5	17	1	ADB456739	Tumour suppression
2215	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2288	14.4	1.5	17	1	ADB456739	Tumour suppression
2216	14.4	1.5	16	1	ADBI4208	Optineurin promote	2289	14.4	1.5	17	1	ADB456739	Tumour suppression
2217	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2290	14.4	1.5	17	1	ADB456739	Tumour suppression
2218	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2291	14.4	1.5	17	1	ADB456739	Tumour suppression
2219	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2292	14.4	1.5	17	1	ADB456739	Tumour suppression
2220	14.4	1.5	16	1	ADBI4208	Optineurin promote	2293	14.4	1.5	17	1	ADB456739	Tumour suppression
c2221	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2294	14.4	1.5	17	1	ADB456739	Tumour suppression
c2222	14.4	1.5	16	1	ADBI4208	Optineurin promote	c2295	14.4	1.5	17	1	ADB456739	Tumour suppression
c2223	14.4	1.5	16	1	ADBI4208	Optineurin promote	2296	14.4	1.5	17	1	ADB456739	Tumour suppression

C2297	14.4	1.5	18	1	AD598409	Sequence tagged bi	2370	13.8	1.4	17	1	AAA22730	Integrin subunit b
C2298	14.4	1.5	18	1	ACA58053	Human familial btp	2371	13.8	1.4	17	1	AAA22842	Integrin subunit b
2299	14.4	1.5	18	1	ADM92832	SNP-containing car	2372	13.8	1.4	17	1	AAA22854	Integrin subunit b
2300	14.4	1.5	18	1	ADN06584	Human FIAP related	C2373	13.8	1.4	17	1	AAA22971	Integrin subunit b
C2301	14.4	1.5	18	1	AD056531	Human cyclin-depen	2374	13.8	1.4	17	1	AAA22827	Integrin subunit b
C2302	14.4	1.5	18	1	AD056556	Human cyclin-depen	2375	13.8	1.4	17	1	AAA22822	Integrin subunit b
2303	14.4	1.5	18	1	AD056556	Human cyclin-depen	C2376	13.8	1.4	17	1	AAA22964	Integrin subunit b
2304	14.4	1.5	18	1	ADP45830	Extend primer 22 u	C2377	13.8	1.4	17	1	AAA22974	Integrin subunit b
2305	14.2	1.5	36	1	AAH91142	Human inflammatory	2378	13.8	1.4	17	1	AAA22731	Integrin subunit b
C2306	14	1.4	14	1	AAV39559	Microsatellite ana	2379	13.8	1.4	17	1	AAA22738	Integrin subunit b
2307	14	1.4	14	1	AAA23392	Integrin subunit b	2380	13.8	1.4	17	1	AAA22754	Integrin subunit b
2308	14	1.4	14	1	AAA23382	Integrin subunit b	2381	13.8	1.4	17	1	AAA22732	Integrin subunit b
C2309	14	1.4	14	1	AAA23406	Integrin subunit b	2382	13.8	1.4	17	1	AAA22823	Integrin subunit b
2310	14	1.4	14	1	AAA23388	Integrin subunit b	2383	13.8	1.4	17	1	AAA22843	Integrin subunit b
2311	14	1.4	14	1	ACA62884	Repeated nucleic a	2384	13.8	1.4	17	1	AAA22824	Integrin subunit b
2312	14	1.4	14	1	ADH70473	Human Vbeta gene r	2385	13.8	1.4	17	1	AAA22824	Integrin subunit b
2313	14	1.4	15	1	AA752086	Human ICM hammerh	2386	13.8	1.4	17	1	AAV91399	Integrin subunit b
2314	14	1.4	15	1	AA752112	Human ICM hammerh	2387	13.8	1.4	17	1	AA736739	Integrin subunit b
2315	14	1.4	15	1	ADH70501	Human Vbeta gene r	2388	13.8	1.4	17	1	AAA25450	Integrin subunit b
2316	14	1.4	15	1	ADQ30131	Murine VRI exon id	2389	13.8	1.4	17	1	AAA25600	Integrin subunit b
2317	14	1.4	15	1	ADQ30131	Optineurin promote	2390	13.8	1.4	17	1	AAA25178	Integrin subunit b
2318	14	1.4	16	1	ADH70756	Human Vbeta gene r	2391	13.8	1.4	17	1	AAA25603	Integrin subunit b
2319	14	1.4	16	1	AA793352	Primer #2 for D105	2392	13.8	1.4	17	1	AAA25444	Integrin subunit b
2320	14	1.4	17	1	AA793352	Integrin subunit b	2393	13.8	1.4	17	1	AAA25445	Integrin subunit b
2321	14	1.4	17	1	AAA22845	Integrin subunit b	2394	13.8	1.4	17	1	AAA98232	Integrin subunit b
C2322	14	1.4	17	1	AAA22806	Integrin subunit b	2395	13.8	1.4	17	1	AAA50197	Integrin subunit b
2323	14	1.4	17	1	AAA22967	Integrin subunit b	2396	13.8	1.4	17	1	AA705509	Integrin subunit b
C2324	14	1.4	17	1	AAA22973	Integrin subunit b	2397	13.8	1.4	17	1	AA705509	Integrin subunit b
2325	14	1.4	17	1	AAA22846	Integrin subunit b	2398	13.8	1.4	17	1	AA705509	Integrin subunit b
2326	14	1.4	17	1	AA705509	Integrin subunit b	2399	13.8	1.4	17	1	AA705509	Integrin subunit b
2327	14	1.4	17	1	AA705509	Integrin subunit b	2400	13.8	1.4	17	1	AA705509	Integrin subunit b
2328	14	1.4	17	1	AB736209	Hammerhead ribozym	2401	13.8	1.4	17	1	ABK00892	Integrin subunit b
2329	14	1.4	17	1	AB736209	Hammerhead ribozym	2402	13.8	1.4	17	1	ABK00891	Integrin subunit b
2330	14	1.4	17	1	ADB04202	Human MD27 scannin	2403	13.8	1.4	17	1	ABK00089	Integrin subunit b
2331	14	1.4	17	1	ADB04204	Human MD27 scannin	C2404	13.8	1.4	17	1	ABK00237	Integrin subunit b
2332	14	1.4	17	1	ADB04203	Human MD27 scannin	2405	13.8	1.4	17	1	ABK00237	Integrin subunit b
2333	14	1.4	17	1	ADB04279	Human MD27 scannin	2406	13.8	1.4	17	1	ABA82250	Integrin subunit b
2334	14	1.4	17	1	ADB04286	Human MD27 scannin	C2407	13.8	1.4	17	1	ABA82250	Integrin subunit b
2335	14	1.4	17	1	ADB04311	Human MD27 scannin	C2408	13.8	1.4	17	1	ABNO0871	Integrin subunit b
2336	14	1.4	17	1	ADB04311	Human MD27 scannin	C2409	13.8	1.4	17	1	ABNO09432	Integrin subunit b
2337	14	1.4	17	1	ADB04311	Human MD27 scannin	C2410	13.8	1.4	17	1	ABNO09435	Integrin subunit b
2338	14	1.4	17	1	ADB04311	Human MD27 scannin	C2411	13.8	1.4	17	1	ABNO09435	Integrin subunit b
2339	14	1.4	17	1	ADB04311	Human MD27 scannin	C2412	13.8	1.4	17	1	ABNO09435	Integrin subunit b
2340	14	1.4	17	1	ADB04311	Human MD27 scannin	C2413	13.8	1.4	17	1	ABNO09435	Integrin subunit b
2341	14	1.4	17	1	ADB04311	Human MD27 scannin	2414	13.8	1.4	17	1	ABK23302	Integrin subunit b
2342	14	1.4	17	1	ADL48718	Human tumour suppress	C2415	13.8	1.4	17	1	ABK23302	Integrin subunit b
2343	14	1.4	17	1	ADL49435	Human tumour suppress	C2416	13.8	1.4	17	1	ABK23302	Integrin subunit b
2344	14	1.4	17	1	ADL49461	Human PKR substrat	C2417	13.8	1.4	17	1	ABK56068	Integrin subunit b
2345	14	1.4	17	1	ADL49461	Human PKR substrat	C2418	13.8	1.4	17	1	ACN01141	Integrin subunit b
2346	14	1.4	17	1	ADL49461	Human PKR substrat	2419	13.8	1.4	17	1	ACN14418	Integrin subunit b
C2347	14	1.4	17	1	ADP08721	Extend primer 58 u	C2419	13.8	1.4	17	1	ACN08942	Integrin subunit b
C2348	14	1.4	17	1	ADP08721	Extend primer 58 u	2420	13.8	1.4	17	1	ACN08942	Integrin subunit b
C2349	14	1.4	17	1	ADP08721	Extend primer 58 u	C2421	13.8	1.4	17	1	ACN08942	Integrin subunit b
C2350	14	1.4	17	1	ADP08721	Extend primer 58 u	C2422	13.8	1.4	17	1	ACN08942	Integrin subunit b
C2351	14	1.4	17	1	ADP08721	Extend primer 58 u	C2423	13.8	1.4	17	1	ACN08942	Integrin subunit b
C2352	14	1.4	17	1	ADP08721	Extend primer 58 u	C2424	13.8	1.4	17	1	ACN08942	Integrin subunit b
C2353	14	1.4	17	1	ADP08721	Extend primer 58 u	C2425	13.8	1.4	17	1	ACN08942	Integrin subunit b
C2354	14	1.4	17	1	ADP08721	Extend primer 58 u	C2426	13.8	1.4	17	1	ACN08942	Integrin subunit b
C2355	14	1.4	17	1	ADP08721	Extend primer 58 u	C2427	13.8	1.4	17	1	ACN08942	Integrin subunit b
C2356	14	1.4	17	1	ADP08721	Extend primer 58 u	C2428	13.8	1.4	17	1	ACN08942	Integrin subunit b
C2357	14	1.4	17	1	ADP08721	Extend primer 58 u	2429	13.8	1.4	17	1	ACN08942	Integrin subunit b
C2358	14	1.4	17	1	ADP08721	Extend primer 58 u	2430	13.8	1.4	17	1	ACN08942	Integrin subunit b
C2359	14	1.4	17	1	ADP08721	Extend primer 58 u	2431	13.8	1.4	17	1	ACN08942	Integrin subunit b
C2360	14	1.4	17	1	ADP08721	Extend primer 58 u	2432	13.8	1.4	17	1	ACN08942	Integrin subunit b
C2361	14	1.4	17	1	ADP08721	Extend primer 58 u	2433	13.8	1.4	17	1	ACN08942	Integrin subunit b
C2362	14	1.4	17	1	ADP08721	Extend primer 58 u	2434	13.8	1.4	17	1	ACN08942	Integrin subunit b
C2363	14	1.4	17	1	ADP08721	Extend primer 58 u	2435	13.8	1.4	17	1	ACN08942	Integrin subunit b
C2364	14	1.4	17	1	ADP08721	Extend primer 58 u	2436	13.8	1.4	17	1	ACN08942	Integrin subunit b
C2365	14	1.4	17	1	ADP08721	Extend primer 58 u	2437	13.8	1.4	17	1	ACN08942	Integrin subunit b
C2366	14	1.4	17	1	ADP08721	Extend primer 58 u	2438	13.8	1.4	17	1	ACN08942	Integrin subunit b
C2367	14	1.4	17	1	ADP08721	Extend primer 58 u	2439	13.8	1.4	17	1	ACN08942	Integrin subunit b
C2368	14	1.4	17	1	ADP08721	Extend primer 58 u	2440	13.8	1.4	17	1	ACN08942	Integrin subunit b
2369	14	1.4	17	1	ADP08721	Extend primer 58 u	2441	13.8	1.4	17	1	ACN08942	Integrin subunit b
2370	14	1.4	17	1	ADP08721	Extend primer 58 u	2442	13.8	1.4	17	1	ACN08942	Integrin subunit b

2443	13.8	1.4	17	1	ABT34859	Tumour suppression	2516	13.8	1.4	17	1	ACC66564	Murine oligonucleo
C2444	13.8	1.4	17	1	ABT35713	Tumour suppression	2517	13.8	1.4	17	1	ACC64076	Murine oligonucleo
C2445	13.8	1.4	17	1	ABT36965	Tumour suppression	2518	13.8	1.4	17	1	ACC64870	Murine oligonucleo
C2446	13.8	1.4	17	1	ABT39805	Tumour suppression	2519	13.8	1.4	17	1	ACA90066	Murine oligonucleo
C2447	13.8	1.4	17	1	ABT39426	Tumour suppression	2520	13.8	1.4	17	1	AAD56441	Cardiovascular dis
C2448	13.8	1.4	17	1	ABT39821	Tumour suppression	2521	13.8	1.4	17	1	AAD56448	2'-F-ANA antisense
C2449	13.8	1.4	17	1	ABT34652	Tumour suppression	2522	13.8	1.4	17	1	AAD56449	2'-F-ANA antisense
C2450	13.8	1.4	17	1	ABT34713	Tumour suppression	2523	13.8	1.4	17	1	AAD56447	2'-F-ANA antisense
C2451	13.8	1.4	17	1	ABT36681	Tumour suppression	2524	13.8	1.4	17	1	AAD56450	2'-F-ANA antisense
C2452	13.8	1.4	17	1	ABT38340	Tumour suppression	2525	13.8	1.4	17	1	ADA50284	Human PCR primer 8
C2453	13.8	1.4	17	1	ABT38870	Tumour suppression	2526	13.8	1.4	17	1	ADB98583	Sequence tagged si
C2454	13.8	1.4	17	1	ABT38923	Tumour suppression	2527	13.8	1.4	17	1	ADB98308	Sequence tagged si
C2455	13.8	1.4	17	1	ABT36025	Tumour suppression	2528	13.8	1.4	17	1	ADB33980	Tumour suppression
C2456	13.8	1.4	17	1	ABT38827	Tumour suppression	2529	13.8	1.4	17	1	ADB40686	Tumour suppression
C2457	13.8	1.4	17	1	ABT40033	Tumour suppression	2530	13.8	1.4	17	1	ADB41889	Tumour suppression
C2458	13.8	1.4	17	1	ABT35129	Tumour suppression	2531	13.8	1.4	17	1	ADB41999	Tumour suppression
C2459	13.8	1.4	17	1	ABT35655	Tumour suppression	2532	13.8	1.4	17	1	ADB42848	Tumour suppression
C2460	13.8	1.4	17	1	ABT37057	Tumour suppression	2533	13.8	1.4	17	1	ADB42904	Tumour suppression
C2461	13.8	1.4	17	1	ABT38389	Tumour suppression	2534	13.8	1.4	17	1	ADB33762	Tumour suppression
C2462	13.8	1.4	17	1	ABT39853	Tumour suppression	2535	13.8	1.4	17	1	ADB41881	Tumour suppression
C2463	13.8	1.4	17	1	ABT34445	Tumour suppression	2536	13.8	1.4	17	1	ADB42307	Tumour suppression
C2464	13.8	1.4	17	1	ABT34807	Tumour suppression	2537	13.8	1.4	17	1	ADB42587	Tumour suppression
C2465	13.8	1.4	17	1	ABT36651	Tumour suppression	2538	13.8	1.4	17	1	ADB40636	Tumour suppression
C2466	13.8	1.4	17	1	ABT36653	Tumour suppression	2539	13.8	1.4	17	1	ADB42220	Tumour suppression
C2467	13.8	1.4	17	1	ABT37037	Tumour suppression	2540	13.8	1.4	17	1	ADB42668	Tumour suppression
C2468	13.8	1.4	17	1	ABT38237	Tumour suppression	2541	13.8	1.4	17	1	ADB42732	Tumour suppression
C2469	13.8	1.4	17	1	ABT40087	Tumour suppression	2542	13.8	1.4	17	1	ADB41555	Tumour suppression
C2470	13.8	1.4	17	1	ABT35675	Tumour suppression	2543	13.8	1.4	17	1	ADB41871	Tumour suppression
C2471	13.8	1.4	17	1	ABT37579	Tumour suppression	2544	13.8	1.4	17	1	ADB42115	Tumour suppression
C2472	13.8	1.4	17	1	ABT37770	Tumour suppression	2545	13.8	1.4	17	1	ADB43876	Tumour suppression
C2473	13.8	1.4	17	1	ABT40151	Tumour suppression	2546	13.8	1.4	17	1	ADB41239	Tumour suppression
C2474	13.8	1.4	17	1	ABT34950	Tumour suppression	2547	13.8	1.4	17	1	ADB40006	Tumour suppression
C2475	13.8	1.4	17	1	ABT36577	Tumour suppression	2548	13.8	1.4	17	1	ADB40041	Tumour suppression
C2476	13.8	1.4	17	1	ABT37081	Tumour suppression	2549	13.8	1.4	17	1	ADB40132	Tumour suppression
C2477	13.8	1.4	17	1	ABT37662	Tumour suppression	2550	13.8	1.4	17	1	ADB42575	Tumour suppression
C2478	13.8	1.4	17	1	ACH06516	NEPB sub-unit modu	2551	13.8	1.4	17	1	ADB42349	Tumour suppression
C2479	13.8	1.4	17	1	ADB04310	Human MD27 scanlin	2552	13.8	1.4	17	1	ADB41338	Tumour suppression
C2480	13.8	1.4	17	1	ADB04414	Human MD27 scanlin	2553	13.8	1.4	17	1	ADB41765	Tumour suppression
C2481	13.8	1.4	17	1	ADB04387	Human MD27 scanlin	2554	13.8	1.4	17	1	ADB43807	Tumour suppression
C2482	13.8	1.4	17	1	ADB04390	Human MD27 scanlin	2555	13.8	1.4	17	1	ADB40879	Tumour suppression
C2483	13.8	1.4	17	1	ADB04420	Human MD27 scanlin	2556	13.8	1.4	17	1	ADB41273	Tumour suppression
C2484	13.8	1.4	17	1	ADB04486	Human MD27 scanlin	2557	13.8	1.4	17	1	ADB43997	Tumour suppression
C2485	13.8	1.4	17	1	ADB04276	Human MD27 scanlin	2558	13.8	1.4	17	1	ADB40673	Tumour suppression
C2486	13.8	1.4	17	1	ADB04320	Human MD27 scanlin	2559	13.8	1.4	17	1	ADB43325	Tumour suppression
C2487	13.8	1.4	17	1	ADB04388	Human MD27 scanlin	2560	13.8	1.4	17	1	ADB44153	Tumour suppression
C2488	13.8	1.4	17	1	ADB04413	Human MD27 scanlin	2561	13.8	1.4	17	1	ADB40382	Tumour suppression
C2489	13.8	1.4	17	1	ADB04421	Human MD27 scanlin	2562	13.8	1.4	17	1	ADB41878	Tumour suppression
C2490	13.8	1.4	17	1	ADB04471	Human MD27 scanlin	2563	13.8	1.4	17	1	ADB41780	Tumour suppression
C2491	13.8	1.4	17	1	ADB04205	Human MD27 scanlin	2564	13.8	1.4	17	1	ADB42420	Tumour suppression
C2492	13.8	1.4	17	1	ADB04377	Human MD27 scanlin	2565	13.8	1.4	17	1	ADB43345	Tumour suppression
C2493	13.8	1.4	17	1	ADB04386	Human MD27 scanlin	2566	13.8	1.4	17	1	ADB43345	Tumour suppression
C2494	13.8	1.4	17	1	ADB04435	Human MD27 scanlin	2567	13.8	1.4	17	1	ADB43838	Tumour suppression
C2495	13.8	1.4	17	1	ADB04466	Human MD27 scanlin	2568	13.8	1.4	17	1	ADB44927	Tumour suppression
C2496	13.8	1.4	17	1	ADB04378	Human MD27 scanlin	2569	13.8	1.4	17	1	ADB44849	Tumour suppression
C2497	13.8	1.4	17	1	ADB04481	Human MD27 scanlin	2570	13.8	1.4	17	1	ADB45873	Tumour suppression
C2498	13.8	1.4	17	1	ADB04375	Human MD27 scanlin	2571	13.8	1.4	17	1	ADB45091	Tumour suppression
C2499	13.8	1.4	17	1	ADB04467	Human MD27 scanlin	2572	13.8	1.4	17	1	ADB45070	Tumour suppression
C2500	13.8	1.4	17	1	ADB04377	Human MD27 scanlin	2573	13.8	1.4	17	1	ADB45775	Tumour suppression
C2501	13.8	1.4	17	1	ADB04321	Human MD27 scanlin	2574	13.8	1.4	17	1	ADB45432	Tumour suppression
C2502	13.8	1.4	17	1	ADB04385	Human MD27 scanlin	2575	13.8	1.4	17	1	ADB44891	Tumour suppression
C2503	13.8	1.4	17	1	ADB04395	Human MD27 scanlin	2576	13.8	1.4	17	1	ADB45471	Tumour suppression
C2504	13.8	1.4	17	1	ADB04482	Human MD27 scanlin	2577	13.8	1.4	17	1	ADB45688	Tumour suppression
C2505	13.8	1.4	17	1	ADB04485	Human MD27 scanlin	2578	13.8	1.4	17	1	ADB44480	Tumour suppression
C2506	13.8	1.4	17	1	ADB04378	Human MD27 scanlin	2579	13.8	1.4	17	1	ADB44569	Tumour suppression
C2507	13.8	1.4	17	1	ADB04449	Human MD27 scanlin	2580	13.8	1.4	17	1	ADB44573	Tumour suppression
C2508	13.8	1.4	17	1	ADB04480	Human MD27 scanlin	2581	13.8	1.4	17	1	ADB45020	Tumour suppression
C2509	13.8	1.4	17	1	ACC45610	Human HBM STS mark	2582	13.8	1.4	17	1	ADB45575	Tumour suppression
C2510	13.8	1.4	17	1	ACC45885	Human HBM STS mark	2583	13.8	1.4	17	1	ADB45717	Tumour suppression
C2511	13.8	1.4	17	1	AB260820	Human K-Ras DNAzym	2584	13.8	1.4	17	1	ADE25242	Plant growth assoc
C2512	13.8	1.4	17	1	AB260569	Human K-Ras DNAzym	2585	13.8	1.4	17	1	ADE14007	Optinurin promote
C2513	13.8	1.4	17	1	ACC65127	Murine oligonucleo	2586	13.8	1.4	17	1	ADE30629	Cholesterol homos
C2514	13.8	1.4	17	1	ACC68489	Murine oligonucleo	2587	13.8	1.4	17	1	ADE30636	Cholesterol homos
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c2589	13.8	1.4	17	1	AD148550	Human tumour suppressor
c2590	13.8	1.4	17	1	AD151546	Human tumour suppressor
c2591	13.8	1.4	17	1	AD152377	Human tumour suppressor
c2592	13.8	1.4	17	1	AD151185	Human tumour suppressor
c2593	13.8	1.4	17	1	AD152079	Human tumour suppressor
c2594	13.8	1.4	17	1	AD152868	Human tumour suppressor
c2595	13.8	1.4	17	1	AD152429	Human tumour suppressor
c2596	13.8	1.4	17	1	AD152776	Human tumour suppressor
c2597	13.8	1.4	17	1	AD151234	Human tumour suppressor
c2598	13.8	1.4	17	1	AD148839	Human tumour suppressor
c2599	13.8	1.4	17	1	AD150971	Human tumour suppressor
c2600	13.8	1.4	17	1	AD151323	Human tumour suppressor
c2601	13.8	1.4	17	1	AD152101	Human tumour suppressor
c2602	13.8	1.4	17	1	AD149325	Human tumour suppressor
c2603	13.8	1.4	17	1	AD149868	Human tumour suppressor
c2604	13.8	1.4	17	1	AD148528	Human tumour suppressor
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c2606	13.8	1.4	17	1	AD148410	Human tumour suppressor
c2607	13.8	1.4	17	1	AD150528	Human tumour suppressor
c2608	13.8	1.4	17	1	AD151596	Human tumour suppressor
c2609	13.8	1.4	17	1	AD147945	Human tumour suppressor
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c2612	13.8	1.4	17	1	AD152224	Human tumour suppressor
c2613	13.8	1.4	17	1	AD152687	Human tumour suppressor
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c2617	13.8	1.4	17	1	AD151116	Human tumour suppressor
c2618	13.8	1.4	17	1	AD152878	Human tumour suppressor
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c2624	13.8	1.4	17	1	AD152615	Human tumour suppressor
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c2626	13.8	1.4	17	1	AD151579	Human tumour suppressor
c2627	13.8	1.4	17	1	AD152221	Human tumour suppressor
c2628	13.8	1.4	17	1	AD153369	Human tumour suppressor
c2629	13.8	1.4	17	1	AD153326	Human tumour suppressor
c2630	13.8	1.4	17	1	AD153360	Human tumour suppressor
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c2638	13.8	1.4	17	1	AD153360	Human tumour suppressor
c2639	13.8	1.4	17	1	AD153360	Human tumour suppressor
c2640	13.8	1.4	17	1	AD153360	Human tumour suppressor
c2641	13.8	1.4	17	1	AD153360	Human tumour suppressor
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c2659	13.8	1.4	17	1	AD153360	Human tumour suppressor
c2660	13.8	1.4	17	1	AD153360	Human tumour suppressor
c2661	13.8	1.4	17	1	AD153360	Human tumour suppressor

2662	13.8	1.4	17	1	AD150754	Human PKR substrate
2663	13.8	1.4	17	1	AD148820	Human IKK-gamma su
2664	13.8	1.4	17	1	AD149422	Human PKR substrate
2665	13.8	1.4	17	1	AD149422	Human PKR substrate
2666	13.8	1.4	17	1	AD150414	Human PKR substrate
2667	13.8	1.4	17	1	AD150736	Human PKR substrate
2668	13.8	1.4	17	1	AD150756	Human PKR substrate
2669	13.8	1.4	17	1	AD149922	Human PKR substrate
2670	13.8	1.4	17	1	AD150191	Human PKR substrate
2671	13.8	1.4	17	1	AD149403	Human PKR substrate
2672	13.8	1.4	17	1	AD149924	Human PKR substrate
2673	13.8	1.4	17	1	AD149945	Human PKR substrate
2674	13.8	1.4	17	1	AD150209	Human PKR substrate
2675	13.8	1.4	17	1	AD150222	Human PKR substrate
2676	13.8	1.4	17	1	AD150755	Human PKR substrate
2677	13.8	1.4	17	1	AD149438	Human PKR substrate
2678	13.8	1.4	17	1	AD149458	Human PKR substrate
2679	13.8	1.4	17	1	AD149462	Human PKR substrate
2680	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2681	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2682	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2683	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2684	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2685	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2686	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2687	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2688	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2689	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2690	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2691	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2692	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2693	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2694	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2695	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2696	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2697	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2698	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2699	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2700	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2701	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2702	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2703	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2704	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2705	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2706	13.8	1.4	17	1	AD150744	Human GRID mRNA su
2707	13.8	1.4	17	1	AD150744	Human GRID mRNA su

ALIGNMENTS

RESULT 1
 ID ACC84455 standard; DNA; 57 BP.
 XX
 AC ACC84455;
 XX
 DT 28-AUG-2003 (first entry)
 DE NTP peptide encoding sequence #2.
 XX
 KW Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
 KW neural thread protein; NTP; tumour; ds.
 XX
 OS Unidentified.
 XX
 FN W0200308443-A2.
 XX
 PD 30-JAN-2003.
 XX
 PF 19-JUL-2002; 2002MO-CA001105.
 XX
 PR 19-JUL-2001; 2001US-0306150P.

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PR 19-JUL-2001; 2001US-0306161P.
PR 16-NOV-2001; 2001US-0331477P.
XX
PA (NYMO-) NYMOX CORP.
XX
PI Averbach PA;
XX
DR WPI; 2003-247999/24.
DR P-PSDB; ABR63250.
XX
PT Novel neural thread protein peptide, referred as cell death peptide,
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.
XX
PS Disclosure; Page 16; 77pp; English.
XX
CC The present invention relates to a neural thread protein (NTP) peptide
CC referred to as cell death peptide. Thought to be cytostatic,
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for
CC treating a condition in a patient requiring removal or destruction of
CC cells, for treating a condition such as benign or malignant tumor,
CC inflammatory disease, autoimmune disease and infectious disease. The
CC peptide useful for treatment is derived from the amino acid sequence for
CC a pancreatic thread protein. The peptide is conjugated, linked or bound
CC to a molecule chosen from antibody or its fragment, antibody-like binding
CC molecule, where the molecule has a higher affinity for binding to a tumor
CC or other target than binding to other cells. Treatment using NTP peptides
CC can remove benign tumors with less risk and fewer of the undesirable side
CC effects of surgery. The present sequence is an NTP encoding sequence
XX
SQ Sequence 57 BP; 12 A; 20 C; 14 G; 11 T; 0 U; 0 Other;

Query Match          5.8%; Score 57; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 CCTGAGCTCAAGCAGCTCCAGCTCCTCAAGCTCCCAAGTGTGGATTACAGGCGT 410
DB 1 CCTGAGCTCAAGCAGCTCCAGCTCCTCAAGCTCCCAAGTGTGGATTACAGGCGT 57

RESULT 2
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ID ACC84456 standard; DNA; 57 BP.
XX
AC ACC84456;
XX
DT 28-AUG-2003 (first entry)
XX
DE NTP peptide encoding sequence #3.
XX
KM Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
KM neural thread protein; NTP; tumour; ds.
XX
OS Unidentified.
XX
PN WO2003008443-A2.
XX
PD 30-JAN-2003.
XX
PF 19-JUL-2002; 2002WO-CA001105.
XX
PR 19-JUL-2001; 2001US-0306150P.
PR 19-JUL-2001; 2001US-0306161P.
PR 16-NOV-2001; 2001US-0331477P.
XX
PA (NYMO-) NYMOX CORP.
XX
PI Averbach PA;
XX
DR WPI; 2003-247999/24.
DR P-PSDB; ABR63251.
XX
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PT Novel neural thread protein peptide, referred as cell death peptide,
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.
XX
PS Disclosure; Page 16; 77pp; English.
XX
CC The present invention relates to a neural thread protein (NTP) peptide
CC referred to as cell death peptide. Thought to be cytostatic,
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for
CC treating a condition in a patient requiring removal or destruction of
CC cells, for treating a condition such as benign or malignant tumor,
CC inflammatory disease, autoimmune disease and infectious disease. The
CC peptide useful for treatment is derived from the amino acid sequence for
CC a pancreatic thread protein. The peptide is conjugated, linked or bound
CC to a molecule chosen from antibody or its fragment, antibody-like binding
CC molecule, where the molecule has a higher affinity for binding to a tumor
CC or other target than binding to other cells. Treatment using NTP peptides
CC can remove benign tumors with less risk and fewer of the undesirable side
CC effects of surgery. The present sequence is an NTP encoding sequence
XX
SQ Sequence 57 BP; 9 A; 21 C; 15 G; 12 T; 0 U; 0 Other;

Query Match          5.8%; Score 57; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 990 CCTCCGGGCTCAAGCAGCTTCTCCTGCTCAAGCTCCCAAGCAGCTGGATTACGGG 1046
DB 1 CCTCCGGGCTCAAGCAGCTTCTCCTGCTCAAGCTCCCAAGCAGCTGGATTACGGG 57

RESULT 3
AAK91064
ID AAK91064 standard; DNA; 66 BP.
XX
AC AAK91064;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human digestive system antigen genomic sequence SHQ ID NO: 4640.
XX
KM Human, digestive system antigen; gene therapy; cancer; appendicitis;
KM ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KM digestive system disorder; Meckel's diverticulum; ds.
XX
OS Homo sapiens.
XX
FN WO200155314-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001324.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
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PR 14-AUG-2000; 2000US-0224518P.
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 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249246P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0251989P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251566P.
 PR 08-DEC-2000; 2000US-0251568P.
 PR 08-DEC-2000; 2000US-0251569P.
 PR 08-DEC-2000; 2000US-0251589P.
 PR 08-DEC-2000; 2000US-0251900P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen Ca, Barash SC, Ruben SM;
 DR WPI; 2001-502630/55.
 XX
 XX Polynucleotides encoding digestive system antigens, useful for
 PT diagnosing, treating, preventing and/or prognosing disorders of the
 PT digestive system, particularly cancer and cancer metastases.
 XX
 XX
 XX
 PS Disclosure; SEQ ID NO 4640; 986pp; English.
 XX
 CC The present invention provides the protein and coding sequences of a
 CC number of human digestive system antigens. These can be used in the
 CC diagnosis, treatment and prevention of digestive system disorders,
 CC including cancer, Meckel's diverticulum, bacterial or parasitic
 CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
 CC ulcerative colitis. The present sequence is a genomic DNA fragment
 CC encoding a digestive system antigen of the invention
 XX
 SQ Sequence 66 BP; 14 A; 14 C; 14 G; 24 T; 0 U; 0 Other;
 Query Match 5.7%; Score 56.4; DB 1; Length 66;
 Best Local Similarity 90.9%; Pred. No. 44;
 Matches 60; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Oy 1070 TTTTGTATTTTCATTAGAGCGGGTTTCACCATATTTTCAGGCTGCTCAAACTCC 1129
 Db 1 TTTTGTATTTTTCATTAGAGCGGGTTTCACCATATTTTCAGGCTGCTCAAACTCC 60

Oy 1130 TGACCT 1135
 Db 61 TGACCT 66

RESULT 4
 AAS32099
 ID AAS32099 standard; DNA; 66 BP.

AC AAS32099;
 XX
 DT 04-DEC-2001 (first entry)

XX Human liver associated genomic DNA #273.

XX Liver associated protein; human; mouse; rabbit; goat; horse; cat; dog;
 KW chicken; sheep; immunosuppressive; antitachytic; vasotropic;
 KW antirheumatic; antiproliferative; cytosolic; cardiant; neuroprotective;
 KW cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer;
 KW ophthalmological; viral; gene therapy; autoimmune disease; neoplasm;
 KW hyperproliferative disorder; breast; liver; cardiovascular disorder; ds;
 KW cerebrovascular disorder; nervous system disorder; bacterial infection;
 KW fungal infection; viral infection; ocular disorder; endocrine disorder;
 KW gastrointestinal disorder; renal disorder; respiratory disorder;
 KW wound healing; skin aging; organ transplantation; tissue regeneration;
 KW anti-infectivity.

OS Homo sapiens.

XX WO20015355-A1.

PD 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US001351.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 11-JUL-2000; 2000US-0217487P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-022519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229509P.

PR 05-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0230437P.

PR 06-SEP-2000; 2000US-0230438P.

PR 09-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231244P.

PR 08-SEP-2000; 2000US-0231413P.

PR 08-SEP-2000; 2000US-0231414P.

PR 08-SEP-2000; 2000US-0232080P.

PR 08-SEP-2000; 2000US-0232081P.

PR 12-SEP-2000; 2000US-0231966P.

PR 14-SEP-2000; 2000US-0232397P.

PR 14-SEP-2000; 2000US-0232398P.

PR 14-SEP-2000; 2000US-0232399P.

PR 14-SEP-2000; 2000US-0232400P.

PR 14-SEP-2000; 2000US-0232401P.

PR 14-SEP-2000; 2000US-0233063P.

PR 14-SEP-2000; 2000US-0233064P.

PR 14-SEP-2000; 2000US-0233065P.

PR 21-SEP-2000; 2000US-0234223P.

PR 21-SEP-2000; 2000US-0234224P.

PR 25-SEP-2000; 2000US-0234997P.

PR 25-SEP-2000; 2000US-0234998P.

PR 26-SEP-2000; 2000US-0235484P.

PR 27-SEP-2000; 2000US-0235834P.

PR 27-SEP-2000; 2000US-0235836P.

PR 29-SEP-2000; 2000US-0236327P.

PR 29-SEP-2000; 2000US-0236367P.

PR 29-SEP-2000; 2000US-0236368P.

PR 29-SEP-2000; 2000US-0236369P.

PR 29-SEP-2000; 2000US-0236370P.

PR 02-OCT-2000; 2000US-0237037P.

PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.

PR 02-OCT-2000; 2000US-0237039P.

PR 02-OCT-2000; 2000US-0237040P.

PR 13-OCT-2000; 2000US-0239935P.

PR 13-OCT-2000; 2000US-0239937P.

PR 20-OCT-2000; 2000US-0240960P.

PR 20-OCT-2000; 2000US-0241221P.

PR 20-OCT-2000; 2000US-0241785P.

PR 20-OCT-2000; 2000US-0241786P.

PR 20-OCT-2000; 2000US-0241787P.

PR 20-OCT-2000; 2000US-0241808P.

PR 20-OCT-2000; 2000US-0241809P.

PR 20-OCT-2000; 2000US-0241826P.

PR 01-NOV-2000; 2000US-0244617P.

PR 08-NOV-2000; 2000US-0246474P.

PR 08-NOV-2000; 2000US-0246475P.

PR 08-NOV-2000; 2000US-0246476P.

PR 08-NOV-2000; 2000US-0246477P.

PR 08-NOV-2000; 2000US-0246478P.

PR 08-NOV-2000; 2000US-0246523P.

PR 08-NOV-2000; 2000US-0246524P.

PR 08-NOV-2000; 2000US-0246525P.

PR 08-NOV-2000; 2000US-0246526P.

PR 08-NOV-2000; 2000US-0246527P.

PR 08-NOV-2000; 2000US-0246528P.

PR 08-NOV-2000; 2000US-0246532P.

PR 08-NOV-2000; 2000US-0246609P.

PR 08-NOV-2000; 2000US-0246610P.

PR 08-NOV-2000; 2000US-0246611P.

PR 17-NOV-2000; 2000US-0249207P.

PR 17-NOV-2000; 2000US-0249208P.

PR 17-NOV-2000; 2000US-0249209P.

PR 17-NOV-2000; 2000US-0249210P.

PR 17-NOV-2000; 2000US-0249211P.

PR 17-NOV-2000; 2000US-0249212P.

XX		17-NOV-2000;	2000US-0249239P.
PR		17-NOV-2000;	2000US-0249300P.
PR		01-DEC-2000;	2000US-0250160P.
PR		01-DEC-2000;	2000US-0250391P.
PR		05-DEC-2000;	2000US-0251030P.
PR		05-DEC-2000;	2000US-0251988P.
PR		05-DEC-2000;	2000US-0256719P.
PR		06-DEC-2000;	2000US-0251479P.
PR		08-DEC-2000;	2000US-0251868P.
PR		08-DEC-2000;	2000US-0251869P.
PR		08-DEC-2000;	2000US-0251989P.
PR		08-DEC-2000;	2000US-0251900P.
PR		11-DEC-2000;	2000US-0254097P.
PR		05-JAN-2001;	2001US-0259678P.
PR		17-JAN-2001;	2001US-00764887.
XX		(HUMA-) HUMAN GENOME SCI INC.	
PA		Rosen CA,	Ruben SM, Barash SC;
XX		WPI; 2003-765398/72.	
DR			
XX		New liver related polypeptide, useful for diagnosis, treatment and/or	
PT		prevention of liver, gastrointestinal, pancreatic, immune, blood related,	
PT		endocrine, reproductive, hyperproliferative or reproductive disorders.	
XX			
PS		Disclosure; SEQ ID NO 575; 181bp; English.	
XX		The invention relates to a novel isolated, liver related polypeptide. The	
CC		polypeptide of the invention demonstrates virucide, fungicide,	
CC		antibacterial, antiparasitic, hepatotropic, antiinflammatory, cytostatic,	
CC		litholytic, antineumatic, antitatheric, neuroprotective, antidabetic,	
CC		anticogulant, thrombolytic, antiarteriosclerotic, cardiant, haemostatic,	
CC		antiarrhythmic, ophthalmological, antiarteriosclerotic, vasotropic,	
CC		osteopathic, nootropic, antiparkinsonian, anticomulsant, neuroleptic,	
CC		vasotropic, cytosolic and gynaeological activities. The polypeptides	
CC		and polynucleotides of the invention may be useful for diagnosis,	
CC		detection, treatment and/or prevention of disorders of the liver such as	
CC		viral, fungal, bacterial or parasitic infections, cirrhosis, Wilson's	
CC		disease, gastrointestinal disorders, pancreatic disorders, gallbladder	
CC		diseases, immune disorders, blood related disorders, hyperproliferative	
CC		disorders, cardiovascular disorders, respiratory disorders,	
CC		musculoskeletal system disorders, neurological diseases, endocrine	
CC		disorders, reproductive system disorders or developmental and inherited	
CC		disorders. The current sequence is that of the human liver-related	
CC		genomic DNA of the invention. The current sequence is not shown within	
CC		the specification per se but was obtained electronically from the USPO	
CC		web-site.	
XX			
CC			
Query Match		5.7%; Score 56.4; DB 1; Length 66;	
Best Local Similarity		90.9%; Pred. No. 44;	
Matches	60; Conservative	0; Mismatches	6; Indels
			Gaps
OY	1070	TTTTTGATTTTCATTAGAGCGGGGTTTACCACTATTGTGCAGCCTGCTCTCAAACGCC	1129
DB	1	TTTTTGATTTTGTAGTAGAAGCGGGGTTTACCATTTGACCAAGCTGCTCTCAAACATCC	60
OY	1130	TGACTT	1135
DB	61	TGACTT	66
RESULT 7			
AD120573			
ID	AD120573	standard; DNA; 60 BP.	
XX	AD120573;		
AC	AD120573;		
XX	15-APR-2004 (first entry)		
DT			
XX	Oligonucleotide sequence enquiry #60.		

XX human; ds; ERNA.
 KW Homo sapiens.
 XX WO2003025229-A1.
 XX 27-MAR-2003.
 XX 19-SEP-2002; 2002WO-AU001286.
 XX 19-SEP-2001; 2001US-0324127P.
 XX (UYQU) UNIV QUEENSLAND.
 XX Mattick J, Gagen M, Stanley S;
 XX WPI; 2003-371830/35.
 DR Identifying an ERNA or a DNA sequence comprising an ERNA-encoding
 PT sequence in the nucleome of a eukaryotic cell, comprising identifying non
 PT protein-encoding nucleotide sequences within an mRNA transcript or a DNA
 PT sequence.
 XX Example 12; SEQ ID NO 63; 137bp; English.
 XX The present invention relates to identifying an ERNA or a DNA sequence
 CC comprising an ERNA-encoding sequence in the nucleome of a eukaryotic cell
 CC comprising identifying non-protein-encoding nucleotide sequences within an
 CC mRNA transcript or a DNA sequence encoding same in the nucleome. The
 CC methods are useful for identifying an ERNA or DNA for modifying a genetic
 CC network in cell to alter the cells phenotype. The present sequence
 CC represents human oligonucleotide sequence enquiry.
 XX Sequence 60 BP; 8 A; 22 C; 16 G; 14 T; 0 U; 0 Other;
 SQ
 Query Match 5.6%; Score 55.2; DB 1; Length 60;
 Best Local Similarity 95.0%; Pred. No. 47;
 Matches 57; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 635 CTCTGTACCCAGGCTGAGTGCAGTGGCGCAATCTTGCTACTGCAACCTCTGCTCC 694
 DB 1 CTCTGTACCCAGGCTGAGTGCAGTGGCGCAATCTTGCTACTGCAACCTCTGCTCC 60
 RESULT 8
 ADI12552/c
 ID ADI12552 standard; DNA; 66 BP.
 XX ADI12552;
 AC ADI12552;
 XX 22-APR-2004 (first entry)
 DT Mutant human BRCA1 genomic DNA resulting from deletion 5 Segid 35.
 DE ds; cancer; human; tumour suppressor;
 KW breast cancer susceptibility gene 1; BRCA1; repetitive Alu;
 KW ovarian cancer; recombination; mutant.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO2003104474-A2.
 XX 18-DEC-2003.
 PD 09-JUN-2003; 2003WO-US018098.
 XX 09-JUN-2003; 2002US-0387132P.
 XX 09-AUG-2002; 2002US-0402430P.
 XX (MYRI-) MYRIAD GENETICS INC.
 PA Scholl T, Hendrickson BC, Ward B, Pruss D;
 PI

XX WPI; 2004-062369/06.
 DR Predicting a predisposition to cancer in a patient comprising detecting a
 XX deletion in the BRCA1 gene that results from the unequal crossover
 PT between a pair of repetitive sequences in the BRCA1 gene.
 XX Disclosure; SEQ ID NO 35; 59bp; English.
 XX This invention relates to a novel method for predicting a predisposition
 CC to cancer in a patient by detecting large deletions in the human tumour
 CC suppressor gene identified as the breast cancer susceptibility gene 1
 CC (BRCA1). Specifically, it refers to deletions that result from the
 CC unequal crossover between a pair of repetitive Alu sequences in the BRCA1
 CC gene, such that the recombined nucleotide sequence containing the
 CC deletion indicates a predisposition to breast and ovarian cancer. The
 CC present invention describes newly discovered deletion mutations that are
 CC believed to be deleterious and cause significant alterations in the
 CC structure or biochemical function of BRCA1. Accordingly, it provides
 CC methods for detecting such mutants, as well as identifying and screening
 CC for cytostatic compounds useful for treating or preventing cancers
 CC associated with a BRCA1 genetic variant. This polynucleotide is a mutant
 CC human BRCA1 genomic DNA fragment that arises as a result of a
 CC recombination event (deletion 5), which causes the omission of exons 15
 CC and 16, given in an exemplification of the invention.
 XX Sequence 66 BP; 15 A; 16 C; 24 G; 11 T; 0 U; 0 Other;
 SQ
 Query Match 5.5%; Score 54.4; DB 1; Length 66;
 Best Local Similarity 90.6%; Pred. No. 55;
 Matches 58; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 687 CTGCTCCCGGGTCAAGTATTCCTCCGCCCCAGCTCTGAGTAGCTGGAGCTACAGG 746
 DB 66 CCGCTCCCGGGTCAAGCAATTCCTGCTCAGCTCTGAGTAGCTGGAGTACAGG 7
 QY 747 CGCC 750
 DB 6 CACC 3
 RESULT 9
 ADI12619/c
 ID ADI12619 standard; DNA; 66 BP.
 XX ADI12619;
 AC ADI12619;
 XX 22-APR-2004 (first entry)
 DT Human BRCA1 DNA upstream from the deletion 5 recombination event.
 DE ds; cancer; human; tumour suppressor;
 KW breast cancer susceptibility gene 1; BRCA1; repetitive Alu;
 KW ovarian cancer; recombination.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO2003104474-A2.
 XX 18-DEC-2003.
 PD 09-JUN-2003; 2003WO-US018098.
 XX 09-JUN-2003; 2002US-0387132P.
 XX 09-AUG-2002; 2002US-0402430P.
 XX (MYRI-) MYRIAD GENETICS INC.
 PA Scholl T, Hendrickson BC, Ward B, Pruss D;
 PI WPI; 2004-062369/06.
 DR Predicting a predisposition to cancer in a patient comprising detecting a

PT deletion in the BRCA1 gene that results from the unequal crossover
PT between a pair of repetitive sequences in the BRCA1 gene.
PS Disclosure; Fig 5, 59pp; English.
XX
CC This invention relates to a novel method for predicting a predisposition
CC to cancer in a patient by detecting large deletions in the human tumour
CC suppressor gene identified as the breast cancer susceptibility gene 1
CC (BRCA1). Specifically, it refers to deletions that result from the
CC unequal crossover between a pair of repetitive Alu sequences in the BRCA1
CC gene, such that the recombined nucleotide sequence containing the
CC deletion indicates a predisposition to breast and ovarian cancer. The
CC present invention describes newly discovered deletion mutations that are
CC believed to be deleterious and cause significant alterations in the
CC structure or biochemical function of BRCA1. Accordingly, it provides
CC methods for detecting such mutants, as well as identifying and screening
CC for cytostatic compounds useful for treating or preventing cancers
CC associated with a BRCA1 genetic variant. This polynucleotide is a human
CC BRCA1 DNA fragment representing the region downstream of the deletion 5
CC recombination event that causes the omission of exons 15 and 16, given in
CC an exemplification of the invention.
XX
SQ Sequence 66 BP, 16 A, 15 C, 23 G, 12 T, 0 U, 0 Other;
Query Match 5.5%; Score 54.4; DB 1; Length 66;
Best Local Similarity 90.6%; Pred. No. 55;
Matches 58; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 687 CTGGCTCCCGGGTTCAGTATTTCTCTGCCCCAGGCTCTGTAGTACGGACTACAG 746
DB 66 CTGGCTCCCGAGTTCAAGCAATTCCTGCTCAGGCTCTGTAGTACGGACTACAG 7
QY 747 CGGC 750
DB 6 CACC 3
Db
RESULT 10
AAK6585
ID AAK6585 standard; DNA; 63 BP.
XX
AC AAK6585;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:41397.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytoelastic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN W0200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-020515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-021513P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 16-AUG-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226682P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0231415P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0234984P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239933P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.

PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
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PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251866P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
PS Disclosure; SEQ ID NO 41397; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytosstatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially

CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK67694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 63 BP; 11 A; 14 C; 16 G; 22 T; 0 U; 0 Other;

Query Match 5.5%; Score 54; DB 1; Length 63;
Best Local Similarity 91.9%; Pred. No. 56;
Matches 57; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 172 TTTTGTAGTGAATGAGCTTTCTCCATGTTGCTGAGGCTGGTCTGGAATCCCGAACC 231
DB 2 TATTTTGTAGTGAATGAGCTTTCTCCATGTTGCTGAGGCTGGTCTGGAATCCCGAACC 61

OY 232 CA 233
DB 62 CA 63

RESULT 11
AAK5681/c
ID AAK5681 standard; DNA; 63 BP.

XX AAK5681;
XX
XX 07-NOV-2001 (first entry)

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40493.

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW Cytostatic; gene therapy; vaccine; metastasis; ds.

OS Homo sapiens.

XX WO200157182-A2.

XX
XX 09-AUG-2001.

PD 17-JAN-2001; 2001WO-US001354.

XX 31-JAN-2000; 2000US-0179065P.

XX 04-FEB-2000; 2000US-0180628P.

XX 24-FEB-2000; 2000US-0184664P.

XX 02-MAR-2000; 2000US-0186350P.

XX 16-MAR-2000; 2000US-0189874P.

XX 17-MAR-2000; 2000US-0190076P.

XX 18-APR-2000; 2000US-0198123P.

XX 19-MAY-2000; 2000US-0205515P.

XX 07-JUN-2000; 2000US-0209467P.

XX 28-JUN-2000; 2000US-0214886P.

XX 30-JUN-2000; 2000US-0215135P.

XX 07-JUL-2000; 2000US-0216647P.

XX 07-JUL-2000; 2000US-0216880P.

XX 11-JUL-2000; 2000US-0217487P.

XX 11-JUL-2000; 2000US-0217496P.

XX 14-JUL-2000; 2000US-0218290P.

XX 26-JUL-2000; 2000US-0220963P.
XX 26-JUL-2000; 2000US-0220964P.
XX 14-AUG-2000; 2000US-0224518P.
XX 14-AUG-2000; 2000US-0224519P.
XX 14-AUG-2000; 2000US-0225213P.
XX 14-AUG-2000; 2000US-0225214P.
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XX 14-AUG-2000; 2000US-0225267P.
XX 14-AUG-2000; 2000US-0225268P.
XX 14-AUG-2000; 2000US-0225269P.
XX 14-AUG-2000; 2000US-0225447P.
XX 14-AUG-2000; 2000US-0225757P.
XX 14-AUG-2000; 2000US-0225758P.
XX 14-AUG-2000; 2000US-0225759P.
XX 18-AUG-2000; 2000US-0226279P.
XX 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229887P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 12-SEP-2000; 2000US-0232081P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
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PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234977P.
PR 25-SEP-2000; 2000US-0234988P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 01-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.

PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 06-DEC-2000; 2000US-0256719P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254979P.
PR 05-JAN-2001; 2001US-0259678P.

XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
PT
PS Disclosure; SEQ ID NO 40493; 3071pp + Sequence Listing; English.

XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 63 BP; 22 A; 16 C; 14 G; 11 T; 0 U; 0 Other;

Query Match 5.5%; Score 54; DB 1; Length 63;
Best Local Similarity 91.9%; Pred. No. 56;
Matches 57; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 172 TTTTATGAGAGATGAGTTTCTCCATGTTGGTACGGTGGTCTCGAAGCTCCGACCT 231
Db 62 TATTATTAGTAGAGATGTTTCAACCTGTGGTACGGTGGTCTCGAAGCTCCGACCT 3
QY 232 CA 233
||

Db 2 CA 1

RESULT 12
ID AAK83961/c
AAK83961 standard; DNA; 57 BP.

XX AAK83961;

DT 07-NOV-2001 (first entry)

XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38773.

DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastrasis; ds.

XX Homo sapiens.

XX WO200157182-A2.

PD 09-AUG-2001.

XX 17-JAN-2001; 2001WO-US001354.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205151P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225577P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.

PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226686P.

PR 22-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 2000US-0227009P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229509P.

PR 05-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0230437P.

PR 06-SEP-2000; 2000US-0230438P.

PR 08-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231244P.

PR 08-SEP-2000; 2000US-0231413P.

PR 08-SEP-2000; 2000US-0231414P.

PR 08-SEP-2000; 2000US-0232080P.

PR 08-SEP-2000; 2000US-0232081P.

PR 12-SEP-2000; 2000US-0231968P.

PR 14-SEP-2000; 2000US-0232397P.

PR 14-SEP-2000; 2000US-0232398P.

PR 14-SEP-2000; 2000US-0232399P.

PR 14-SEP-2000; 2000US-0232400P.

PR 14-SEP-2000; 2000US-0233063P.

PR 14-SEP-2000; 2000US-0233064P.

PR 14-SEP-2000; 2000US-0233065P.

PR 21-SEP-2000; 2000US-0234223P.

PR 21-SEP-2000; 2000US-0234274P.

PR 25-SEP-2000; 2000US-0234997P.

PR 25-SEP-2000; 2000US-0234998P.

PR 26-SEP-2000; 2000US-0235484P.

PR 27-SEP-2000; 2000US-0235834P.

PR 27-SEP-2000; 2000US-0235836P.

PR 29-SEP-2000; 2000US-0236327P.

PR 29-SEP-2000; 2000US-0236367P.

PR 29-SEP-2000; 2000US-0236368P.

PR 29-SEP-2000; 2000US-0236369P.

PR 29-SEP-2000; 2000US-0236370P.

PR 02-OCT-2000; 2000US-0236802P.

PR 02-OCT-2000; 2000US-0237037P.

PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.

PR 02-OCT-2000; 2000US-0237040P.

PR 13-OCT-2000; 2000US-0239935P.

PR 13-OCT-2000; 2000US-0239937P.

PR 20-OCT-2000; 2000US-0240960P.

PR 20-OCT-2000; 2000US-0241221P.

PR 20-OCT-2000; 2000US-0241785P.

PR 20-OCT-2000; 2000US-0241786P.

PR 20-OCT-2000; 2000US-0241787P.

PR 20-OCT-2000; 2000US-0241808P.

PR 20-OCT-2000; 2000US-0241809P.

PR 20-OCT-2000; 2000US-0241826P.

PR 01-NOV-2000; 2000US-0244617P.

PR 06-NOV-2000; 2000US-0246474P.

PR 08-NOV-2000; 2000US-0246475P.

PR 08-NOV-2000; 2000US-0246476P.

PR 08-NOV-2000; 2000US-0246477P.

PR 08-NOV-2000; 2000US-0246478P.

PR 08-NOV-2000; 2000US-0246523P.

PR 08-NOV-2000; 2000US-0246524P.

PR 08-NOV-2000; 2000US-0246525P.

PR 08-NOV-2000; 2000US-0246526P.

PR 08-NOV-2000; 2000US-0246527P.

PR 08-NOV-2000; 2000US-0246528P.

PR 08-NOV-2000; 2000US-0246532P.

PR 08-NOV-2000; 2000US-0246609P.

PR 08-NOV-2000; 2000US-0246610P.

PR 08-NOV-2000; 2000US-0246611P.

PR 08-NOV-2000; 2000US-0246613P.

PR 17-NOV-2000; 2000US-0249207P.

PR 17-NOV-2000; 2000US-0249208P.

PR 17-NOV-2000; 2000US-0249209P.

PR 17-NOV-2000; 2000US-0249210P.

PR 17-NOV-2000; 2000US-0249211P.

PR 17-NOV-2000; 2000US-0249212P.

PR 17-NOV-2000; 2000US-0249213P.

PR 17-NOV-2000; 2000US-0249214P.

PR 17-NOV-2000; 2000US-0249215P.

PR 17-NOV-2000; 2000US-0249216P.

PR 17-NOV-2000; 2000US-0249217P.

PR 17-NOV-2000; 2000US-0249244P.

PR 17-NOV-2000; 2000US-0249245P.

PR 17-NOV-2000; 2000US-0249246P.

PR 17-NOV-2000; 2000US-0249265P.

PR 17-NOV-2000; 2000US-0249297P.

PR 17-NOV-2000; 2000US-0249299P.

XX (SIMP/) SIMPSON A J G.
 PA (NETO/) NETO E D.
 PA (BREN/) BRENTANI R R.
 XX Simpson AUG, Neto ED, Brentani RR;
 PI WPI, 2003-182626/18.
 XX
 XX Determining open reading frames of genome of an organism e.g. a human
 PT suffering from cancer involves use of single oligonucleotide primer at
 PT low stringency for preparing single-stranded cDNA from mRNA of
 PT individual.

PS Example 9; Page 286; 9599p; English.

CC The invention describes a method of determining open reading frames in
 CC the genome of organism, comprising contacting mRNA from cell of organism
 CC with a single oligonucleotide primer (1) at low stringency, preparing
 CC single-stranded cDNA by reverse transcribing mRNA with (1), amplifying
 CC cDNA, sequencing the product, and repeating the contacting, preparing
 CC and amplifying steps with different primers and sequencing resulting
 CC nucleic acids. The method is useful for determining that a known
 CC nucleotide sequence from a genome of an organism corresponds to a
 CC nucleic acid molecule from a genome of an organism; and for sequencing
 CC all or part of a genome of an organism. mRNA is obtained from mammalian
 CC or human cell which is associated with a pathological condition e.g. a
 CC colon cancer or breast cancer cell. The method is useful for analyses of
 CC populations of subjects and can be used to carry out genetic analyses of
 CC large or small populations. Further, it can be used to study living
 CC systems to determine if, e.g. there have been genetic shifts which render
 CC an individual or population more or less likely to be afflicted with
 CC diseases such as cancer, to determine antibiotic resistance or non-
 CC tolerance, and so forth. The method can also be used in the study of
 CC congenital diseases, and the risk of affliction to a foetus, as well as
 CC the study of whether the conditions are likely to be passed to offspring
 CC through ova or sperm. The analyses for pathological conditions can be
 CC carried out in all animals, plants, birds, fish, etc. Using this method,
 CC in the area of agriculture, for example the genomes of food crops can be
 CC studied to determine if resistance genes are present, defects in plant
 CC genomes can also be studied in this way. Similarly, the method permits
 CC determination of the pathogens which integrate into the genome, such as
 CC retroviruses and other integrating viruses such as influenza virus, have
 CC undergone shifts or mutations, which may require different approaches to
 CC therapy. This method is also applied to eukaryotic pathogens, such as
 CC trypanosomes, different types of Plasmodium, etc. The method essentially
 CC eliminates sequencing of non-coding portions. This sequence represents a
 CC polynucleotide isolated from human colon cancer cell cDNA library
 XX
 SQ Sequence 65 BP; 13 A; 15 C; 27 G; 10 T; 0 U; 0 Other;

Query Match. 5.3%; Score 52.8; DB 1; Length 65;
 Best Local Similarity 89.1%; Pred. No. 66;
 Matches 57; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 690 CCTCCGGGTTCAAGTATTCTCCGCCAGCCTCTGAGTAGCTGGGACTACAGGCGC 749
 DB 64 CTTCCGGGTTCAAGCATTCTCTGCTCAGCCTCCGAGTAGTGGGACTACAGGCGC 5

OY 750 CCAC 753
 DB 4 CCGC 1

RESULT 15
 ID ACC84454
 AC ACC84454 standard; DNA; 60 BP.

XX AC AC84454;
 XX DT 28-AUG-2003 (first entry)
 XX

DE NTP peptide encoding sequence #1.
 XX Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
 KW neural thread protein; NTP; tumour; ds.
 XX Unidentified.
 OS

PN W02003008443-A2.

XX 30-JAN-2003.

XX 19-JUL-2002; 2002WO-CA001105.

XX 19-JUL-2001; 2001US-0306150P.

XX 19-JUL-2001; 2001US-030615P.

XX 16-NOV-2001; 2001US-0331477P.

XX (NTMO-) NTMOX CORP.

XX Averbach PA;
 PI WPI, 2003-247999/24.
 DR P-F8DB; ABR63249.

XX Novel neural thread protein peptide, referred as cell death peptide,
 PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
 PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.
 PS Disclosure; Page 15; 777p; English.

XX The present invention relates to a neural thread protein (NTP) peptide
 CC referred to as cell death peptide. Thought to be cytostatic,
 CC antibacterial, immunosuppressive and antiinflammatory. It is useful for
 CC treating a condition in a patient requiring removal or destruction of
 CC cells, for treating a condition such as benign or malignant tumor,
 CC inflammatory disease, autoimmune disease and infectious disease. The
 CC peptide useful for treatment is derived from the amino acid sequence for
 CC a pancreatic thread protein. The peptide is conjugated, linked or bound
 CC to a molecule chosen from antibody or its fragment, antibody-like binding
 CC molecule, where the molecule has a higher affinity for binding to a tumor
 CC or other target than binding to other cells. Treatment using NTP peptides
 CC can remove benign tumors with less risk and fewer of the undesirable side
 CC effects of surgery. The present sequence is an NTP encoding sequence
 XX

SQ Sequence 60 BP; 9 A; 21 C; 15 G; 15 T; 0 U; 0 Other;

Query Match. 5.2%; Score 51; DB 1; Length 60;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 699 TTCAAGTATTCTCTCCGCCAGCCTCTGAGTAGCTGGGACTACAGGCGC 749
 DB 10 TTCAAGTATTCTCTCTGCCAGCCTCTGAGTAGCTGGGACTACAGGCGC 60

RESULT 16
 ID AD120585
 AC AD120585 standard; DNA; 60 BP.

XX AD120585;

XX 15-APR-2004 (first entry)

DE Oligonucleotide sequence enquiry #72.

XX human; ds; eRNA.

XX Homo sapiens.

XX W02003025229-A1.

XX 27-MAR-2003.

XX

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PF 19-SEP-2002; 2002WO-AU001286.
XX
XX 19-SEP-2001; 2001US-0324127P.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX
XX Mattick J, Gagen M, Stanley S;
XX
XX WPI; 2003-371830/35.
XX
XX Identifying an mRNA or a DNA sequence comprising an mRNA-encoding
XX sequence in the nucleome of a eukaryotic cell, comprising identifying non
XX protein-encoding nucleotide sequences within an mRNA transcript or a DNA
XX sequence.
XX
XX Example 12; SEQ ID NO 75; 137pp; English.
XX
XX The present invention relates to identifying an RNA or a DNA sequence
XX comprising an RNA-encoding sequence in the nucleome of a eukaryotic cell
XX comprising identifying non-protein-encoding nucleotide sequences within an
XX mRNA transcript or a DNA sequence encoding same in the nucleome. The
XX methods are useful for identifying an RNA or DNA for modifying a genetic
XX network in cell to alter the cells phenotype. The present sequence
XX represents human oligonucleotide sequence enquiry.
XX
XX Sequence 60 BP; 10 A; 22 C; 16 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 5.1%; Score 50.4; DB 1; Length 60;
XX Best Local Similarity 90.0%; Pred. No. 82;
XX Matches 54; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX 637 CCGTACCCAGGCTGAGTGCAGTGGGCGCATCTTGAGCTCACTGCAACCTCTCCGCCG 696
XX 1 CCGTACCCAGGCTGAGTGCAGTGGGCGCATCTTGAGCTCACTGCAACCTCTCCGCCG 60
XX
XX RESULT 17
XX ACC79017/c
XX ID ACC79017 standard; DNA; 61 BP.
XX
XX ACC79017;
XX
XX 29-JUL-2003 (first entry)
XX
XX Human genome SNP related oligonucleotide ss1000934.
XX
XX Human; regulation; single nucleotide polymorphism; SNP; gene therapy;
XX transcription factor binding site cluster; probe; primer; gene; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT 31
XX FT variation /*tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX
XX WO2003025198-A2.
XX
XX 27-MAR-2003.
XX
XX 11-SEP-2002; 2002WO-US028842.
XX
XX 17-SEP-2001; 2001US-0322723P.
XX 30-NOV-2001; 2001US-0334543P.
XX
XX (ITGE-) INT GENOMICS LLC.
XX
XX Nowotny V;
XX
XX WPI; 2003-354608/33.
XX
XX New set of regulatory single nucleotide polymorphism (SNP)
XX polymorphisms, useful in diagnostic assays, in testing systems for
```

```
PT finding new drugs, or for treating or preventing a disease associated
XX with the regulatory SNP.
XX
XX Example 2; Page 21; 37pp; English.
XX
XX The present invention describes a set of regulatory single nucleotide
XX polymorphism (SNP) polymorphisms or its complementary set of
XX polymorphisms comprising polymorphisms of at least 6 contiguous
XX nucleotides, where each polymorphisms of the set contains a regulatory
XX SNP with 5' and/or 3' genomic flanking sequence. A set of regulatory SNP
XX polymorphisms contains several regulatory SNPs which collectively map
XX to several transcription factor binding site cluster (TF) sequences so
XX that each SNP lies within a TFC sequence, and a genomic nucleic acid
XX sequence from 30 nucleotides 5' to 30 nucleotides 3' to each SNP is
XX identical or complementary except for the SNP, to a portion of a genomic
XX nucleic acid sequence from 30 nucleotides 5' to 30' nucleotides 3' to the
XX TFC sequence. The set of regulatory SNP polymorphisms can be used in
XX gene therapy. The regulatory SNP polymorphisms are useful in diagnostic
XX assays, in testing systems for finding new drugs, or for treating or
XX preventing a disease associated with the regulatory SNP. The
XX polymorphisms are also useful as probes or primers for detecting the
XX regulatory SNPs. The present sequence represents a human genome related
XX oligonucleotide comprising a SNP, which is used in an example from the
XX present invention
XX
XX Sequence 61 BP; 11 A; 19 C; 21 G; 9 T; 0 U; 1 Other;
XX
XX Query Match 5.1%; Score 50; DB 1; Length 61;
XX Best Local Similarity 88.3%; Pred. No. 87;
XX Matches 53; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
XX
XX 643 CCCAGGCTGAGTGCAGTGGGCGCATCTTGAGCTCACTGCAACCTCTCCGCCGTTCA 702
XX 60 CCCAGGCTGAGTGCAGTGGGCGCATCTTGAGCTCACTGCAACCTCTCCGCCGTTCA 1
XX
XX RESULT 18
XX AD112551/c
XX ID AD112551 standard; DNA; 56 BP.
XX
XX AD112551;
XX
XX 22-APR-2004 (first entry)
XX
XX Mutant human BRCA1 genomic DNA resulting from deletion 5 SegID 34.
XX
XX de; cancer; human; tumour suppressor;
XX breast cancer susceptibility gene 1; BRCA1; repetitive Alu;
XX ovarian cancer; recombination; mutant.
XX
XX Homo sapiens.
XX
XX WO2003104474-A2.
XX
XX 18-DEC-2003.
XX
XX 09-JUN-2003; 2003WO-US018098.
XX
XX 07-JUN-2002; 2002US-0387132P.
XX 09-AUG-2002; 2002US-0402430P.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Scholl T, Hendrickson BC, Ward B, Pruss D;
XX
XX WPI; 2004-062369/06.
XX
XX Predicting a predisposition to cancer in a patient comprising detecting a
XX deletion in the BRCA1 gene that results from the unequal crossover
XX between a pair of repetitive sequences in the BRCA1 gene.
XX
XX Disclosure; SEQ ID NO 34; 59pp; English.
XX
```

CC This invention relates to a novel method for predicting a predisposition
CC to cancer in a patient by detecting large deletions in the human tumour
CC suppressor gene identified as the breast cancer susceptibility gene 1
CC (BRCA1). Specifically, it refers to deletions that result from the
CC unequal crossover between a pair of repetitive Alu sequences in the BRCA1
CC gene, such that the recombined nucleotide sequence containing the
CC deletion indicates a predisposition to breast and ovarian cancer. The
CC present invention describes newly discovered deletion mutations that are
CC believed to be deleterious and cause significant alterations in the
CC structure or biochemical function of BRCA1. Accordingly, it provides
CC methods for detecting such mutants, as well as identifying and screening
CC for cytostatic compounds useful for treating or preventing cancers
CC associated with a BRCA1 genetic variant. This polynucleotide is a mutant
CC human BRCA1 genomic DNA fragment that arises as a result of a
CC recombination event (deletion 5), which causes the omission of exons 15
CC and 16, given in an exemplification of the invention.

XX
SQ Sequence 56 BP; 13 A; 14 C; 18 G; 11 T; 0 U; 0 Other;

Query Match 4.9%; Score 48.6; DB 1; Length 56;
Best Local Similarity 92.7%; Pred. No. 96;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 693 CCGGGTTCAAGTATTCTCTCCGCCAGCCTCTGAGTACTGGAGCTACAGGC 747
Db 56 CCGGGTTCAAGCATTTCTCTGCTCTGAGTACTGGAGTATTACAGGC 2

RESULT 19
AA179765
ID AA179765 standard; DNA; 51 BP.
XX
AC AA179765;
DT 09-NOV-2001 (first entry)
XX
DE Human nonconservative amino acid changing SNP nucleic acid SEQ:6706.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantification; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
PN WO200140521-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US032758.
XX
PR 30-NOV-1999; 99US-0168138P.
PR 29-NOV-2000; 2000US-00726173.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkova RA, Leach M;
XX
DR WPI; 2001-356160/37.
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX
PS Claim 1; Page 2557; 2653pp; English.

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA173114 to AA175329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides

CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples

XX
SQ Sequence 51 BP; 8 A; 17 C; 15 G; 11 T; 0 U; 0 Other;

Query Match 4.9%; Score 48.4; DB 1; Length 51;
Best Local Similarity 98.0%; Pred. No. 91;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 638 TGTGACCCAGGCTGAGTGACATGCGCCCAATCTTGCTCACTGCAACCTC 687
Db 1 TGTGACCCAGGCTGAGTGACATGCGCCCAATCTTGCTCACTGCAACCTC 50

RESULT 20
AD120575
ID AD120575 standard; DNA; 60 BP.
XX
AC AD120575;
DT 15-APR-2004 (first entry)
XX
DE Oligonucleotide sequence enquiry #62.
XX
KW human; ds; eRNA.
XX
OS Homo sapiens.
XX
PN WO2003025229-A1.
XX
PD 27-MAR-2003.
XX
PF 19-SEP-2002; 2002WO-AU001286.
XX
PR 19-SEP-2001; 2001US-0324127P.
XX
PA (UNYU) UNIV QUEENSLAND.
XX
PI Mactick J, Gagen M, Stanley S;
XX
DR WPI; 2003-371830/35.
XX
PT Identifying an eRNA or a DNA sequence comprising an eRNA-encoding
PT sequence in the nucleome of a eukaryotic cell, comprising identifying non
PT protein-encoding nucleotide sequences within an mRNA transcript or a DNA
PT sequence.
XX
PS Example 12; SEQ ID NO 65; 137pp; English.

CC The present invention relates to identifying an eRNA or a DNA sequence
CC comprising an eRNA-encoding sequence in the nucleome of a eukaryotic cell
CC comprising identifying non-protein-encoding nucleotide sequences within an
CC mRNA transcript or a DNA sequence encoding same in the nucleome. The
CC methods are useful for identifying an eRNA or DNA for modifying a genetic
CC network in cell to alter the cells phenotype. The present sequence
CC represents human oligonucleotide sequence enquiry.

XX
SQ Sequence 60 BP; 9 A; 18 C; 18 G; 15 T; 0 U; 0 Other;

Query Match 4.9%; Score 48.2; DB 1; Length 60;
Best Local Similarity 94.3%; Pred. No. 1.1e+02;
Matches 50; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 696 GGGTTCAAGTATTCTCTGCTCTGAGTACTGGAGTATTACAGGC 748
|||||

Db 2 GGCTTCAAGTATCTCTCCTCAGCCTCCGAGTAGCTGGAGCTACAGCG 54

RESULT 21

AAA77228
ID AAA77228 standard, cDNA, 51 BP.

AAA77228;

16-NOV-2000 (first entry)

Human clone cg43971764 polymorphic site, SEQ ID NO:911.

Human; single nucleotide polymorphism; SNP; chromosome 15; detection;
identification; gene therapy; ss.

Homo sapiens.

Key Location/Qualifiers
FT replace(26,C)
FT /*tag= a

MO200029623-A2.

25-MAY-2000.

17-NOV-1999; 99WO-US027293.

17-NOV-1998; 98US-0109024P.

16-NOV-1999; 99US-00443199.

(CURA-) CURAGEN CORP.

Shinkets RA, Leach MD;

WPI; 2000-387826/33.

Human nucleic acids containing single nucleotide polymorphisms, useful
for treating a subject suffering, or at risk from a pathology due to the
presence of a sequence polymorphism.

Claim 1; Page 433; 543pp; English.

Sequences AAA7318-A77509 represent 1192 human nucleic acid sequences
which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 1112
(AAA76338-A77429) are consecutive pairs of nucleotides which contain
silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are consecutive
pairs of nucleotides containing SNPs which result in changes in the
corresponding amino acid sequences (AAB11749-B11828). The SNPs in
sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid
changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result
in non-conservative changes. The SNPs in sequences 1187 to 1192
(AAA77504-A77509) generate frameshift mutations. The invention also
relates to a method of detecting a polymorphic site in a nucleic acid and
a method of determining the relatedness of two nucleic acids. It also
encompasses peptides containing polymorphic sites, antibodies raised
against such peptides, and a method of detecting polymorphic
proteins/peptides using the antibodies. The nucleic acids are useful for
gene therapy of an individual having, suspected of having, or at risk of
developing a pathological condition due to the presence of a sequence
polymorphism. Such treatment would comprise administration of the wild-
type nucleic acid sequence. Antibodies raised against polymorphic
peptides can also be used in the treatment of such individuals

Sequence 51 BP; 11 A; 20 C; 13 G; 7 T; 0 U; 0 Other;

Query Match 4.8%; Score 47.8; DB 1; Length 51;

Best Local Similarity 96.1%; Pred. No. 97;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

847 CTTGGGCTCCCAAGTGTGGATTACAGCGCGAGCCACAGCCCGC 897

1 CTTGAGCTCCCAAGTGTGGATTACAGCGCGAGCCACAGCCCGC 51

RESULT 22

AA176251/C
ID AA176251 standard, DNA, 51 BP.

AA176251;

09-NOV-2001 (first entry)

Human silent SNP containing nucleic acid SEQ:3192.

Human; single nucleotide polymorphism; SNP; genome; gene therapy;
protein therapy; vaccine; probe; diagnostic assay; detection;
quantitation; restorative therapy; polymorphic; ds.

Homo sapiens.

MO200140521-A2.

07-JUN-2001.

30-NOV-2000; 2000WO-US032758.

30-NOV-1999; 99US-0168138P.

29-NOV-2000; 2000US-00726173.

(CURA-) CURAGEN CORP.

Shinkets RA, Leach M;

WPI; 2001-356160/37.

Polymorphic nucleic acid sequences, useful in genetic testing and
therapy.

Claim 1; Page 1027; 2653pp; English.

AA173060 to AA179867 represent isolated human polymorphic polynucleotide
sequences (I), which contain single nucleotide polymorphisms (SNPs).
AA173114 to AA175329 represent peptides related to human polymorphic
polynucleotide sequences. The sequences can be used in gene and protein
therapy, and in vaccine production. (I) and the polypeptides encoded by
them may be used in the prevention, diagnosis and treatment of diseases
associated with inappropriate expression of polymorphic polypeptides. For
example, (I) may be used to treat disorders by rectifying mutations or
deletions in a patient's genome that affect the activity of polypeptides
by expressing inactive proteins or to supplement the patient's own
production of polypeptide. Additionally, (I) and its complementary
sequences may also be used as DNA probes in diagnostic assays to detect
and quantitate the presence of similar nucleic acids in samples, and
therefore which patients may be in need of restorative therapy. The
polypeptides encoded by (I) may be used as antigens in the production of
antibodies specific for polymorphic polypeptides. The antibodies may also
be used to down regulate expression and activity. The antibodies may also
be used as diagnostic agents for detecting the presence of polymorphic
polypeptides in samples

Sequence 51 BP; 12 A; 16 C; 15 G; 8 T; 0 U; 0 Other;

Query Match 4.8%; Score 47.8; DB 1; Length 51;

Best Local Similarity 96.1%; Pred. No. 97;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

639 GTACCCAGGCTGAGTGCAGTGCACATCTTGCTCACTGACACTCTG 689

51 GTACCCAGGCTGAGTGCAGTGCAGTGCATCTTGCTCACTGACACTCTG 1

RESULT 23

AA178079
ID AA178079 standard, DNA, 51 BP.

XX

AC AA178079;
XX 09-NOV-2001 (first entry)
XX Human silent SNP containing nucleic acid SEQ:5020.
DE
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX WO200140521-A2.
XX
XX 07-JUN-2001.
XX
XX 30-NOV-2000; 2000WO-US032758.
XX
XX 30-NOV-1999; 99US-0168138P.
XX 29-NOV-2000; 2000US-00726173.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach M;
XX WPI, 2001-356160/37.
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX
XX Claim 1; Page 2046; 2653bp; English.
XX
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAWS3114 to AAWS3329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 9 A; 20 C; 14 G; 8 T; 0 U; 0 Other;
Query Match 4.8%; Score 47.8; DB 1; Length 51;
Best Local Similarity 96.1%; Pred. No. 97;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 641 CACCCAGGCTGAGTGCAGTGGCGCAATCTTGGCTCACTGCAACCTCTGCC 691
DB 1 CACCCAGGCTGAGTGCAGTGGCGCAATCTTGGCTCACTGCAACCTCTGCC 51

RESULT 24
AA173248/C
ID AA173248 standard; DNA; 51 BP.
XX
XX AA173248;
AC
XX 09-NOV-2001 (first entry)
XX
XX Human silent SNP containing nucleic acid SEQ:189.
XX

KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
XX WO200140521-A2.
XX
XX 07-JUN-2001.
XX
XX 30-NOV-2000; 2000WO-US032758.
XX
XX 30-NOV-1999; 99US-0168138P.
XX 29-NOV-2000; 2000US-00726173.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach M;
XX WPI, 2001-356160/37.
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX
XX Claim 1; Page 113; 2653bp; English.
XX
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAWS3114 to AAWS3329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 12 A; 8 C; 23 G; 8 T; 0 U; 0 Other;
Query Match 4.8%; Score 47.8; DB 1; Length 51;
Best Local Similarity 96.1%; Pred. No. 97;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 974 CTCAGTGAACCTCTGCTCCCGGCTCAAGCAATCTCTCTGCTCAAGCT 1024
DB 51 CTCAGTGAACCTCTGCTCCCGGCTCAAGCAATCTCTCTGCTCAAGCT 1

RESULT 25
AD112542/C
ID AD112542 standard; DNA; 49 BP.
XX
XX AD112542;
AC
XX 22-APR-2004 (first entry)
XX
XX Mutant human BRCA1 genomic DNA resulting from deletion 3 Segid 25.
DE
XX ds; cancer; human; tumour suppressor;
KW breast cancer susceptibility gene 1; BRCA1; repetitive Alu;
KW ovarian cancer; recombination; mutant.
XX
XX Homo sapiens.
XX

XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
PS Claim 1; Page 56; 2653pp; English.
XX
XX
CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA173114 to AA175329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
SQ Sequence 51 BP; 10 A; 15 C; 18 G; 8 T; 0 U; 0 Other;
XX
XX
XX Query Match 4.7%; Score 46.8; DB 1; Length 51;
XX Best Local Similarity 96.0%; Pred. No. 1.1e+02;
XX Matches 48; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 638 TGTCAACCCAGCTGAGTGCAGTGCAGCAATCTTGCTCCTCACTGCAACCTC 687
DB 51 TGTCCGCCAGCTGAGTGCAGTGCAGCAATCTTGCTCCTCACTGCAACCTC 2
RESULT 28
AA177229
ID AA177229 standard; cDNA; 51 BP.
XX
XX AAA177229;
XX
XX 16-NOV-2000 (first entry)
XX
XX Human clone cg43971764 polymorphic site, SEQ ID NO:912.
XX
XX Human; single nucleotide polymorphism; SNP; chromosome 15; detection;
XX identification; gene therapy; ss.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX FT variation replace(26,1)
XX FT /*tag= a
XX
XX WO200029623-A2.
XX
XX 25-MAY-2000.
XX
XX 17-NOV-1999; 99WO-US027293.
XX
XX PF 17-NOV-1999; 99US-0109024P.
XX
XX PR 17-NOV-1998; 98US-0109024P.
XX
XX PR 16-NOV-1999; 99US-00443199.
XX
XX (CURA-) CURAGEN CORP.
XX
XX PA
XX
XX Shimkets RA, Leach MD;
XX
XX MPI; 2000-387626/33.
XX
XX Human nucleic acids containing single nucleotide polymorphisms, useful
XX for treating a subject suffering, or at risk from a pathology due to the
PT

PT presence of a sequence polymorphism.
XX
XX
PS Claim 1; Page 433; 543pp; English.
XX
XX
CC Sequences AA176318-A177509 represent 1192 human nucleic acid sequences
CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 1112
CC (AA176318-A177429) are consecutive pairs of nucleotides which contain
CC silent SNPs. Sequences 1113 to 1192 (AA177430-A177509) are consecutive
CC pairs of nucleotides containing SNPs which result in changes in the
CC corresponding amino acid sequences (AA177429-11128). The SNPs in
CC sequences 1113 to 1128 (AA177430-A177445) lead to conservative amino acid
CC changes, while those in sequences 1129 to 1186 (AA177446-A177509) result
CC in non-conservative changes. The SNPs in sequences 1187 to 1192
CC (AA177504-A177509) generate frameshift mutations. The invention also
CC relates to a method of detecting a polymorphic site in a nucleic acid and
CC a method of determining the relatedness of two nucleic acids. It also
CC encompasses peptides containing polymorphic sites, antibodies raised
CC against such peptides, and a method of detecting polymorphic
CC proteins/peptides using the antibodies. The nucleic acids are useful for
CC gene therapy of an individual having, suspected of having, or at risk of
CC developing a pathological condition due to the presence of a sequence
CC polymorphism. Such treatment would comprise administration of the wild-
CC type nucleic acid sequence. Antibodies raised against polymorphic
CC peptides can also be used in the treatment of such individuals
SQ Sequence 51 BP; 11 A; 21 C; 13 G; 6 T; 0 U; 0 Other;
XX
XX
XX Query Match 4.7%; Score 46.2; DB 1; Length 51;
XX Best Local Similarity 94.1%; Pred. No. 1.2e+02;
XX Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 847 CCTGGGCTCCCAAGTGTGGATTACAGGCGTGAAGCCACCGCCGGC 897
DB 1 CCTAGGCTCCCAAGTGTGGATTACAGGCGTGAAGCCACCGCCGGC 51
RESULT 29
AA173249/C
ID AA173249 standard; DNA; 51 BP.
XX
XX AAA173249;
XX
XX 09-NOV-2001 (first entry)
XX
XX Human silent SNP containing nucleic acid SEQ:190.
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
XX protein therapy; vaccine; probe; diagnostic assay; detection;
XX quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
XX
XX
XX WO200140521-A2.
XX
XX 07-JUN-2001.
XX
XX 30-NOV-2000; 2000WO-US032758.
XX
XX PF 30-NOV-1999; 99US-0168138P.
XX
XX PR 29-NOV-2000; 2000US-00726173.
XX
XX (CURA-) CURAGEN CORP.
XX
XX PA
XX
XX Shimkets RA, Leach M;
XX
XX MPI; 2001-356160/37.
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
XX therapy.
XX
XX Claim 1; Page 113; 2653pp; English.
XX
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC

CC sequences (1), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (1) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (1) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (1) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (1) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 13 A; 8 C; 22 G; 8 T; 0 U; 0 Other;
XX
Query Match 4.7%; Score 46.2; DB 1; Length 51;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 974 CTCACGTGACCTCTGCTCCGCGGCTCAAGCGATTCCTCTGTCAGCCT 1024
DB 51 CTCACGTGACCTCTGCTCCGCGGCTCAAGCGATTCCTCTGTCAGCCT 1
XX
RESULT 30
AA178078
ID AA178078 standard; DNA; 51 BP.
XX
AC AA178078;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:5019.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
PN MO200140521-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000MO-US032758.
XX
PR 30-NOV-1999; 99US-0168138P.
XX
PR 29-NOV-2000; 2000US-00726173.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkete RA, Leach M;
XX
DR WPI; 2001-356160/37.
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
XX therapy.
XX
PS Claim 1; Page 2046; 2653bp; English.
XX
CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (1) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For

CC example, (1) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (1) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (1) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 8 A; 20 C; 15 G; 8 T; 0 U; 0 Other;
XX
Query Match 4.7%; Score 46.2; DB 1; Length 51;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 641 CACCCAGGCTGAGTGCAGTGGCCGACATTCGCTCACTGCAACCTGGCC 691
DB 1 CACCCAGGCTGAGTGCAGTGGCCGACATTCGCTCACTGCAACCTGGCC 51
XX
RESULT 31
AA179818
ID AA179818 standard; DNA; 51 BP.
XX
AC AA179818;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human nonconservative amino acid changing SNP nucleic acid SEQ:6759.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
PN MO200140521-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000MO-US032758.
XX
PR 30-NOV-1999; 99US-0168138P.
XX
PR 29-NOV-2000; 2000US-00726173.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkete RA, Leach M;
XX
DR WPI; 2001-356160/37.
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
XX therapy.
XX
PS Claim 1; Page 2573; 2653bp; English.
XX
CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (1) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (1) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (1) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and

CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 9 A; 16 C; 14 G; 12 T; 0 U; 0 Other;
Query Match 4.7%; Score 46.2; DB 1; Length 51;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 695 CGGGTTCAAGTATTCTCTCCGCCAGCCTCTGAGTAGCTGGAGCTACAG 745
DB 1 CGGGTTCAAGCATCTCTCTGCTCAGCCTCTGAGTAGCTGGAGCTACAG 51
RESULT 32
AA176250/c
ID AA176250 standard; DNA; 51 BP.
XX
AC AA176250;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:3191.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
PN WO200140521-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US032758.
XX
PR 30-NOV-1999; 99US-0168138P.
PR 29-NOV-2000; 2000US-00726173.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-356160/37.
XX
PT polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX
PS Claim 1; Page 1026; 2653pp; English.
CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA53114 to AA53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples

XX
SQ Sequence 51 BP; 12 A; 15 C; 15 G; 9 T; 0 U; 0 Other;
Query Match 4.7%; Score 46.2; DB 1; Length 51;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 639 GTCAACCAGGCTGAGTGCAGTGGCGCATCTTGGCTCACTGCAACTCTG 689
DB 51 GTCAACCAGGCTGAGTGCAGTGGCATGATCTTGGCTCACTGCAACTCTG 1
RESULT 33
AA17676/c
ID AA17676 standard; DNA; 51 BP.
XX
AC AA17676;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:4617.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
PN WO200140521-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US032758.
XX
PR 30-NOV-1999; 99US-0168138P.
PR 29-NOV-2000; 2000US-00726173.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-356160/37.
XX
PT polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX
PS Claim 1; Page 1923; 2653pp; English.
CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA53114 to AA53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
SQ Sequence 51 BP; 12 A; 10 C; 21 G; 8 T; 0 U; 0 Other;
Query Match 4.7%; Score 46.2; DB 1; Length 51;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CC the invention may also be useful for gene therapy. The genes and proteins
CC of the invention are useful for modulating the maturation of an immune
CC system cell, kidney cell, pancreas cell, retinal cell, spleen cell or
CC reticuloendothelial cell, modulating interactions between lymphoid and
CC non-lymphoid immune system cells, as molecular markers, as drug targets,
CC assessing kidney, pancreas or spleen function and for detecting,
CC diagnosing, staging, monitoring, prognosticating, preventing or treating
CC diseases and conditions associated with genes of the bone marrow, kidney,
CC spleen, pancreas, retina, spleen or lymphoid disease (for example,
CC neutropenia, leucopenia, cancer, multiple myeloma, renal failure,
CC glomerular disease, diabetes, retinal degeneration, optic neuritis,
CC glaucoma or anaemia. The present sequence is that of a human tissue-
CC specific gene promoter DNA sequence which is related to the invention.

XX Sequence 50 BP; 11 A; 14 C; 16 G; 9 T; 0 U; 0 Other;

Query Match 4.6%; Score 45.2; DB 1; Length 50;
Best Local Similarity 94.0%; Pred. No. 1.3e+02;
Matches 47; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 836 TGATGTGCTGCTGCTGCTGCCAAGTGTGGATTCAGGCGTGAAGCC 885

DB 50 TGATCCACTGCTGCTGCTGCCAAGTGTGGATTCAGGCGTGAAGCC 1

RESULT 36

AA173067/C
ID AA173067 standard; DNA; 51 BP.

AC AA173067;

DT 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ:8.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;

KM protein therapy; vaccine; probe; diagnostic assay; detection;

KM quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

OS WO200140521-A2.

PN 07-JUN-2001.

PD 30-NOV-2000; 2000WO-US032758.

PF 30-NOV-1999; 99US-0168138P.

PR 29-NOV-2000; 2000US-00726173.

PA (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach M;

DR WPI; 2001-356160/37.

XX Polymorphic nucleic acid sequences, useful in genetic testing and

PT therapy.

PS Claim 1; Page 56; 2653pp; English.

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples

XX Sequence 51 BP; 11 A; 15 C; 17 G; 8 T; 0 U; 0 Other;

Query Match 4.6%; Score 45.2; DB 1; Length 51;
Best Local Similarity 94.0%; Pred. No. 1.3e+02;
Matches 47; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 638 TGTACCCAGGCTGAGTGCAGTGCAGATCTTGCTCACTGCAACTC 687

DB 51 TGTGCCAGGCTGAGTGCAGTGCAGATCTTGCTCACTGCAACTC 2

AA174554/C
ID AA174554 standard; DNA; 51 BP.

AC AA174554;

DT 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ:1495.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;

KM protein therapy; vaccine; probe; diagnostic assay; detection;

KM quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

OS WO200140521-A2.

PN 07-JUN-2001.

PD 30-NOV-2000; 2000WO-US032758.

PF 30-NOV-1999; 99US-0168138P.

PR 29-NOV-2000; 2000US-00726173.

PA (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach M;

DR WPI; 2001-356160/37.

XX Polymorphic nucleic acid sequences, useful in genetic testing and

PT therapy.

PS Claim 1; Page 511; 2653pp; English.

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC polypeptides in samples
XX Sequence 51 BP; 10 A; 15 C; 17 G; 9 T; 0 U; 0 Other;

Query Match 4.6%; Score 45.2; DB 1; Length 51;
Best Local Similarity 94.0%; Pred. No. 1.3e+02;
Matches 47; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 635 CTCTGTACCCGAGGTGAGTGCAGTGGCGCAATCTTGGCTCACTGCAAC 684
DB 50 CTGTGTACCCGAGGTGAGTGCAGTGGCGCAATCTTGGCTCACTGCAAC 1

RESULT 38
AA173064/C
ID AA173064 standard; DNA; 51 BP.

XX AA173064;
AC
XX
XX
DT 09-NOV-2001 (first entry)

XX Human silent SNP containing nucleic acid SEQ.5.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX WO200140521-A2.

XX 07-JUN-2001.

XX 30-NOV-2000; 2000MO-US032758.

XX 30-NOV-1999; 99US-0168138P.

XX 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

XX Shimkete RA, Leach M;

XX WPI; 2001-356160/37.

XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.

XX Claim 1; Page 55; 2653pp; English.

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX Sequence 51 BP; 14 A; 10 C; 19 G; 8 T; 0 U; 0 Other;

Query Match 4.5%; Score 44.8; DB 1; Length 51;
Best Local Similarity 95.8%; Pred. No. 1.4e+02;

Matches 46; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 966 AATCTGGCTCACTGCAACCTTGGCTCCCGGAGCTCAAGCATTTCTCC 1013
DB 48 AATCTGGCTCACTGCAACCTTGGCTCCCGGAGCTCAAGCATTTCTCC 1

RESULT 39
AA177324
ID AA177324 standard; DNA; 51 BP.

XX AA177324;

XX 09-NOV-2001 (first entry)

XX Human silent SNP containing nucleic acid SEQ.4265.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX WO200140521-A2.

XX 07-JUN-2001.

XX 30-NOV-2000; 2000MO-US032758.

XX 30-NOV-1999; 99US-0168138P.

XX 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

XX Shimkete RA, Leach M;

XX WPI; 2001-356160/37.

XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.

XX Claim 1; Page 1815; 2653pp; English.

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX Sequence 51 BP; 8 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 4.5%; Score 44.8; DB 1; Length 51;
Best Local Similarity 95.8%; Pred. No. 1.4e+02;
Matches 46; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 843 CTGCTGCTGCTCCCAAGTGTGGGATTACAGGCTGACCAAC 890
DB 4 CCGCTGCTGCTCCCAAGTGTGGGATTACAGGCTGACCAAC 51

RESULT 40
 AAA77498
 ID AAA77498 standard; cDNA; 51 BP.
 AC AAA77498;
 DT 16-NOV-2000 (first entry)
 DE Human Alu subfamily S9 gene polymorphic site, SEQ ID NO:1181.
 DE Human, single nucleotide polymorphism; SNP; detection; identification;
 KM gene therapy; ss.
 OS Homo sapiens.
 FH Key location/Qualifiers
 FT variation replace(26,T)
 FT /*tag= a
 WO200029623-A2.
 PD 25-MAY-2000.
 PF 17-NOV-1999; 99WO-US027293.
 PR 17-NOV-1998; 98US-0109024P.
 PR 16-NOV-1999; 99US-00443199.
 PA (CURA-) CURAGEN CORP.
 PI Shinkets RA, Leach MD;
 DR WPI; 2000-387826/33.
 DR P-PSDB; AAB11817.
 PT Human nucleic acids containing single nucleotide polymorphisms, useful
 PT for treating a subject suffering, or at risk from a pathology due to the
 PT presence of a sequence polymorphism.
 PS Claim 1; Page 515; 543pp; English.
 XX Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
 CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 1112
 CC (AAA76318-A77429) are consecutive pairs of nucleotides which contain
 CC silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are consecutive
 CC pairs of nucleotides containing SNPs which result in changes in the
 CC corresponding amino acid sequences (AAB11749-B11828). The SNPs in
 CC sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid
 CC changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result
 CC in non-conservative changes. The SNPs in sequences 1187 to 1192
 CC (AAA77504-A77509) generate frameshift mutations. The invention also
 CC relates to a method of detecting a polymorphic site in a nucleic acid and
 CC a method of determining the relatedness of two nucleic acids. It also
 CC encompasses peptides containing polymorphic sites, antibodies raised
 CC against such peptides, and a method of detecting polymorphic
 CC proteins/peptides using the antibodies. The nucleic acids are useful for
 CC gene therapy of an individual having, suspected of having, or at risk of
 CC developing a pathological condition due to the presence of a sequence
 CC polymorphism. Such treatment would comprise administration of the wild-
 CC type nucleic acid sequence. Antibodies raised against polymorphic
 CC peptides can also be used in the treatment of such individuals
 SQ Sequence 51 BP; 12 A; 18 C; 10 G; 11 T; 0 U; 0 Other;

Query Match 4.5%; Score 44.6; DB 1; Length 51;
 Best Local Similarity 92.2%; Pred. No. 1.4e+02;
 Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 355 CTGAGCTCAGAGCTCCTCAGCTCCCAAGCTGGGATTACA 405
 DB 1 CTGAGCTCAGAGCTCCTCAGCTCCCAAGCTGGGATTACA 51

RESULT 41
 AAA77230
 ID AAA77230 standard; cDNA; 51 BP.
 AC AAA77230;
 DT 16-NOV-2000 (first entry)
 DE Human clone cg43972482 polymorphic site, SEQ ID NO:913.
 DE Human, single nucleotide polymorphism; SNP; chromosome 8; detection;
 KM identification; gene therapy; ss.
 OS Homo sapiens.
 FH Key location/Qualifiers
 FT variation replace(26,C)
 FT /*tag= a
 WO200029623-A2.
 PD 25-MAY-2000.
 PF 17-NOV-1999; 99WO-US027293.
 PR 17-NOV-1998; 98US-0109024P.
 PR 16-NOV-1999; 99US-00443199.
 PA (CURA-) CURAGEN CORP.
 PI Shinkets RA, Leach MD;
 DR WPI; 2000-387826/33.
 DR Human nucleic acids containing single nucleotide polymorphisms, useful
 PT for treating a subject suffering, or at risk from a pathology due to the
 PT presence of a sequence polymorphism.
 PS Claim 1; Page 433; 543pp; English.
 XX Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
 CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 1112
 CC (AAA76318-A77429) are consecutive pairs of nucleotides which contain
 CC silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are consecutive
 CC pairs of nucleotides containing SNPs which result in changes in the
 CC corresponding amino acid sequences (AAB11749-B11828). The SNPs in
 CC sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid
 CC changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result
 CC in non-conservative changes. The SNPs in sequences 1187 to 1192
 CC (AAA77504-A77509) generate frameshift mutations. The invention also
 CC relates to a method of detecting a polymorphic site in a nucleic acid and
 CC a method of determining the relatedness of two nucleic acids. It also
 CC encompasses peptides containing polymorphic sites, antibodies raised
 CC against such peptides, and a method of detecting polymorphic
 CC proteins/peptides using the antibodies. The nucleic acids are useful for
 CC gene therapy of an individual having, suspected of having, or at risk of
 CC developing a pathological condition due to the presence of a sequence
 CC polymorphism. Such treatment would comprise administration of the wild-
 CC type nucleic acid sequence. Antibodies raised against polymorphic
 CC peptides can also be used in the treatment of such individuals
 SQ Sequence 51 BP; 9 A; 11 C; 16 G; 15 T; 0 U; 0 Other;

Query Match 4.5%; Score 44.6; DB 1; Length 51;
 Best Local Similarity 92.2%; Pred. No. 1.4e+02;
 Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 177 TTAGTAGAGAGGAGTTCTCAGTGTGCTGAGGCTGCTGAACTCCG 227
 DB 1 TTAGTAGAGAGGAGGTTTCCACCATTTGCTGAGGCTGCTGAACTCCG 51


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RESULT 42
AAL31459
ID AAL31459 standard; DNA; 51 BP.
XX
AC AAL31459;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #4667.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035498.
XX
PR 28-DEC-1999; 99US-0173419P.
XX
PR 27-DEC-2000; 2000US-00173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinketsu RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX
PT autoimmune diseases and infections.
XX
PS Claim 1; Page 2729; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukemia), diseases of the nervous system and an infection of pathogenic
CC organisms
XX
SQ Sequence 51 BP; 11 A; 20 C; 12 G; 8 T; 0 U; 0 Other;
XX
XX
Query Match 4.5%; Score 44.6; DB 1; Length 51;
Best Local Similarity 92.2%; Pred. No. 1.4e+02;
Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 843 CTTGCTCTGCGCTCCCAAGTCTGAGTACAGGCGTGAAGCCACCGCC 893
DB 1 CCGCGCTTGGCTCCCAAGTCTGAGTACAGGCGTGAAGCCACCGCC 51
RESULT 43
AAL29843
ID AAL29843 standard; DNA; 51 BP.
```

```
XX
AC AAL29843;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #3051.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035498.
XX
PR 28-DEC-1999; 99US-0173419P.
XX
PR 27-DEC-2000; 2000US-00173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinketsu RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX
PT autoimmune diseases and infections.
XX
PS Claim 1; Page 2260; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukemia), diseases of the nervous system and an infection of pathogenic
CC organisms
XX
SQ Sequence 51 BP; 7 A; 24 C; 9 G; 11 T; 0 U; 0 Other;
XX
XX
Query Match 4.5%; Score 44.6; DB 1; Length 51;
Best Local Similarity 92.2%; Pred. No. 1.4e+02;
Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 974 CTCATGCAACCTCTGCTCCCGGGCTCAAGCATTTCTGTCAGCCT 1024
DB 1 CTCATGCAAGCTCTGCAAGCTCCCGGGCTCAAGCATTTCTGTCAGCCT 51
RESULT 44
AAL173062/C
ID AAL173062 standard; DNA; 51 BP.
XX
AC AAL173062;
XX
```

DT 09-NOV-2001 (first entry)
XX Human silent SNP containing nucleic acid SEQ:3.
DE
XX
XX Human, single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KM quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
OS
XX WO200140521-A2.
FN
XX
XX 07-JUN-2001.
PD
XX
XX 30-NOV-2000; 2000WO-US032758.
PF
XX
XX 30-NOV-1999; 99US-0168138P.
PR
XX 29-NOV-2000; 2000US-00726173.
PA
XX (CURA-) CURAGEN CORP.
PI
XX Shimkets RA, Leach M;
PS WPI; 2001-356160/37.
DR
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
PT
XX
XX Claim 1; Page 55; 2653pp; English.
PS
XX
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA173114 to AA175332 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
XX
SQ Sequence 51 BP; 12 A; 11 C; 21 G; 7 T; 0 U; 0 Other;
XX
XX
XX Query Match 4.5%; Score 44.6; DB 1; Length 51;
XX Best Local Similarity 92.2%; Pred. No. 1.4e+02;
XX Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 971 CGGCTCAGTCAACCTCGCTCCGCGGCTCAAGGATCTCTGCTCAG 1021
DB 51 CGGCTCAGTCAACCTCGCTCCGCGGCTCAAGGATCTCTGCTCAG 1

KW quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
OS
XX WO200140521-A2.
FN
XX
XX 07-JUN-2001.
PD
XX
XX 30-NOV-2000; 2000WO-US032758.
PF
XX
XX 30-NOV-1999; 99US-0168138P.
PR
XX 29-NOV-2000; 2000US-00726173.
PA
XX (CURA-) CURAGEN CORP.
PI
XX Shimkets RA, Leach M;
PS WPI; 2001-356160/37.
DR
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
PT
XX
XX Claim 1; Page 1876; 2653pp; English.
PS
XX
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA173114 to AA175332 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
XX
SQ Sequence 51 BP; 18 A; 14 C; 10 G; 9 T; 0 U; 0 Other;
XX
XX
XX Query Match 4.5%; Score 44.6; DB 1; Length 51;
XX Best Local Similarity 92.2%; Pred. No. 1.4e+02;
XX Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 175 TTTTGTAGATGAGTGTCTCCATGTTGGTCAAGGCTGTCTGAATCC 225
DB 51 TTTTGTAGATGAGTGTCTCCATGTTGGTCAAGGCTGTCTGAATCC 1

RESULT 45
AA177522/C
ID AA177522 standard; DNA; 51 BP.
XX
XX AA177522;
AC
XX
XX 09-NOV-2001 (first entry)
DT
XX
XX Human silent SNP containing nucleic acid SEQ:4463.
DE
XX Human, single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW

RESULT 46
AA178388
ID AA178388 standard; DNA; 51 BP.
XX
XX AA178388;
AC
XX
XX 09-NOV-2001 (first entry)
DT
XX
XX Human silent SNP containing nucleic acid SEQ:5329.
DE
XX Human, single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200140521-A2.
PN
XX

XX polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX
XX Claim 1; Page 1924; 2653pp; English.
XX
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA55314 to AA55329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
XX Sequence 51 BP; 12 A; 9 C; 21 G; 9 T; 0 U; 0 Other;
SQ
Query Match 4.5%; Score 44.6; DB 1; Length 51;
Best Local Similarity 92.2%; Pred. No. 1.4e+02;
Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy 971 CGGCTCACTGCACCTCTGCTCCGAGCTCAAGGATTCTCTCTCAG 1021
Db 51 CGGCTCACTGCACCTCTGCTCCGAGCTCAAGGATTCTCTCTCAG 1
RESULT 49
AAH89407
ID AAH89407 standard; DNA; 51 BP.
AC AAH89407;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 188.
XX
XX Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200151670-A2.
PN 19-JUL-2001.
XX
XX 05-JAN-2001; 2001WO-US000322.
PD
XX
XX 07-JAN-2000; 2000US-0174962P.
PR
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX Shimketa RA, Leach MD;
PI
XX
XX WPI; 2001-451871/48.
DR
XX
XX P-PSDB; AAM00294.
DR
XX
XX Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT infection and diabetes.
XX
XX Claim 1; Page 160; 475pp; English.
PS
XX

CC The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tubercous
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC autoimmunity. The present sequence is a polymorphism-containing
CC oligonucleotide fragment of the invention
XX
XX Sequence 51 BP; 8 A; 23 C; 8 G; 12 T; 0 U; 0 Other;
SQ
Query Match 4.5%; Score 44.6; DB 1; Length 51;
Best Local Similarity 92.2%; Pred. No. 1.4e+02;
Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy 974 CTCACCTGCACCTCTGCTCCGAGCTCAAGGATTCTCTCTCAGCCT 1024
Db 1 CTCACCTGCACCTCTGCTCCGAGCTCAAGGATTCTCTCTCAGCCT 51
RESULT 50
AAH89406
ID AAH89406 standard; DNA; 51 BP.
AC AAH89406;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 187.
XX
XX Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; de.
XX
XX Homo sapiens.
OS
XX
XX WO200151670-A2.
PN 19-JUL-2001.
XX
XX 05-JAN-2001; 2001WO-US000322.
PD
XX
XX 07-JAN-2000; 2000US-0174962P.
PR
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX Shimketa RA, Leach MD;
PI
XX
XX WPI; 2001-451871/48.
DR
XX
XX P-PSDB; AAM00293.
DR
XX
XX Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT infection and diabetes.
XX
XX Claim 1; Page 159; 475pp; English.
PS
XX
XX The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tubercous
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC autoimmunity. The present sequence is a polymorphism-containing
CC oligonucleotide fragment of the invention
XX
XX Sequence 51 BP; 8 A; 22 C; 8 G; 13 T; 0 U; 0 Other;
SQ

Query Match 4.5%; Score 44.6; DB 1; Length 51;
Best Local Similarity 92.2%; Pred. No. 1.4e+02;
Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 674 CTCACCTGCACCACTCTGCGCTCCGCGGTCAAGTATTCCTGCGCCAGCCT 724
DB 1 CTCACCTGCACCACTCTGCGCTCCGCGGTCAAGTATTCCTGCGCCAGCCT 51

RESULT 51

ABL00260
ID ABL00260 standard; DNA; 51 BP.

XX ABL00260;

XX 05-MAR-2002 (first entry)

XX Human silent noncoding SNP oligonucleotide SEQ ID NO:251.

XX Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;

KW immunosuppressive; antineoplastic; neuroprotective; anticancer;

KW autoimmune disease; inflammation; cancer; nervous system disease;

KW infection; polymorphic protein; ds.

XX Homo sapiens.

XX MO200138586-A2.

XX 31-MAY-2001.

XX 22-NOV-2000; 2000WO-US032311.

XX 24-NOV-1999; 99US-0167383P.

XX (CURA-) CURAGEN CORP.

XX Shimketa RA, Leach M;

XX WPI; 2001-355949/37.

XX Isolated human nucleic acids comprising one or more single nucleotide

PT polymorphisms, useful for treating a subject suffering from a pathology,

PT e.g. autoimmune diseases, ascribed to the presence of a sequence

PT polymorphism.

XX Claim 1; Page 323; 674pp; English.

XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides

CC comprising one or more single nucleotide polymorphisms (SNPs).

CC to ABB56903 represent human peptides encoded by some of the SNP

CC oligonucleotides. The sequences from the present invention can have

CC immunosuppressive, cytostatic, antineoplastic, neuroprotective and

CC and antibodies from the present invention can be used for treating a

CC subject suffering from, at risk for, or suspected of, suffering from a

CC pathology ascribed to the presence of a sequence polymorphism. The

CC the nervous system, and infection by pathogenic microorganisms. The SNPs

CC are also useful for determining which forms of a characterised

CC polymorphism are present in individuals. The antibodies may be used in

CC the detection, quantitation and/or cellular or tissue localisation of a

CC polymorphic protein (e.g., for use in measuring levels of the polymorphic

CC protein within appropriate physiological samples)

XX Sequence 51 BP; 9 A; 17 C; 13 G; 12 T; 0 U; 0 Other;

XX Query Match 4.5%; Score 44.6; DB 1; Length 51;

XX Best Local Similarity 92.2%; Pred. No. 1.4e+02;

XX Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 954 GTGCAATGGCAATCTGCGCTCACTGCACCTCTGCGCGGTCAAG 1004

DB 1 GTGCAATGGCAATCTGCGCTCACTGCACCTCTGCGCGGTCAAG 51

RESULT 52

AAH89761
ID AAH89761 standard; DNA; 50 BP.

XX AAH89761;

XX 01-OCT-2001 (first entry)

XX Human coding sequence polymorphic site SEQ ID NO: 542.

XX Human; single nucleotide polymorphism; SNP; paternity test;

KW forensic test; aberrant protein expression; ds.

XX Homo sapiens.

XX MO200151670-A2.

XX 19-JUL-2001.

XX 05-JAN-2001; 2001WO-US000322.

XX 07-JAN-2000; 2000US-0174962P.

XX (CURA-) CURAGEN CORP.

XX Shimketa RA, Leach MD;

XX WPI; 2001-451871/48.

XX P-P-SDB; AAM00644.

XX Isolated human polynucleotides containing single nucleotide

PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,

PT infection and diabetes.

XX Claim 1; Page 260; 475pp; English.

XX The present invention relates to human nucleic acids containing single

CC nucleotide polymorphisms (SNPs). These can be used in forensic and

CC paternity tests, and to aid in the treatment of diseases associated with

CC aberrant protein expression, including cancer, amyloidosis, diabetes,

CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,

CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,

CC meningitis, muscular disorders, dementia, neurological diseases, tuberculous

CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or

CC autoimmunity. The present sequence is a polymorphism-containing

CC oligonucleotide fragment of the invention

XX Sequence 50 BP; 10 A; 10 C; 11 G; 19 T; 0 U; 0 Other;

XX Query Match 4.4%; Score 43.8; DB 1; Length 50;

XX Best Local Similarity 95.7%; Pred. No. 1.5e+02;

XX Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 750 CCACCAAGCCTAGCTATTTTGTATTTTGTAGTAGAGTGGGTT 796

DB 3 CCACCAAGCCTAGCTATTTTGTATTTTGTAGTAGAGTGGGTT 49

RESULT 53

AAH89763
ID AAH89763 standard; DNA; 50 BP.

XX AAH89763;

XX 01-OCT-2001 (first entry)

XX Human coding sequence polymorphic site SEQ ID NO: 544.

XX Human; single nucleotide polymorphism; SNP; paternity test;

KW forensic test; aberrant protein expression; ds.

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XX OS Homo sapiens.
XX PN WO200151670-A2.
XX PD 19-JUL-2001.
XX PF 05-JAN-2001; 2001WO-US000322.
XX PR 07-JAN-2000; 2000US-0174962P.
XX PA (CURA-) CURAGEN CORP.
XX PI Shimkets RA, Leach MD;
XX DR WPI; 2001-451871/48.
XX P-PSDB; AAM00646.
PT Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT infection and diabetes.
XX PS Claim 1; Page 260; 475pp; English.
XX CC The present invention relates to human nucleic acids containing single
XX CC nucleotide polymorphisms (SNPs). These can be used in forensic and
XX CC paternity tests, and to aid in the treatment of diseases associated with
XX CC aberrant protein expression, including cancer, amyloidosis, diabetes,
XX CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
XX CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
XX CC meningitis, muscular disorders, dementia, neurological diseases, tubercous
XX CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
XX CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
XX CC autoimmunity. The present sequence is a polymorphism-containing
XX CC oligonucleotide fragment of the invention
XX SQ Sequence 50 BP; 10 A; 10 C; 11 G; 19 T; 0 U; 0 Other;
XX
Query Match 4.4%; Score 43.8; DB 1; Length 50;
Best Local Similarity 95.7%; Pred.No. 1.5e+02;
Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 750 CCACCAAGCGCTAATTTTGTATTTTGTATTTAGAGAGAGGGGT 796
DB 2 CCACCAAGCGCTAATTTTGTATTTTGTATTTAGAGAGAGCGGGT 48
RESULT 54
AAH89759
ID AAH89759 standard; DNA; 50 BP.
XX AC AAH89759;
XX DT 01-OCT-2001 (first entry)
XX DE Human coding sequence polymorphic site SEQ ID NO: 540.
XX KM Human; single nucleotide polymorphism; SNP; paternity test;
XX KM forensic test; aberrant protein expression; ds.
XX OS Homo sapiens.
XX PN WO200151670-A2.
XX PD 19-JUL-2001.
XX PF 05-JAN-2001; 2001WO-US000322.
XX PR 07-JAN-2000; 2000US-0174962P.
XX PA (CURA-) CURAGEN CORP.
XX PI Shimkets RA, Leach MD;
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XX DR WPI; 2001-451871/48.
XX P-PSDB; AAM00642.
PT Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT infection and diabetes.
XX PS Claim 1; Page 259; 475pp; English.
XX CC The present invention relates to human nucleic acids containing single
XX CC nucleotide polymorphisms (SNPs). These can be used in forensic and
XX CC paternity tests, and to aid in the treatment of diseases associated with
XX CC aberrant protein expression, including cancer, amyloidosis, diabetes,
XX CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
XX CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
XX CC meningitis, muscular disorders, dementia, neurological diseases, tubercous
XX CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
XX CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
XX CC autoimmunity. The present sequence is a polymorphism-containing
XX CC oligonucleotide fragment of the invention
XX SQ Sequence 50 BP; 10 A; 11 C; 11 G; 18 T; 0 U; 0 Other;
XX
Query Match 4.4%; Score 43.8; DB 1; Length 50;
Best Local Similarity 95.7%; Pred.No. 1.5e+02;
Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 750 CCACCAAGCGCTAATTTTGTATTTTGTATTTAGAGAGAGGGGT 796
DB 4 CCACCAAGCGCTAATTTTGTATTTTGTATTTAGAGAGAGCGGGT 50
RESULT 55
AAI75600/C
ID AAI75600 standard; DNA; 51 BP.
XX AC AAI75600;
XX DT 09-NOV-2001 (first entry)
XX DE Human silent SNP containing nucleic acid SEQ:2541.
XX KM Human; single nucleotide polymorphism; SNP; genome; gene therapy;
XX KM protein therapy; vaccine; probe; diagnostic assay; detection;
XX KM quantitation; restorative therapy; polymorphic; ds.
XX OS Homo sapiens.
XX PN WO200140521-A2.
XX PD 07-JUN-2001.
XX PF 30-NOV-2000; 2000WO-US032758.
XX PR 30-NOV-1999; 99US-0168138P.
XX PR 29-NOV-2000; 2000US-00726173.
XX PA (CURA-) CURAGEN CORP.
XX PI Shimkets RA, Leach M;
XX DR WPI; 2001-356160/37.
XX PT Polymorphic nucleic acid sequences, useful in genetic testing and
XX PT therapy.
XX PS Claim 1; Page 829; 2653pp; English.
XX CC AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
XX CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
XX CC AAM53114 to AAM53329 represent peptides related to human polymorphic
XX CC polynucleotide sequences. The sequences can be used in gene and protein
```


CC systemic lupus erythromatous and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms

XX Sequence 51 BP; 9 A; 20 C; 12 G; 10 T; 0 U; 0 Other;

Query Match 4.4%; Score 43.6; DB 1; Length 51;
Best Local Similarity 92.0%; Pred. No. 1.6e+02;
Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 990 CCTCCGGGCTCAGGATTCCTCTCAGCTCCCAAGAGCTGGGA 1039
DB 2 CCTCCGGGCTCAGGATTCCTCCGCTCAGCTCCCAAGAGCTGGGA 51

RESULT 58
AA173532/c
ID AA173532 standard; DNA; 51 BP.

XX AA173532;

DT 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ:473.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX WO200140521-A2.

PD 07-JUN-2001.

PF 30-NOV-2000; 2000WO-US032758.

PR 30-NOV-1999; 99US-0168138P.

PR 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;

DR WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and
therapy.

PS Claim 1; Page 199; 2653pp; English.

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA173114 to AA175329 represent peptides related to human polymorphic
polynucleotide sequences. The sequences can be used in gene and protein
therapy, and in vaccine production. (I) and the polypeptides encoded by
them may be used in the prevention, diagnosis and treatment of diseases
associated with inappropriate expression of polymorphic polypeptides. For
example, (I) may be used to treat disorders by rectifying mutations or
deletions in a patient's genome that affect the activity of polypeptides
by expressing inactive proteins or to supplement the patients own
production of polypeptide. Additionally, (I) and its complementary
sequences may also be used as DNA probes in diagnostic assays to detect
and quantitate the presence of similar nucleic acids in samples, and
therefore which patients may be in need of restorative therapy. The
polypeptides encoded by (I) may be used as antigens in the production of
antibodies specific for polymorphic polypeptides. The antibodies may also
be used to down regulate expression and activity. The antibodies may also
be used as diagnostic agents for detecting the presence of polymorphic
polypeptides in samples

XX Sequence 51 BP; 10 A; 14 C; 18 G; 9 T; 0 U; 0 Other;

Query Match 4.4%; Score 43.6; DB 1; Length 51;
Best Local Similarity 92.0%; Pred. No. 1.6e+02;
Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 842 GCTTCCTCGGCTCCCAAGAGTCTGGGATTAACAGCGGCGACACAG 891
DB 50 GCTTCCTCGGCTCCCAAGAGTCTGGGATTAACAGCGGCGACACAG 1

RESULT 59
AA179585/c

ID AA179585 standard; DNA; 51 BP.

XX AA179585;

DT 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ:5526.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX WO200140521-A2.

PD 07-JUN-2001.

PF 30-NOV-2000; 2000WO-US032758.

PR 30-NOV-1999; 99US-0168138P.

PR 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;

DR WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and
therapy.

PS Claim 1; Page 2504; 2653pp; English.

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA173114 to AA175329 represent peptides related to human polymorphic
polynucleotide sequences. The sequences can be used in gene and protein
therapy, and in vaccine production. (I) and the polypeptides encoded by
them may be used in the prevention, diagnosis and treatment of diseases
associated with inappropriate expression of polymorphic polypeptides. For
example, (I) may be used to treat disorders by rectifying mutations or
deletions in a patient's genome that affect the activity of polypeptides
by expressing inactive proteins or to supplement the patients own
production of polypeptide. Additionally, (I) and its complementary
sequences may also be used as DNA probes in diagnostic assays to detect
and quantitate the presence of similar nucleic acids in samples, and
therefore which patients may be in need of restorative therapy. The
polypeptides encoded by (I) may be used as antigens in the production of
antibodies specific for polymorphic polypeptides. The antibodies may also
be used to down regulate expression and activity. The antibodies may also
be used as diagnostic agents for detecting the presence of polymorphic
polypeptides in samples

XX Sequence 51 BP; 11 A; 14 C; 17 G; 9 T; 0 U; 0 Other;

Query Match 4.4%; Score 43.6; DB 1; Length 51;
Best Local Similarity 92.0%; Pred. No. 1.6e+02;
Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 646 AGCTGAGTGCAGTGGCGCAATCTTGCTCAGTGCACACTCTGCTCCC 695

Db 51 AGGCTGAGTGCAGTGGCGGTGATCTTGGCTCACTGCACCTCC 2

RESULT 60
AA174555/C
ID AA174555 standard; DNA; 51 BP.

XX AA174555;

DT 09-NOV-2001 (first entry)

XX Human silent SNP containing nucleic acid SEQ:1496.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
XX protein therapy; vaccine; probe; diagnostic assay; detection;
XX quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX MO200140521-A2.

XX 07-JUN-2001.

XX 30-NOV-2000; 2000MO-US032758.

XX 30-NOV-1999; 99US-0168138P.

XX 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI; 2001-356160/37.

XX Polymorphic nucleic acid sequences, useful in genetic testing and
XX therapy.

XX Claim 1; Page 511; 2653pp; English.

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
XX sequences (I), which contain single nucleotide polymorphisms (SNPs).
XX AA173114 to AA175329 represent peptides related to human polymorphic
XX polynucleotide sequences. The sequences can be used in gene and protein
XX therapy, and in vaccine production. (I) and the polypeptides encoded by
XX them may be used in the prevention, diagnosis and treatment of diseases
XX associated with inappropriate expression of polymorphic polypeptides. For
XX example, (I) may be used to treat disorders by rectifying mutations or
XX deletions in a patient's genome that affect the activity of polypeptides
XX by expressing inactive proteins or to supplement the patients own
XX production of polypeptide. Additionally, (I) and its complementary
XX sequences may also be used as DNA probes in diagnostic assays to detect
XX and quantitate the presence of similar nucleic acids in samples, and
XX therefore which patients may be in need of restorative therapy. The
XX polypeptides encoded by (I) may be used as antigens in the production of
XX antibodies specific for polymorphic polypeptides. The antibodies may also
XX be used to down regulate expression and activity. The antibodies may also
XX be used as diagnostic agents for detecting the presence of polymorphic
XX polypeptides in samples

XX Sequence 51 BP; 10 A; 14 C; 17 G; 10 T; 0 U; 0 Other;

XX Query Match 4.4%; Score 43.6; DB 1; Length 51;

XX Best Local Similarity 92.0%; Pred. No. 1.6e+02;

XX Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

XX 635 CTCTGTACCCAGGCTGAGTGCAGTGGCGCAATCTTGGCTCACTGCAC 684

XX 50 CTCTGTACCCAGGCTGAGTGCAGTGGCGCAATCTTGGCTCACTGCAC 1

RESULT 61

AA173861

ID AA173861 standard; DNA; 51 BP.

XX AA173861;

DT 09-NOV-2001 (first entry)

XX Human silent SNP containing nucleic acid SEQ:802.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
XX protein therapy; vaccine; probe; diagnostic assay; detection;
XX quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX MO200140521-A2.

XX 07-JUN-2001.

XX 30-NOV-2000; 2000MO-US032758.

XX 30-NOV-1999; 99US-0168138P.

XX 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI; 2001-356160/37.

XX Polymorphic nucleic acid sequences, useful in genetic testing and
XX therapy.

XX Claim 1; Page 299; 2653pp; English.

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
XX sequences (I), which contain single nucleotide polymorphisms (SNPs).
XX AA173114 to AA175329 represent peptides related to human polymorphic
XX polynucleotide sequences. The sequences can be used in gene and protein
XX therapy, and in vaccine production. (I) and the polypeptides encoded by
XX them may be used in the prevention, diagnosis and treatment of diseases
XX associated with inappropriate expression of polymorphic polypeptides. For
XX example, (I) may be used to treat disorders by rectifying mutations or
XX deletions in a patient's genome that affect the activity of polypeptides
XX by expressing inactive proteins or to supplement the patients own
XX production of polypeptide. Additionally, (I) and its complementary
XX sequences may also be used as DNA probes in diagnostic assays to detect
XX and quantitate the presence of similar nucleic acids in samples, and
XX therefore which patients may be in need of restorative therapy. The
XX polypeptides encoded by (I) may be used as antigens in the production of
XX antibodies specific for polymorphic polypeptides. The antibodies may also
XX be used to down regulate expression and activity. The antibodies may also
XX be used as diagnostic agents for detecting the presence of polymorphic
XX polypeptides in samples

XX Sequence 51 BP; 9 A; 17 C; 13 G; 12 T; 0 U; 0 Other;

XX Query Match 4.4%; Score 43.6; DB 1; Length 51;

XX Best Local Similarity 92.0%; Pred. No. 1.6e+02;

XX Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

XX 638 TGTACCCAGGCTGAGTGCAGTGGCGCAATCTTGGCTCACTGCACCTC 687

XX 1 TGTACCCAGGCTGAGTGCAGTGGCGGTGATCTTGGCTCACTGCACCTC 50

RESULT 62

AA177807

AA177807 standard; DNA; 51 BP.

AA177807;

09-NOV-2001 (first entry)

XX 26-APR-2001.
PD 13-OCT-2000; 2000WO-US028436.
XX 15-OCT-1999; 99US-0160096P.
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX Picoult-Newburg L, Pohl M;
XX WPI; 2001-290930/30.
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX Claim 1; Page 56; 83pp; English.
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
XX primer extension (SNPE) primers, and the sequences of regions flanking
XX sites of single nucleotide polymorphisms SNPs. The present invention
XX includes kits for determining the presence or absence of a SNP, using the
XX oligonucleotides of the invention. The PCR primers are used to amplify a
XX SNP flanking sequence, the SNPE primer is used as a genotyping primer.
XX The oligonucleotides are useful for genotyping a nucleic acid sample by
XX performing a single-nucleotide primer extension reaction. The
XX oligonucleotides are useful for determining the presence, absence or
XX identity of a SNP and for genotyping nucleic acid samples, for e.g. to
XX assess by association analysis the genotype of an individual or group of
XX individuals, having a pathological phenotypic trait suspected of being
XX caused by one or more SNPs. Phenotypic traits include diseases e.g.
XX agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
XX dystrophy, familial hypercholesterolemia, polycystic kidney disease,
XX osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
XX traits also include symptoms of or susceptibility to multifactorial
XX disease of which a component is or may be genetic such as autoimmune
XX diseases, including, rheumatoid arthritis, multiple sclerosis,
XX inflammation, cancer, nervous system diseases and infection by pathogenic
XX microorganisms. The method is also useful in forensic investigations and
XX paternity analysis. The present sequence represents a fragment of human
XX DNA flanking the site of a single nucleotide polymorphism
XX
XX Sequence 51 BP; 9 A; 16 C; 13 G; 13 T; 0 U; 0 Other;
SQ
Query Match 4.4%; Score 43.6; DB 1; Length 51;
Best Local Similarity 92.0%; Pred. No. 1.6e+02;
Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 645 CAGGCTGAGTGCAGTGCAGCAATCTTGCTCACTGCACCTTGCTCC 694
DB 1 CAGGCTGAGTGCAGTGCAGCAATCTTGCTCACTGCACCTTGCTCC 50
RESULT 65
AA173065/c
ID AA173065 standard; DNA; 51 BP.
XX AA173065;
XX 09-NOV-2001 (first entry)
XX Human silent SNP containing nucleic acid SEQ.6.
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
XX protein therapy; vaccine; probe; diagnostic assay; detection;
XX quantitation; restorative therapy; polymorphic; ds.
XX Homo sapiens.
XX OS
XX 30-NOV-1999; 99US-0168138P.
XX PN W0200140521-A2.
XX PR 29-NOV-2000; 2000US-00726173.
XX 07-JUN-2001.

XX 30-NOV-2000; 2000WO-US032758.
XX 30-NOV-1999; 99US-0168138P.
XX 29-NOV-2000; 2000US-00726173.
XX (CURA-) CURAGEN CORP.
XX Shinkets RA, Leach M;
XX WPI; 2001-356160/37.
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
XX therapy.
XX Claim 1; Page 56; 2653pp; English.
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
XX sequences (I), which contain single nucleotide polymorphisms (SNPs).
XX AA173114 to AA175329 represent peptides related to human polymorphic
XX polynucleotide sequences. The sequences can be used in gene and protein
XX therapy, and in vaccine production. (I) and the polypeptides encoded by
XX them may be used in the prevention, diagnosis and treatment of diseases
XX associated with inappropriate expression of polymorphic polypeptides. For
XX example, (I) may be used to treat disorders by rectifying mutations or
XX deletions in a patient's genome that affect the activity of polypeptides
XX by expressing inactive proteins or to supplement the patient's own
XX production of polypeptide. Additionally, (I) and its complementary
XX sequences may also be used as DNA probes in diagnostic assays to detect
XX and quantitate the presence of similar nucleic acids in samples, and
XX therefore which patients may be in need of restorative therapy. The
XX polypeptides encoded by (I) may be used as antigens in the production of
XX antibodies specific for polymorphic polypeptides. The antibodies may also
XX be used to down regulate expression and activity. The antibodies may also
XX be used as diagnostic agents for detecting the presence of polymorphic
XX polypeptides in samples
XX
XX Sequence 51 BP; 13 A; 10 C; 20 G; 8 T; 0 U; 0 Other;
SQ
Query Match 4.4%; Score 43.2; DB 1; Length 51;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 45; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 966 AATCTGGCTCACTGCACCTTGCTCCCGGCTCAACGATTCCTCC 1013
DB 48 AATCTGGCTCACTGCACCTTGCTCCCGGCTCAACGATTCCTCC 1
RESULT 66
AA177325
ID AA177325 standard; DNA; 51 BP.
XX AA177325;
XX 09-NOV-2001 (first entry)
XX Human silent SNP containing nucleic acid SEQ.4266.
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
XX protein therapy; vaccine; probe; diagnostic assay; detection;
XX quantitation; restorative therapy; polymorphic; ds.
XX Homo sapiens.
XX OS
XX W0200140521-A2.
XX PN 07-JUN-2001.
XX 30-NOV-2000; 2000WO-US032758.
XX PF 30-NOV-1999; 99US-0168138P.
XX PR 29-NOV-2000; 2000US-00726173.
XX

PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX WPI; 2001-356160/37.
XX
XX polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
PS
XX Claim 1; Page 1815; 2653pp; English.
XX
XX AA173060 to AA17867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA173114 to AA173329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC thereafter which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
XX polypeptides in samples
XX
SQ Sequence 51 BP; 8 A; 20 C; 14 G; 9 T; 0 U; 0 Other;
XX
Query Match 4.4%; Score 43.2; DB 1; Length 51;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 45; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 843 CTGCTCGGCTCCCAAGTGTGGATTACAGCGGTGAGCCACAC 890
DB 4 CCGGCTCGGCTCCCAAGTGTGGATTACAGCGGTGAGCCACAC 51
XX
RESULT 67
AAA77231
ID AAA77231 standard; cDNA; 51 BP.
XX
AC AAA77231;
XX
DT 16-NOV-2000 (first entry)
XX
DE Human clone cg43972482 polymorphic site, SEQ ID NO:914.
XX
XX Human; single nucleotide polymorphism; SNP; chromosome 8; detection;
KM identification; gene therapy; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH variation replace(26,T)
FT /*tag= a
XX
XX WO200029623-A2.
XX
XX 25-MAY-2000.
XX
XX 17-NOV-1999; 99WO-US027293.
XX
XX 17-NOV-1998; 98US-0109024P.
XX
XX 16-NOV-1999; 99US-00443199.
XX
XX (CURA-) CURAGEN CORP.
PA Shimkets RA, Leach MD;
XX
PI

XX
XX WPI; 2000-387826/33.
XX
XX Human nucleic acids containing single nucleotide polymorphisms, useful
PT for treating a subject suffering; or at risk from a pathology due to the
PT presence of a sequence polymorphism.
XX
XX Claim 1; Page 433; 543pp; English.
XX
XX Sequences AA176318-A177509 represent 1192 human nucleic acid sequences
CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 1112
CC (AA176318-A177429) are consecutive pairs of nucleotides which contain
CC silent SNPs. Sequences 1113 to 1192 (AA177430-A177509) are consecutive
CC pairs of nucleotides containing SNPs which result in changes in the
CC corresponding amino acid sequences (AA11749-B11828). The SNPs in
CC sequences 1113 to 1128 (AA177430-A177445) lead to conservative amino acid
CC changes, while those in sequences 1129 to 1186 (AA177446-A177503) result
CC in non-conservative changes. The SNPs in sequences 1187 to 1192
CC (AA177504-A177509) generate frameshift mutations. The invention also
CC relates to a method of detecting a polymorphic site in a nucleic acid and
CC a method of determining the relatedness of two nucleic acids. It also
CC encompasses peptides containing polymorphic sites, antibodies raised
CC against such peptides, and a method of detecting polymorphic
CC proteins/peptides using the antibodies. The nucleic acids are useful for
CC gene therapy of an individual having, suspected of having, or at risk of
CC developing a pathological condition due to the presence of a sequence
CC polymorphism. Such treatment would comprise administration of the wild-
CC type nucleic acid sequence. Antibodies raised against polymorphic
XX peptides can also be used in the treatment of such individuals
XX
SQ Sequence 51 BP; 9 A; 12 C; 16 G; 14 T; 0 U; 0 Other;
XX
Query Match 4.3%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 1.7e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 177 TTAGTAGAGATGAGTTCTTCATGTTGGTCAGGCTGCTCGAATCCCG 227
DB 1 TTAGTAGAGAGCGGGGTTTCACATGCTGTCAGGCTGCTCGAATCCCG 51
XX
RESULT 68
AAA77499
ID AAA77499 standard; cDNA; 51 BP.
XX
AC AAA77499;
XX
DT 16-NOV-2000 (first entry)
XX
DE Human Alu subfamily SQ gene polymorphic site, SEQ ID NO:1182.
XX
XX Human; single nucleotide polymorphism; SNP; detection; identification;
KM gene therapy; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH variation replace(26,C)
FT /*tag= a
XX
XX WO200029623-A2.
XX
XX 25-MAY-2000.
XX
XX 17-NOV-1999; 99WO-US027293.
XX
XX 17-NOV-1998; 98US-0109024P.
XX
XX 16-NOV-1999; 99US-00443199.
XX
XX (CURA-) CURAGEN CORP.
PA Shimkets RA, Leach MD;
XX
PI

DR WPI; 2000-387826/33.
DR P-PSDB; AAB11818.
XX
XX Human nucleic acids containing single nucleotide polymorphisms, useful
PT for treating a subject suffering, or at risk from a pathology due to the
PT presence of a sequence polymorphism.
XX
XX Claim 1; Page 515; 543bp; English.
XX
XX Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 1112
CC (AAA76318-A77429) are consecutive pairs of nucleotides which contain
CC silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are consecutive
CC pairs of nucleotides containing SNPs which result in changes in the
CC corresponding amino acid sequences (AAB11749-B11828). The SNPs in
CC sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid
CC changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result
CC in non-conservative changes. The SNPs in sequences 1187 to 1192
CC (AAA77504-A77509) generate frameshift mutations. The invention also
CC relates to a method of detecting a polymorphic site in a nucleic acid and
CC a method of determining the relatedness of two nucleic acids. It also
CC encompasses peptides containing polymorphic sites, antibodies raised
CC against such peptides, and a method of detecting polymorphic
CC proteins/peptides using the antibodies. The nucleic acids are useful for
CC gene therapy of an individual having, suspected of having, or at risk of
CC developing a pathological condition due to the presence of a sequence
CC polymorphism. Such treatment would comprise administration of the wild-
CC type nucleic acid sequence. Antibodies raised against polymorphic
CC peptides can also be used in the treatment of such individuals
XX
SQ Sequence 51 BP; 12 A; 17 C; 10 G; 12 T; 0 U; 0 Other;
XX
XX
Query Match 4.3%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 1.7e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
QY 355 CTGAGCTCAGCAGTCACCTGCTCAGCTCCCAAGTCTGGATTACA 405
Db 1 CTGACCTCAAGTGATCCACCTGCTTACCTCCCAAGTCTGGATTACA 51
XX
RESULT 69
AAL31284/c
ID AAL31284 standard; DNA; 51 BP.
XX
XX AAL31284;
XX
XX 24-JAN-2002 (first entry)
XX
XX Human SNP oligonucleotide #4492.
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cyrostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinase; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
XX Homo sapiens.
XX
XX WO200147944-A2.
XX
XX 05-JUL-2001.
XX
XX 28-DEC-2000; 2000WO-US035498.
XX
XX 28-DEC-1999; 99US-0173419P.
XX 27-DEC-2000; 2000US-00173419.
XX (CURA-) CURAGEN CORP.
XX

PI Shimkets RA, Leach M;
XX
XX WPI; 2001-465210/50.
XX
XX Polymorphic nucleic acids encoding e.g. amyases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
XX
XX Claim 1; Page 2678; 4143bp; English.
XX
XX The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amyases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukemias), diseases of the nervous system and an infection of pathogenic
CC organisms
XX
SQ Sequence 51 BP; 10 A; 15 C; 17 G; 9 T; 0 U; 0 Other;
XX
XX
Query Match 4.3%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 1.7e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
QY 845 TGCGTCGCGCTCCCAAGTGTGGATTACAGGCGTGACCAACAGCCCG 895
Db 51 TGCGTCGCGCTCCCAAGTGTGGATTACAGGCGTGACCAACAGCCCG 1
XX
RESULT 70
AAL31458
ID AAL31458 standard; DNA; 51 BP.
XX
XX AAL31458;
XX
XX 24-JAN-2002 (first entry)
XX
XX Human SNP oligonucleotide #4666.
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cyrostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinase; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
XX Homo sapiens.
XX
XX WO200147944-A2.
XX
XX 05-JUL-2001.
XX
XX 28-DEC-2000; 2000WO-US035498.
XX
XX 28-DEC-1999; 99US-0173419P.
XX 27-DEC-2000; 2000US-00173419.
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach M;
XX
XX WPI; 2001-465210/50.
XX

XX polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PS autoimmune diseases and infections.
XX Claim 1; Page 2728; 4143pp; English.
PS
XX The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinases, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms
SQ Sequence 51 BP; 11 A; 19 C; 10 G; 11 T; 0 U; 0 Other;
XX
XX
Query Match 4.3%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 1.7e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1008 TTCTCTGTCAGCCTCCAGACAGCTGGATTACGGGACCTCCACCA 1058
DB 1 TTCTCTGCTCAGCCTCCAGTAGCTGGATTACAGGACGTAACCA 51
RESULT 71
AAL31460
ID AAL31460 standard; DNA; 51 BP.
XX
XX AAL31460;
AC
XX
XX 24-JAN-2002 (first entry)
DT
XX
XX Human SNP oligonucleotide #4668.
DE
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinase; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200147944-A2.
PN
XX
XX 05-JUL-2001.
PD
XX
XX 28-DEC-2000; 2000WO-US035498.
PF
XX
XX 28-DEC-1999; 99US-0173419P.
PR
XX
XX 27-DEC-2000; 2000US-00173419.
PS
XX
XX (CURA-) CURAGEN CORP.
FA
XX
XX Shimkets RA, Leach M;
PI
XX
XX MPI; 2001-465210/50.
DR
XX
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer.

PT autoimmune diseases and infections.
XX
XX Claim 1; Page 2729; 4143pp; English.
PS
XX The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinases, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms
SQ Sequence 51 BP; 10 A; 16 C; 14 G; 11 T; 0 U; 0 Other;
XX
XX
Query Match 4.3%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 1.7e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 849 TCGGCTCCCAAGTGTGATTACAGCGTGAAGCCACCGCCGCTT 899
DB 1 TTGGCTCCCAAGTGTGATTACAGCATGAGCCACCGCTGGCT 51
RESULT 72
AAT77523/C
ID AAT77523 standard; DNA; 51 BP.
XX
XX AAT77523;
AC
XX
XX 09-NOV-2001 (first entry)
DT
XX
XX Human silent SNP containing nucleic acid SEQ:4464.
DE
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200140521-A2.
PN
XX
XX 07-JUN-2001.
PD
XX
XX 30-NOV-2000; 2000WO-US032758.
PF
XX
XX 30-NOV-1999; 99US-0168138P.
PR
XX
XX 29-NOV-2000; 2000US-00726173.
PS
XX
XX (CURA-) CURAGEN CORP.
FA
XX
XX Shimkets RA, Leach M;
PI
XX
XX MPI; 2001-356160/37.
DR
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
PS
XX
XX Claim 1; Page 1877; 2653pp; English.
CC
XX AAT73060 to AAT79867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptide sequences related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by

CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples

SO Sequence 51 BP; 17 A; 14 C; 11 G; 9 T; 0 U; 0 Other;

Query Match 4.3%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 1.7e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 175 TTTTGTAGAGATGAGTTTCTCCATGTTGTCAGGCTGCTCGAATCC 225
DB 51 TTTTGTAGAGATGAGGTTTCTCCATGTTGTCAGGCTGCTCGAATCC 1

RESULT 73

AA178387
ID AA178387 standard; DNA; 51 BP.

XX AA178387;

DT 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ:5328.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;

KW protein therapy; vaccine; probe; diagnostic assay; detection;

XX quantitation; restorative therapy; polymorphic; ds.

OS Homo sapiens.

PN WO200140521-A2.

PD 07-JUN-2001.

PF 30-NOV-2000; 2000MO-US032758.

PR 30-NOV-1999; 99US-0168138P.

PR 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

PA Shimkets RA, Leach M;

PI WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and
therapy.

PS Claim 1; Page 2140; 2653pp; English.

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA173114 to AA175329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (I) and its complementary

CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples

SO Sequence 51 BP; 9 A; 16 C; 16 G; 10 T; 0 U; 0 Other;

Query Match 4.3%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 1.7e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 646 AGGCTGAGTGAAGTGGCGCATCTTGGCTCACTGCAACCTGCTCCCG 696
DB 1 AGGCTGAGTGAAGTGGCGCATCTTGGCTCACTGCAACCTGCTCCCG 51

RESULT 74

AA176192/c
ID AA176192 standard; DNA; 51 BP.

XX AA176192;

DT 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ:3133.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;

KW protein therapy; vaccine; probe; diagnostic assay; detection;

XX quantitation; restorative therapy; polymorphic; ds.

OS Homo sapiens.

PN WO200140521-A2.

PD 07-JUN-2001.

PF 30-NOV-2000; 2000MO-US032758.

PR 30-NOV-1999; 99US-0168138P.

PR 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

PA Shimkets RA, Leach M;

PI WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and
therapy.

PS Claim 1; Page 1009; 2653pp; English.

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA173114 to AA175329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (I) and its complementary

CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also

CC be used as diagnostic agents for detecting the presence of polymorphic
XX polypeptides in samples

SQ Sequence 51 BP; 14 A; 16 C; 12 G; 9 T; 0 U; 0 Other;

Query Match 4.3%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 1.7e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 177 TTATAGAGATGAGTTCATGTCAGGCTGCTCGAATCCG 227
DB 51 TTATAGAGAGCGGGTTCCATGTCAGGCTGCTCGAATCCG 1

RESULT 75
AA177583/C
ID AA177583 standard; DNA; 51 BP.

XX AA177583;

XX AC 09-NOV-2001 (first entry)

XX DT 09-NOV-2001 (first entry)

XX DE Human silent SNP containing nucleic acid SEQ:4524.

XX KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.

XX OS Homo sapiens.

XX PN WO200140521-A2.

XX PD 07-JUN-2001.

XX PF 30-NOV-2000; 2000WO-US032758.

XX PR 30-NOV-1999; 99US-0168138P.

XX PR 29-NOV-2000; 2000US-00726173.

XX PA (CURA-) CURAGEN CORP.

XX P1 Shimkets RA, Leach M;

XX DR WPI; 2001-356160/37.

XX PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.

XX PS Claim 1; Page 1895; 2653pp; English.

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA173114 to AA175329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples

SQ Sequence 51 BP; 15 A; 7 C; 20 G; 9 T; 0 U; 0 Other;

Query Match 4.3%; Score 43; DB 1; Length 51;

Best Local Similarity 90.2%; Pred. No. 1.7e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 681 CAACCTGCTCCCGGGTTCAAGTATTTCTCCGCCCCGAGCCCTCGAGT 731
DB 51 CAACCTGCTCCCGGGTTCAAGTATTTCTCCGCCCCGAGCCCTCGAGT 1

RESULT 76
AA173060/C
ID AA173060 standard; DNA; 51 BP.

XX AA173060;

XX AC 09-NOV-2001 (first entry)

XX DE Human silent SNP containing nucleic acid SEQ:1.

XX KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.

XX OS Homo sapiens.

XX PN WO200140521-A2.

XX PD 07-JUN-2001.

XX PF 30-NOV-2000; 2000WO-US032758.

XX PR 30-NOV-1999; 99US-0168138P.

XX PR 29-NOV-2000; 2000US-00726173.

XX PA (CURA-) CURAGEN CORP.

XX P1 Shimkets RA, Leach M;

XX DR WPI; 2001-356160/37.

XX PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.

XX PS Claim 1; Page 54; 2653pp; English.

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA173114 to AA175329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples

SQ Sequence 51 BP; 13 A; 11 C; 21 G; 6 T; 0 U; 0 Other;

Query Match 4.3%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 1.7e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 684 CCTGCTCCCGGGTTCAAGTATTTCTCCGCCCCGAGCCCTCGAGTAGC 734
DB 51 CCTGCTCCCGGGTTCAAGTATTTCTCCGCCCCGAGCCCTCGAGTAGC 1

PR 30-NOV-1999; 99US-0168138P.
 PR 29-NOV-2000; 2000US-00726173.
 XX (CURA-) CURAGEN CORP.
 PA Shimkets RA, Leach M;
 PI WPI; 2001-356160/37.
 DR WPI; 2001-356160/37.
 XX Polymorphic nucleic acid sequences, useful in genetic testing and
 PT therapy.
 PS Claim 1; Page 979; 2653pp; English.
 XX
 CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
 CC AA173060 to AA179867 represent peptides related to human polymorphic
 CC polynucleotide sequences. The sequences can be used in gene and protein
 CC therapy, and in vaccine production. (I) and the polypeptides encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate expression of polymorphic polypeptides. For
 CC example, (I) may be used to treat disorders by rectifying mutations or
 CC deletions in a patient's genome that affect the activity of polypeptides
 CC by expressing inactive proteins or to supplement the patients own
 CC production of polypeptide. Additionally, (I) and its complementary
 CC sequences may also be used as DNA probes in diagnostic assays to detect
 CC and quantitate the presence of similar nucleic acids in samples, and
 CC therefore which patients may be in need of restorative therapy. The
 CC polypeptides encoded by (I) may be used as antigens in the production of
 CC antibodies specific for polymorphic polypeptides. The antibodies may also
 CC be used to down regulate expression and activity. The antibodies may also
 CC be used as diagnostic agents for detecting the presence of polymorphic
 CC polypeptides in samples
 XX
 SQ Sequence 51 BP; 11 A; 8 C; 24 G; 8 T; 0 U; 0 Other;
 XX
 Query Match 4.3%; Score 43; DB 1; Length 51;
 Best Local Similarity 90.2%; Pred. No. 1.7e+02;
 Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 XX
 QY 974 CTCACGTCAACCTCTGCTCCGCGCTCAAGCATTTCTGCTCAGCCT 1024
 DB 51 CTCACGTCAACCTCTGCTCCGCGCTCAAGCATTTCTGCTCAGCCT 1
 XX
 RESULT 82
 ID AA176247/C
 XX AA176247 standard; DNA; 51 BP.
 AC AA176247;
 XX
 DT 09-NOV-2001 (first entry)
 XX
 DE Human silent SNP containing nucleic acid SEQ:3188.
 XX
 KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
 KW protein therapy; vaccine; probe; diagnostic assay; detection;
 KW quantitation; restorative therapy; polymorphic; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200140521-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 30-NOV-2000; 2000WO-US032758.
 XX
 PR 30-NOV-1999; 99US-0168138P.
 XX
 PR 29-NOV-2000; 2000US-00726173.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach M;
 XX

XX
 DR WPI; 2001-356160/37.
 XX Polymorphic nucleic acid sequences, useful in genetic testing and
 PT therapy.
 PS Claim 1; Page 1026; 2653pp; English.
 XX
 CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
 CC AA173060 to AA179867 represent peptides related to human polymorphic
 CC polynucleotide sequences. The sequences can be used in gene and protein
 CC therapy, and in vaccine production. (I) and the polypeptides encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate expression of polymorphic polypeptides. For
 CC example, (I) may be used to treat disorders by rectifying mutations or
 CC deletions in a patient's genome that affect the activity of polypeptides
 CC by expressing inactive proteins or to supplement the patients own
 CC production of polypeptide. Additionally, (I) and its complementary
 CC sequences may also be used as DNA probes in diagnostic assays to detect
 CC and quantitate the presence of similar nucleic acids in samples, and
 CC therefore which patients may be in need of restorative therapy. The
 CC polypeptides encoded by (I) may be used as antigens in the production of
 CC antibodies specific for polymorphic polypeptides. The antibodies may also
 CC be used to down regulate expression and activity. The antibodies may also
 CC be used as diagnostic agents for detecting the presence of polymorphic
 CC polypeptides in samples
 XX
 SQ Sequence 51 BP; 10 A; 14 C; 18 G; 9 T; 0 U; 0 Other;
 XX
 Query Match 4.3%; Score 43; DB 1; Length 51;
 Best Local Similarity 90.2%; Pred. No. 1.7e+02;
 Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 XX
 QY 697 GGTCAAGTATTCTCCGCGCTCAAGCATTTCTGCTCAGCCT 747
 DB 51 GGTCAAGTATTCTCCGCGCTCAAGCATTTCTGCTCAGCCT 1
 XX
 RESULT 83
 ID AA178389
 XX AA178389 standard; DNA; 51 BP.
 AC AA178389;
 XX
 DT 09-NOV-2001 (first entry)
 XX
 DE Human silent SNP containing nucleic acid SEQ:5330.
 XX
 KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
 KW protein therapy; vaccine; probe; diagnostic assay; detection;
 KW quantitation; restorative therapy; polymorphic; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200140521-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 30-NOV-2000; 2000WO-US032758.
 XX
 PR 30-NOV-1999; 99US-0168138P.
 XX
 PR 29-NOV-2000; 2000US-00726173.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach M;
 XX
 PT WPI; 2001-356160/37.
 PT Polymorphic nucleic acid sequences, useful in genetic testing and
 PT therapy.
 XX

CC	Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis, glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis, meningitis, muscular disorders, dementia, neurological diseases, tubercous sclerosis, male infertility, hypercalcaemia, blood pressure disorders, osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or autoimmunity. The present sequence is a polymorphism-containing oligonucleotide fragment of the invention	XX
CC		XX
XX	Sequence 51 BP; 11 A; 13 C; 15 G; 12 T; 0 U; 0 Other;	SQ
XX		XX
XX	Query Match 4.3%; Score 43; DB 1; Length 51;	
XX	Best Local Similarity 90.2%; Pred. No. 1.7e+02;	
XX	Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
XX		
XX	1083 ATTAGAGCGGGGTTTCACCATTTGTGACGCTGGTCTCAACTCCTGAC 1133	
XX	1 AGTAGAGACGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAACTCCTGAC 51	Db
XX		
XX	RESULT 85	
XX	AAH89506 standard; DNA; 51 BP.	ID
XX	AAH89506;	AC
XX	01-OCT-2001 (first entry)	DT
XX		DE
XX	Human coding sequence polymorphic site SEQ ID NO: 287.	XX
XX		XX
XX	Human; single nucleotide polymorphism; SNP; paternity test;	KM
XX	forensic test; aberrant protein expression; ds.	XX
XX		OS
XX	Homo sapiens.	XX
XX	MO200151670-A2.	PN
XX	19-JUL-2001.	PD
XX		XX
XX	05-JAN-2001; 2001MO-US000322.	PF
XX		XX
XX	07-JAN-2000; 2000US-0174962P.	PR
XX	(CUBA-) CURAGEN CORP.	XX
XX		PA
XX	Shinkets RA, Leach MD;	PI
XX		XX
XX	WPI; 2001-451871/48.	DR
XX	P-PEDB; AAM00389.	XX
XX		PT
XX	Isolated human polynucleotides containing single nucleotide	XX
XX	polymorphisms, useful for the treatment and diagnosis of e.g. cancer,	XX
XX	infection and diabetes.	XX
XX		PS
XX	Claim 1; Page 186; 475pp; English.	XX
XX		CC
XX	The present invention relates to human nucleic acids containing single	CC
XX	nucleotide polymorphisms (SNPs). These can be used in forensic and	CC
XX	paternity tests, and to aid in the treatment of diseases associated with	CC
XX	aberrant protein expression, including cancer, amyloidosis, diabetes,	CC
XX	Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,	CC
XX	glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,	CC
XX	meningitis, muscular disorders, dementia, neurological diseases, tubercous	CC
XX	sclerosis, male infertility, hypercalcaemia, blood pressure disorders,	CC
XX	osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or	CC
XX	autoimmunity. The present sequence is a polymorphism-containing	CC
XX	oligonucleotide fragment of the invention	XX
XX		XX
XX	Sequence 51 BP; 12 A; 13 C; 14 G; 12 T; 0 U; 0 Other;	SQ
XX		XX
XX	Query Match 4.3%; Score 43; DB 1; Length 51;	
XX	Best Local Similarity 90.2%; Pred. No. 1.7e+02;	
XX	Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	

PF 13-OCT-2000; 2000WO-US028436.
XX
XX 15-OCT-1999; 99US-0160096P.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX Picoult-Newburg L, Pohl M;
XX
XX WPI, 2001-290930/30.
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
XX
XX Claim 1; Page 60; 83pp; English.
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms (SNPs). The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotype trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, leach-Nyman syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic, such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a fragment of human
CC DNA flanking the site of a single nucleotide polymorphism
XX
SQ Sequence 51 BP; 7 A; 17 C; 16 G; 11 T; 0 U; 0 Other;
Query Match 4.3%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 1.7e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 646 AGGCTGAGTGCAGTGGCGCAATCTTGGCTCACTGCAACCTTGCCTCCG 696
DB 1 AGGCTGGGGTGCAGTGGTGCATCTCGGCTCACTGCAACCTTACTCCG 51
RESULT 89
ABL00123/c
ID ABL00123 standard; DNA; 51 BP.
XX
XX ABL00123;
AC
XX 05-MAR-2002 (first entry)
DT
XX
XX Human silent noncoding SNP oligonucleotide SEQ ID NO:114.
DE
XX
XX Human; single nucleotide polymorphism; SNP; polymorphism; cytosstatic;
KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
KW autoimmune disease; inflammation; cancer; nervous system disease;
KW infection; polymorphic protein; ds.
XX
XX Homo sapiens.
OS
XX WO200138586-A2.
PN
XX 31-MAY-2001.
PD
XX 22-NOV-2000; 2000WO-US032311.
PF

XX
XX 24-NOV-1999; 99US-0167383P.
PR
XX (CURA-) CURAGEN CORP.
PA
XX Shimkets RA, Leach M;
XX
XX WPI, 2001-355949/37.
XX
XX Isolated human nucleic acids comprising one or more single nucleotide
PT polymorphisms, useful for treating a subject suffering from a pathology,
PT e.g. autoimmune diseases, ascribed to the presence of a sequence
PT polymorphism.
XX
XX
XX Claim 1; Page 280; 674pp; English.
XX
XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
CC to ABB56903 represent human peptides encoded by some of the SNP
CC oligonucleotides. The sequences from the present invention can have
CC immunosuppressive, cytosstatic, antiinflammatory, neuroprotective and
CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
CC and antibodies from the present invention can be used for treating a
CC subject suffering from, at risk for, or suspected of, suffering from a
CC pathology ascribed to the presence of a sequence polymorphism. The
CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
CC the nervous system, and infection by pathogenic microorganisms. The SNPs
CC are also useful for determining which forms of a characterised
CC polymorphism are present in individuals. The antibodies may be used in
CC the detection, quantitation and/or cellular or tissue localisation of a
CC polymorphic protein (e.g., for use in measuring levels of the polymorphic
CC protein within appropriate physiological samples)
XX
SQ Sequence 51 BP; 16 A; 14 C; 11 G; 10 T; 0 U; 0 Other;
Query Match 4.3%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 1.7e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 181 TAGAGTGCAGATTCTTCATGTTGGTGCAGGCTGCTCGAACCTCCGACCT 231
DB 51 TAGAGTGGGGTTTCACCATGTGTGCTTAGGCTGCTCAACCTCTACCT 1
RESULT 90
ABL00021
ID ABL00021 standard; DNA; 51 BP.
XX
XX ABL00021;
AC
XX 05-MAR-2002 (first entry)
DT
XX
XX Human silent noncoding SNP oligonucleotide SEQ ID NO:12.
DE
XX
XX Human; single nucleotide polymorphism; SNP; polymorphism; cytosstatic;
KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
KW autoimmune disease; inflammation; cancer; nervous system disease;
KW infection; polymorphic protein; ds.
XX
XX Homo sapiens.
OS
XX WO200138586-A2.
PN
XX 31-MAY-2001.
PD
XX 22-NOV-2000; 2000WO-US032311.
PF
XX 24-NOV-1999; 99US-0167383P.
XX
XX (CURA-) CURAGEN CORP.
PA
XX Shimkets RA, Leach M;
XX
XX

DR WPI; 2001-355949/37.
XX Isolated human nucleic acids comprising one or more single nucleotide
PT polymorphisms, useful for treating a subject suffering from a pathology,
PT e.g. autoimmune diseases, ascribed to the presence of a sequence
PT polymorphism.
XX
XX Claim 1; Page 248; 674pp; English.
XX
XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
CC to ABB59903 represent human peptides encoded by some of the SNP
CC oligonucleotides. The sequences from the present invention can have
CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
CC and antibodies from the present invention can be used for treating a
CC subject suffering from, at risk for, or suspected of, suffering from a
CC pathology ascribed to the presence of a sequence polymorphism. The
CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
CC the nervous system, and infection by pathogenic microorganisms. The SNPs
CC are also useful for determining which forms of a characterised
CC polymorphism are present in individuals. The antibodies may be used in
CC the detection, quantitation and/or cellular or tissue localisation of a
CC polymorphic protein (e.g., for use in measuring levels of the polymorphic
CC protein within appropriate physiological samples)
XX
XX Sequence 51 BP; 7 A; 20 C; 13 G; 11 T; 0 U; 0 Other;
SQ
XX
XX Query Match 4.3%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 1.7e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 987 CTGGCTCCGGGGGCTCAAGGATTCCTCTGCTCAGGCTCCAGACAGCTGG 1037
DB 1 CCGCCTCTGGGTTCAAGGATTCCTCTGCTCAGGCTCCAGACAGCTGG 51
RESULT 91
AA176817
ID AA176817 standard; DNA; 51 BP.
XX
XX AA176817;
XX
XX 09-NOV-2001 (first entry)
XX
XX Human silent SNP containing nucleic acid SEQ:3758.
DE
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
OS
XX WO200140521-A2.
XX
XX 07-JUN-2001.
PD
XX 30-NOV-2000; 2000WO-US032758.
PF
XX 30-NOV-1999; 99US-0168138P.
PR
XX 29-NOV-2000; 2000US-00726173.
PR
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach M;
PI
XX WPI; 2001-356160/37.
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX
XX Claim 1; Page 1201; 2653pp; English.
XX

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
XX Sequence 51 BP; 8 A; 17 C; 13 G; 13 T; 0 U; 0 Other;
SQ
XX
XX Query Match 4.3%; Score 42.6; DB 1; Length 51;
Best Local Similarity 91.8%; Pred. No. 1.8e+02;
Matches 45; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 193 TTCTCCATGTGTGTCAGGCTGTGTCGAATCCGACCTCAGATGATCC 241
DB 1 TTGCGCATGTGTGCGCAGGCTGTGTCGAATCTCTGACCTCAGATGATCC 49
RESULT 92
AD112541/c
ID AD112541 standard; DNA; 44 BP.
XX
XX AD112541;
XX
XX 22-APR-2004 (first entry)
XX
XX Mutant human BRCA1 genomic DNA resulting from deletion 3 Segid 24.
DE
XX de; cancer; human; tumour suppressor;
KW breast cancer susceptibility gene 1; BRCA1; repetitive Alu;
KW ovarian cancer; recombination; mutant.
XX
XX Homo sapiens.
OS
XX WO2003104474-A2.
XX
XX 18-DEC-2003.
PD
XX 09-JUN-2003; 2003WO-US018098.
PF
XX 07-JUN-2002; 2002US-0387132P.
PR
XX 09-AUG-2002; 2002US-0402430P.
PR
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Scholl T, Hendrickson BC, Ward B, Pruse D;
PI
XX WPI; 2004-062369/06.
XX
XX Predicting a predisposition to cancer in a patient comprising detecting a
PT deletion in the BRCA1 gene that results from the unequal crossover
PT between a pair of repetitive sequences in the BRCA1 gene.
XX
XX Disclosure; SEQ ID NO 24; 59pp; English.
XX
XX This invention relates to a novel method for predicting a predisposition
CC to cancer in a patient by detecting large deletions in the human tumour
CC suppressor gene identified as the breast cancer susceptibility gene 1
CC (BRCA1). Specifically, it refers to deletions that result from the
CC unequal crossover between a pair of repetitive Alu sequences in the BRCA1

CC gene, such that the recombinant nucleotide sequence containing the
CC deletion indicates a predisposition to breast and ovarian cancer. The
CC present invention describes newly discovered deletion mutations that are
CC believed to be deleterious and cause significant alterations in the
CC structure or biochemical function of BRCA1. Accordingly, it provides
CC methods for detecting such mutants, as well as identifying and screening
CC for cytostatic compounds useful for treating or preventing cancers
CC associated with a BRCA1 genetic variant. This polynucleotide is a mutant
CC human BRCA1 genomic DNA fragment that arises as a result of a
CC recombinant event (deletion 3), which causes the omission of exons 16
CC and 17, given in an exemplification of the invention.

CC
XX
SQ Sequence 44 BP; 11 A; 12 C; 14 G; 7 T; 0 U; 0 Other;

Query Match 4.3%; Score 42.4; DB 1; Length 44;
Best Local Similarity 97.7%; Pred. No. 1.6e+02;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 833 TTGTGATCTGCTGCTCGGCTCCCAAGTGTGGATTACAG 876
DB 44 TTGTGATCTGCTGCTCGGCTCCCAAGTGTGGATTACAG 1

RESULT 93
AAH38364/C

ID AAH38364 standard; DNA; 51 BP.

AC AAH38364;

XX 14-AUG-2001 (first entry)

DT Human SNP flanking oligonucleotide SEQ ID 1160.

XX
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KM SNP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
KM Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KM polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KM acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KM inflammation; forensic investigation; paternity analysis; ds.

OS Homo sapiens.

XX WO200129262-A2.

XX 26-APR-2001.

XX 13-OCT-2000; 2000MO-US028436.

XX 15-OCT-1999; 99US-0160096P.

XX (ORCH-) ORCHID BIOSCIENCES INC.

XX Picoult-Newburg L, Pohl M;

XX WPI; 2001-290930/30.

XX
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.

XX
XX
XX Claim 1; Page 55; 83pp; English.

XX
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNP primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of

CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC diseases of which a component is or may be genetic such as autoimmune
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a fragment of human
CC DNA flanking the site of a single nucleotide polymorphism

XX
XX
SQ Sequence 51 BP; 8 A; 14 C; 17 G; 12 T; 0 U; 0 Other;

Query Match 4.3%; Score 42.4; DB 1; Length 51;
Best Local Similarity 97.7%; Pred. No. 1.8e+02;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 854 CTCCCAAGTGTGGATTACAGCGTGAAGCCACACCGCCGCG 897
DB 51 CTCCCAAGTGTGGATTACAGCGTGAAGCCACACCGCCGCG 8

RESULT 94
AAZ69411/C

ID AAZ69411 standard; DNA; 47 BP.

AC AAZ69411;

XX 10-SEP-2001 (first entry)

DT Human map-related biallelic marker SEQ ID NO:3767.

XX
XX
XX Human genome; biallelic marker; high density disequilibrium map;
KM genomic map; haplotype; phenotype; polymorphic base; genotyping;
KM genotyping; hybridisation; identification; characterisation; diagnosis;
KM single nucleotide polymorphism; SNP; ds.

OS Homo sapiens.

XX
XX
XX Key Location/Qualifiers
FT Variation replace(24,T)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"

XX WO9954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-1B000822.

XX 21-APR-1998; 98US-0082614P.

XX 23-NOV-1998; 98US-0109732P.

XX (GENSET) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX
XX
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.

XX
XX
XX Claim 3; Page 1034; 2745pp; English.

XX
XX
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ6579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.

CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ. ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3327, 3327 and
CC 3357, are not actually given a sequence in the Sequence Listing from the
CC present invention
CC
CC
CC
CC
CC Sequence 47 BP; 13 A; 8 C; 19 G; 7 T; 0 U; 0 Other;
XX
XX

Query Match	4.3%	Score 42.2;	DB 1;	Length 47;
Best Local Similarity	93.6%	Pred. No. 1.7e+02;		
Matches 44; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Oy	673	GCTCACTGCAACCTTGCCTCCCGGGTTCAAGTTATTCCTGCCCC	719
Db	47	GCTCACTGCAACCTTGCTCCTCCCGAGTTCAAGTAGATTCTCCTGCCCC	1

RESULT 95
AA174450/c
ID AA174450 standard; DNA; 51 BP.

AC	AAI74450;
XX	
DT	09-NOV-2001 (first entry)

Human silent SNP containing nucleic acid SEQ:1391.

KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
 KW protein therapy; vaccine; probe; diagnostic assay; detection;
 KW quantitation; restorative therapy; polymorphic; ds.

Homo sapiens.

PN WO200140521-A2.

07-JUN-2001.

30-NOV-2000; 2000WO-US032758.

PR 30-NOV-1999; 99US-0168138P.

[illegible]

XX

XX

XX

PT therapy.

PS Claim 1; Page 479; 2653pp; English.

AA173066 to AA179867 represent isolated human polymorphic polynucleotide sequences (1), the sequences (1) contain single nucleotide polymorphisms (SNPs). AA53314 to AA53329 represent peptides related to human polymorphic polynucleotide sequences. The sequences can be used in gene and protein therapy, and in vaccine production. (1) and the polypeptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of polymorphic polypeptides. For example, (1) may be used to treat disorders by rectifying mutations or deletions in a patient's genome that affect the activity of polypeptides by expressing inactive proteins or to supplement the patient's own production of polypeptide. Additionally, (1) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The polypeptides encoded by (1) may be used as antigens in the production of antibodies specific for polymorphic polypeptides. The antibodies may also be used to down regulate expression and activity. The antibodies may also

CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
XX
Sequence 51 BP; 10 A; 11 C; 19 G; 11 T; 0 U; 0 Other;

Sequence 51 BP; 10 A; 11 C; 19 G; 11 T; 0 U; 0 Other;

Query Match 4.3%; Score 42.2; DB 1; Length 51;

```

Best Local Alignment: 20/20; 222/222;
Matches 44; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 369 TCCACCTGCGCTCAGCCTCCCAAAGTGTGGATTACAGGCGTGACG 415
||| ||||||||| ||||||||| |||||
Db 49 TCCTCTGCCTCAGCCTCCCAAAGTCGTGGATTACAGGCATGCACC 3

RESULT 96
AAI76248/c
ID AAI76248 standard; DNA; 51 BP.

AA	
DT	09-NOV-2001 (first entry)
XX	
DE	Human silent SNP containing nucleic acid SEQ:3189

AA Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KM protein therapy; vaccine; probe; diagnostic assay; detection;
KM quantitation; restorative therapy; polymorphic; ds.

Homo sapiens.

AA WO200140521-A2
PN

PD 07-JUN-2001.

30-NOV-2000; 2000WO-US032758.

AA 30-NOV-1999; 99US-0168138P
PR

[illegible][illegible]

XX
FI
OITIMCCEB UN, DEACCI

XX	278
XX	279

PT therapy.

PS Claim 1; Page 1026; 2653pp; English.

AA AAT73060 to AAT79867 represent isolated human polymorphic polynucleotide sequences (I), which contain single nucleotide polymorphisms (SNPs). AAM5314 to AAM53329 represent peptides related to human polymorphic polynucleotide sequences. The sequences can be used in gene and protein therapy, and in vaccine production. (I) and the polypeptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of polymorphic polypeptides. For example, (I) may be used to treat disorders by rectifying mutations or deletions in a patient's genome that affect the activity of polypeptides by expressing inactive proteins or to supplement the patients own production of polypeptide. Additionally, (I) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The polypeptides encoded by (I) may be used as antigens in the production of antibodies specific for polymorphic polypeptides. The antibodies may also be used to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of polymorphic polypeptides in samples

SO Sequence 51 BP; 15 A; 10 C; 18 G; 8 T; 0 U; 0 Other;

Query Match 4.3%; Score 42.2; DB 1; Length 51.

Best Local Similarity 93.6%; Pred. No. 1.9e+02;
Matches 44; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 667 ATCTTGCTCACTGACACCTCTGCTCCCGGTTCAATATTCTCC 713
DB 47 ATCTTGCTCACTGACACCTCTGCTCCCGGTTCAATATTCTCC 1

RESULT 97

AA175601/C
ID AA175601 standard; DNA; 51 BP.

XX AA175601;

DT 09-NOV-2001 (first entry)

XX Human silent SNP containing nucleic acid SEQ:2542.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;

XX protein therapy; vaccine; probe; diagnostic assay; detection;

XX quantitation; restorative therapy; polymorphic; ds.

OS Homo sapiens.

PN WO200140521-A2.

PD 07-JUN-2001.

PF 30-NOV-2000; 2000WO-US032758.

PR 30-NOV-1999; 99US-0168138P.

PR 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

XX Shinketsu RA, Leach M;

XX WPI; 2001-356160/37.

XX Polymorphic nucleic acid sequences, useful in genetic testing and

XX therapy.

PS Claim 1; Page 829; 2653pp; English.

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA173114 to AA1753329 represent peptides related to human polymorphic

CC polynucleotide sequences. The sequences can be used in gene and protein

CC therapy, and in vaccine production. (I) and the polypeptides encoded by

CC them may be used in the prevention, diagnosis and treatment of diseases

CC associated with inappropriate expression of polymorphic polypeptides. For

CC example, (I) may be used to treat disorders by rectifying mutations or

CC deletions in a patient's genome that affect the activity of polypeptides

CC by expressing inactive proteins or to supplement the activity of polypeptides

CC production of polypeptide. Additionally, (I) and its complementary

CC sequences may also be used as DNA probes in diagnostic assays to detect

CC and quantitate the presence of similar nucleic acids in samples, and

CC therefore which patients may be in need of restorative therapy. The

CC polypeptides encoded by (I) may be used as antigens in the production of

CC antibodies specific for polymorphic polypeptides. The antibodies may also

CC be used to down regulate expression and activity. The antibodies may also

CC be used as diagnostic agents for detecting the presence of polymorphic

CC polypeptides in samples

XX Sequence 51 BP; 13 A; 13 C; 16 G; 9 T; 0 U; 0 Other;

SQ

Query Match 4.3%; Score 42.2; DB 1; Length 51;

Best Local Similarity 93.6%; Pred. No. 1.9e+02;
Matches 44; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 634 ACTGTGTACCCAGGCTGAGTGCAGTGGCGCAATCTTGGCTCACTG 680
DB 48 ACTGTGTACCCAGGCTGAGTGCAGTGGCGCAATCTTGGCTCACTG 2

RESULT 98

ACC84458
ID ACC84458 standard; DNA; 42 BP.

XX ACC84458;

DT 28-AUG-2003 (first entry)

XX NTP peptide encoding sequence #5.

XX Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;

XX neural thread protein; NTP; tumour; ds.

XX Unidentified.

PN WO2003008443-A2.

PD 19-JUN-2002; 2002WO-CA001105.

PR 19-JUN-2001; 2001US-0306150P.

PR 19-JUN-2001; 2001US-0306151P.

PR 16-NOV-2001; 2001US-0331477P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA;

XX WPI; 2003-247999/24.

XX P-PSDB; ABR63253.

XX Novel neural thread protein peptide, referred as cell death peptide,

XX useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,

XX atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.

XX Disclosure; Page 16; 77pp; English.

XX The present invention relates to a neural thread protein (NTP) peptide

XX referred to as cell death peptide. Thought to be cytostatic,

XX antibacterial, immunosuppressive and antiinflammatory. It is useful for

XX treating a condition in a patient requiring removal or destruction of

XX cells, for treating a condition such as benign or malignant tumor,

XX inflammatory disease, autoimmune disease and infectious disease. The

XX peptide useful for treatment is derived from the amino acid sequence for

XX a pancreatic thread protein. The peptide is conjugated, linked or bound

XX to a molecule chosen from antibody or its fragment, antibody-like binding

XX molecule, where the molecule has a higher affinity for binding to a tumor

XX or other target than binding to other cells. Treatment using NTP peptides

XX can remove benign tumors with less risk and fewer of the undesirable side

XX effects of surgery. The present sequence is an NTP encoding sequence

XX Sequence 42 BP; 8 A; 15 C; 10 G; 9 T; 0 U; 0 Other;

SQ

Query Match 4.2%; Score 42; DB 1; Length 42;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 369 TCCACCTGCTCAGCTCCCAAGTGTGAGTTACAGGCT 410
DB 1 TCCACCTGCTCAGCTCCCAAGTGTGAGTTACAGGCT 42

RESULT 99

ACC84457
ID ACC84457 standard; DNA; 42 BP.

XX ACC84457;

DT 28-AUG-2003 (first entry)

XX

PI Wollgemuth J., Fry K., Matlock G., Altman P., Prentice J., Phillips J;
PI ly N., Woodward R., Quettermous T., Johnson F;
XX WPI; 2002-636525/68.
DR
XX
PT New system for leukocyte expression profiling, diagnosing a disease, or
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT or congestive heart failure, comprises diagnostic oligonucleotides.
XX
PS Claim 1; Page 577; Opp; English.
XX
CC The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
SQ Sequence 50 BP; 12 A; 14 C; 16 G; 8 T; 0 U; 0 Other;

Query Match 4.2%; Score 42; DB 1; Length 50;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 927 GAATCTCACTCTGTATACCAGGCTGGAGTGCATGCGCCAATCTGGGCTC 976
DB 50 GAGTCCTCACTCTGTATACCCAGGCTGGAGTGCATGCGCGCAACTTGCTC 1

RESULT 102
ID AACI4922/C
XX AACI4922 standard; cDNA; 51 BP.
AC AACI4922;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 18997.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.
OS Homo sapiens.
XX
PN EPI033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 93US-0122487P.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J., Duclert A., Giordano J;
XX
DR WPI; 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 1; SEQ ID NO 18997; 71pp + Sequence listing; English.

The present sequence is one of a large number of 5' ESTs derived from
cDNAs encoding secreted proteins. No ORF has yet been conclusively
identified within the present sequence. The 5' ESTs were prepared from

CC	total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC	sequences usually correspond mainly to the 3' untranslated region (UTR)
CC	of the mRNA because they are often obtained from oligo-dT primed cDNA
CC	libraries. Such ESTs are not well suited for isolating cDNA sequences
CC	derived from the 5' ends of mRNAs and even in those cases where longer
CC	cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC	ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC	to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC	diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC	They are used to obtain upstream regulatory sequences and to design
CC	expression and secretion vectors
XX	
SQ	Sequence 51 BP; 23 A; 13 C; 9 G; 6 T; 0 U; 0 Other;
OY	Query Match 4.2%; Score 42; DB 1; Length 51; Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Dn	Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
	908 TTTTGGTTGTTGAATGAGTAATCATCTCGTGTACCGAGCGTGAGTGC 957 50 TTTTTTTTTTGGATGATGAGTCCTCACTCTGTGCCCCAGCGTGAGTGC 1
RESULT 103	
ADCl6982/C	ID ADCl6982 standard; DNA; 51 BP.
AC	ADCl6982;
XX	
DT	18-DEC-2003 (first entry)
XX	
DE	Human single nucleotide polymorphism (SNP) region Seq IDB4.
XX	
KM	sequence polymorphism analysis; human identity; human relatedness;
KM	single nucleotide polymorphism; SNP; genetic disease; cytosratic;
KM	immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
KM	fatty acid metabolism; glycolysis; amino acid metabolism;
KM	paternity analysis; forensic; autoimmune disease; cancer; nervous system;
OS	infection; pathogenic microorganism; human; ds.
XX	
Homo sapiens.	
FH	Key Location/Qualifiers
FT	variation replace(26,A)
FT	/tag= a
FT	/standard_name= "Single nucleotide polymorphism"
PN	MO200029622-A2.
XX	
PD	25-MAY-2000.
XX	
PF	17-NOV-1999; 99WO-US027283.
XX	
PR	17-NOV-1998; 98US-0103024P.
PR	16-NOV-1999; 99US-00443199.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
Pt	Shinkets RA, Leach MD;
XX	
DR	WPI; 2000-399731/34.
XX	
PT	Novel polynucleotide and polypeptide including one or more single
PT	nucleotide polymorphisms, useful for diagnosing and treating conditions
PT	associated with the presence of sequence polymorphism in humans and
PT	animals.
XX	
PS	Claim 1; SEQ ID NO 84; 187bp; English.
XX	
CC	This invention relates to novel isolated nucleotide sequences which
CC	comprise 217 defined polymorphic sequences. Sequence polymorphism-based
CC	analysis of nucleic acid sequences can augment or replace previously
CC	known methods for determining the identity and relatedness of

CC individuals. Single nucleotide polymorphisms (SNPs) tend to occur with
CC great frequency throughout the genome and may be located close to loci of
CC interest. Such variations can cause or be closely linked to pathological
CC conditions (genetic diseases). Hence the SNPs of the invention may be
CC useful in the development of compounds with cytostatic,
CC immunosuppressive, antiinflammatory, neuroprotective or antimicrobial
CC activities. Regulators of metabolic pathways such as fatty acid
CC metabolism, glycolysis, and amino acid metabolism may also be developed.
CC The compounds may be useful for treating a subject suffering from or at
CC risk for a pathology associated with the presence of a sequence
CC polymorphism. SNP detection is also useful in paternity analysis and
CC forensic application. Polymorphisms may contribute to the phenotype of an
CC organism and phenotypic traits include genetic diseases such as
CC autoimmune diseases, cancer, diseases of the nervous system and infection
CC by pathogenic microorganisms. The present sequence is the sequence
CC surrounding and including a human SNP of the invention.

XX SQ Sequence 51 BP, 12 A, 11 C, 17 G, 11 T, 0 U, 0 Other;

Query Match 4.2%; Score 42; DB 1; Length 51;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 356 TTAGCTCAAGCAGTCCAGCTGCTCAGCTCCCAAGTGTGGATTACA 405
DB 50 TCAGCTCAAGTATCCAGCTGCTCGGCTCCCAAGTGTGGATTACA 1

RESULT 104
AA127794/c
ID AAL27794 standard; DNA; 51 BP.
XX
XX AAL27794;

DT 24-JAN-2002 (first entry)
XX
XX Human SNP oligonucleotide #1002.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytoskeletal;
XX neuroprotective; antitubercular; gene therapy; vaccine; amylose; cancer;
XX amyloid protein; angiotensin; apoptosis related protein; cadherin;
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX complement related protein; cytochrome; kinesin; cytokine; interleukin;
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX multifactorial disease; autoimmune disease; infection;
XX nervous system disease; ss.

OS Homo sapiens.

XX
XX WO200147944-A2.

PN 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US035498.

XX 28-DEC-1999; 99US-0173419P.

XX 27-DEC-2000; 2000US-00173419.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI; 2001-465210/50.

XX polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX autoimmune diseases and infections.

XX Claim 1; Page 1666; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic
XX variants of proteins related to amylases, amyloid proteins, angiotensin,
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogene,

CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms

XX SQ Sequence 51 BP, 10 A, 13 C, 16 G, 12 T, 0 U, 0 Other;

Query Match 4.2%; Score 42; DB 1; Length 51;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 994 CCGGGCTCAAGGAGATTCTCTGCTCAGCTCCCAAGCAGCTGGATTAC 1043
DB 51 CAGGGCTCAAGGAATCTCTCTCTCAGCTCCCAAGGAGCTGGATTAC 2

RESULT 105
AA173932
ID AA173932 standard; DNA; 51 BP.
XX
XX AA173932;

DT 09-NOV-2001 (first entry)
XX
XX Human silent SNP containing nucleic acid SEQ.873.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
XX protein therapy; vaccine; probe; diagnostic assay; detection;
XX quantitation; restorative therapy; polymorphic; ds.

OS Homo sapiens.

XX
XX WO200140521-A2.

PN 07-JUN-2001.

XX 30-NOV-2000; 2000WO-US032758.

XX 30-NOV-1999; 99US-0168138P.

XX 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI; 2001-356160/37.

XX polymorphic nucleic acid sequences, useful in genetic testing and
XX therapy.

XX Claim 1; Page 321; 2653pp; English.

XX AA173060 to AA179867 represent isolated human polymorphic polymorphic
XX sequences (I), which contain single nucleotide polymorphisms (SNPs).
XX AA173060 to AA173067 represent peptides related to human polymorphic
XX polymorphic nucleic acid sequences. The sequences can be used in gene and protein
XX therapy, and in vaccine production. (I) and the polymorphisms encoded by
XX them may be used in the prevention, diagnosis and treatment of diseases
XX associated with inappropriate expression of polymorphic polymorphisms. For
XX example, (I) may be used to treat disorders by rectifying mutations or
XX deletions in a patient's genome that affect the activity of polymorphisms
XX by expressing inactive proteins or to supplement the patients own
XX production of polymorphisms. Additionally, (I) and its complementary
XX sequences may also be used as DNA probes in diagnostic assays to detect

XX 09-NOV-2001 (first entry)
XX
XX Human silent SNP containing nucleic acid SEQ:5241.
DE
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KM protein therapy; vaccine; probe; diagnostic assay; detection;
KM quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
OS
XX WO200140521-A2.
FN
XX
XX 07-JUN-2001.
PD
XX
XX 30-NOV-2000; 2000WO-US032758.
PF
XX 30-NOV-1999; 99US-0168138P.
PR 29-NOV-2000; 2000US-00726173.
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX Shinkets RA, Leach M;
PI WPI; 2001-356160/37.
DR
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX
XX Claim 1; Page 2114; 2653pp; English.
PS
XX
XX AAT73060 to AAT79867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptide sequences related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 12 A; 17 C; 14 G; 8 T; 0 U; 0 Other;
Query Match 4.2%; Score 42; DB 1; Length 51;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 847 CCTCGGCTCCCAAGTGTGGATTACAGGCGTAGCCACCAACCCCGG 896
DB 2 CCTGGCTCCCAAGTGTGGATTACAGGCGTAGCCACCAACCCCGG 51
RESULT 111
AAT73860
ID AAT73860 standard; DNA; 51 BP.
XX
XX AAT73860;
AC
XX
XX 09-NOV-2001 (first entry)
DT
XX
XX Human silent SNP containing nucleic acid SEQ:801.
DE
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KM

KM protein therapy; vaccine; probe; diagnostic assay; detection;
KM quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
OS
XX WO200140521-A2.
FN
XX
XX 07-JUN-2001.
PD
XX
XX 30-NOV-2000; 2000WO-US032758.
PF
XX 30-NOV-1999; 99US-0168138P.
PR 29-NOV-2000; 2000US-00726173.
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX Shinkets RA, Leach M;
PI WPI; 2001-356160/37.
DR
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX
XX Claim 1; Page 299; 2653pp; English.
PS
XX
XX AAT73060 to AAT79867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptide sequences related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 9 A; 16 C; 13 G; 13 T; 0 U; 0 Other;
Query Match 4.2%; Score 42; DB 1; Length 51;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 638 TGTACCCAGGCTGAGTGCAGTGGCGCAATCTTGGCTCACTGCAACTC 687
DB 1 TGTACCCAGGCTGAGTGCAGTGGCGCAATCTTGGCTCACTGCAACTC 50
RESULT 112
AAT73760
ID AAT73760 standard; DNA; 51 BP.
XX
XX AAT73760;
AC
XX
XX 09-NOV-2001 (first entry)
DT
XX
XX Human silent SNP containing nucleic acid SEQ:701.
DE
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KM protein therapy; vaccine; probe; diagnostic assay; detection;
KM quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
OS
XX WO200140521-A2.
FN

XX 07-JUN-2001.
PD 30-NOV-2000; 2000MO-US032758.
XX 30-NOV-1999; 99US-0168138P.
XX 29-NOV-2000; 2000US-00726173.
PR (CURA-) CURAGEN CORP.
XX Shinkets RA, Leach M;
XX WPI; 2001-356160/37.
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
PS Claim 1; Page 268; 2653pp; English.
XX
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA173060 to AA179867 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 9 A; 19 C; 13 G; 10 T; 0 U; 0 Other;
Query Match 4.2%; Score 42; DB 1; Length 51;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 648 GCTGAGTGCAGTGGGCAATCTTGGCTACCTGCAACCTGCTCCCG 697
DB 1 GCTGAGTGCAGTGGGCAATCTTGGCTACCTGCAACCTGCTCCCG 50
RESULT 113
AA177806
ID AA177806 standard; DNA; 51 BP.
XX
XX AA177806;
XX
DT 09-NOV-2001 (first entry)
XX
XX Human silent SNP containing nucleic acid SEQ:4747.
DE
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
XX protein therapy; vaccine; probe; diagnostic assay; detection;
XX quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
XX
XX WO200140521-A2.
XX
XX 07-JUN-2001.
XX
XX 30-NOV-2000; 2000MO-US032758.
XX
XX 30-NOV-1999; 99US-0168138P.

PR 29-NOV-2000; 2000US-00726173.
XX (CURA-) CURAGEN CORP.
XX Shinkets RA, Leach M;
XX WPI; 2001-356160/37.
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
PS Claim 1; Page 1963; 2653pp; English.
XX
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA173060 to AA179867 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 7 A; 22 C; 9 G; 13 T; 0 U; 0 Other;
Query Match 4.2%; Score 42; DB 1; Length 51;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 672 GGCTCACTGCAACCTGCTCCCGGTTCAAGTATTTCTGCCCCAG 721
DB 2 GGCTCACTGCAACCTGCTCCCGGTTCAAGTATTTCTGCCCCAG 51
RESULT 114
AA173533/C
ID AA173533 standard; DNA; 51 BP.
XX
XX AA173533;
XX
DT 09-NOV-2001 (first entry)
XX
XX Human silent SNP containing nucleic acid SEQ:474.
DE
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
XX protein therapy; vaccine; probe; diagnostic assay; detection;
XX quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
XX
XX WO200140521-A2.
XX
XX 07-JUN-2001.
XX
XX 30-NOV-2000; 2000MO-US032758.
XX
XX 30-NOV-1999; 99US-0168138P.
XX 29-NOV-2000; 2000US-00726173.
XX (CURA-) CURAGEN CORP.
XX Shinkets RA, Leach M;
XX PI

DR WPI; 2001-356160/37.
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
PS Claim 1; Page 199; 2653pp; English.
XX AA173060 to AA17867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA53114 to AA53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 9 A; 14 C; 19 G; 9 T; 0 U; 0 Other;
Query Match 4.2%; Score 42; DB 1; Length 51;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 842 GCGTCGCTCGGCTCCCAAGTCGCGATTACAGCGCGCCACCCAG 891
DB 50 GCCCGCTCGGCTCCCAAGTCGCGATTACAGCGCTTGAATCACCAG 1
RESULT 115
ABL00195
ID ABL00195 standard; DNA; 51 BP.
XX
AC ABL00195;
XX
DT 05-MAR-2002 (first entry)
XX
DE Human silent noncoding SNP oligonucleotide SEQ ID NO:186.
XX
KW Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
KW autoimmune disease; inflammation; cancer; nervous system disease;
KW infection; polymorphic protein; de.
XX
OS Homo sapiens.
XX
PN WO200138586-A2.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-US032311.
XX
PR 24-NOV-1999; 99US-0167383P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkels RA, Leach M;
XX
DR WPI; 2001-355949/37.
XX
PT Isolated human nucleic acids comprising one or more single nucleotide
PT polymorphisms, useful for treating a subject suffering from a pathology,
PT e.g. autoimmune diseases, ascribed to the presence of a sequence
PT polymorphism.

XX
PS Claim 1; Page 303; 674pp; English.
XX
CC ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
CC to ABB56903 represent human peptides encoded by some of the SNP
CC oligonucleotides. The sequences from the present invention can have
CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
CC and antibodies from the present invention can be used for treating a
CC subject suffering from, at risk for, or suspected of, suffering from a
CC pathology ascribed to the presence of a sequence polymorphism. The
CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
CC the nervous system, and infection by pathogenic microorganisms. The SNPs
CC are also useful for determining which forms of a characterized
CC polymorphism are present in individuals. The antibodies may be used in
CC the detection, quantitation and/or cellular or tissue localisation of a
CC polymorphic protein (e.g., for use in measuring levels of the polymorphic
CC protein within appropriate physiological samples)
XX
SQ Sequence 51 BP; 8 A; 23 C; 8 G; 12 T; 0 U; 0 Other;
Query Match 4.2%; Score 42; DB 1; Length 51;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 981 CAACCTCGCTCCGCGGCTCAAGCATTCCTCTCTCAGCCTCCAG 1030
DB 1 CAACCTCGCTCCGCGGCTCAAGCATTCCTCTCTCAGCCTCCAG 50
RESULT 116
AD112525/C
ID AD112525 standard; DNA; 48 BP.
XX
AC AD112525;
XX
DT 22-APR-2004 (first entry)
XX
DE Human BRCA1 DNA junction sequence comprising large deletion Segid 5.
XX
KW ds; cancer; human; tumour suppressor;
KW breast cancer susceptibility gene 1; BRCA1; repetitive Alu;
KW ovarian cancer; junction sequence; recombination; mutant.
XX
OS Homo sapiens.
XX
PN WO2003104474-A2.
XX
PD 18-DEC-2003.
XX
PF 09-JUN-2003; 2003WO-US018098.
XX
PR 07-JUN-2002; 2002US-0387132P.
PR 09-AUG-2002; 2002US-0402430P.
XX
PA (MYRI-) MYRIAD GENETICS INC.
XX
PI Scholl T, Hendrickson BC, Ward B, Pruss D;
XX
DR WPI; 2004-062369/06.
XX
PT Predicting a predisposition to cancer in a patient comprising detecting a
PT deletion in the BRCA1 gene that results from the unequal crossover
PT between a pair of repetitive sequences in the BRCA1 gene.
XX
PS Claim 16; SEQ ID NO 5; 59pp; English.
XX
CC This invention relates to a novel method for predicting a predisposition
CC to cancer in a patient by detecting large deletions in the human tumour
CC suppressor gene identified as the breast cancer susceptibility gene 1
CC (BRCA1). Specifically, it refers to deletions that result from the
CC unequal crossover between a pair of repetitive Alu sequences in the BRCA1

CC gene, such that the recombinant nucleotide sequence containing the
CC deletion indicates a predisposition to breast and ovarian cancer. The
CC present invention describes newly discovered deletion mutations that are
CC believed to be deleterious and cause significant alterations in the
CC structure or biochemical function of BRCA1. Accordingly, it provides
CC methods for detecting such mutants, as well as identifying and screening
CC for cytostatic compounds useful for treating or preventing cancers
CC associated with a BRCA1 genetic variant. This polynucleotide is a DNA
CC fragment representing a junction sequence that arises as a result of a
CC recombination event in human BRCA1 that causes the omission of exons 15
CC and 16, given in an exemplification of the invention.

XX SQ Sequence 48 BP; 13 A; 12 C; 14 G; 9 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.6; DB 1; Length 48;
Best Local Similarity 91.7%; Pred. No. 1.9e+02;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 696 GGGTCAAGTATTTCTCTGCCCCAGCCCTCTGAGTAGCTGAGACTAC 743
DB 48 GGGTCAAGCATTTCTCTGCTCTGAGCCCTCTGAGTAGCTGAGACTAC 1

RESULT 117

AA175849
ID AA175849 standard; DNA; 51 BP.

XX AA175849;

XX 09-NOV-2001 (first entry)

XX Human silent SNP containing nucleic acid SEQ:2790.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;

XX protein therapy; vaccine; probe; diagnostic assay; detection;

XX quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX MO200140521-A2.

XX 07-JUN-2001.

XX 30-NOV-2000; 2000WO-US032758.

XX 30-NOV-1999; 99US-0168138P.

XX 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI; 2001-356160/37.

XX Polymorphic nucleic acid sequences, useful in genetic testing and
XX therapy.

XX Claim 1; Page 904; 2653pp; English.

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide

XX sequences (I), which contain single nucleotide polymorphisms (SNPs).

XX AA55114 to AA55329 represent peptides related to human polymorphic

XX polynucleotide sequences. The sequences can be used in gene and protein

XX therapy, and in vaccine production. (I) and the polypeptides encoded by

XX them may be used in the prevention, diagnosis and treatment of diseases

XX associated with inappropriate expression of polymorphic polypeptides. For

XX example, (I) may be used to treat disorders by rectifying mutations or

XX deletions in a patient's genome that affect the activity of polypeptides

XX by expressing inactive proteins or to supplement the patients own

XX production of polypeptide. Additionally, (I) and its complementary

XX sequences may also be used as DNA probes in diagnostic assays to detect

XX and quantitate the presence of similar nucleic acids in samples, and

XX therefore which patients may be in need of restorative therapy. The

CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples

XX SQ Sequence 51 BP; 12 A; 21 C; 6 G; 12 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.6; DB 1; Length 51;
Best Local Similarity 91.7%; Pred. No. 2e+02;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 966 AATCGGCTGACGACACCTCTGCTCGGGGCTCAAGCATTTCTCC 1013
DB 4 AATCGACGCTGACGACACCTCTGCTCGGGGCTCAAGCATTTCTCC 51

RESULT 118

ABL00141/C
ID ABL00141 standard; DNA; 51 BP.

XX ABL00141;

XX 05-MAR-2002 (first entry)

XX Human silent noncoding SNP oligonucleotide SEQ ID NO:132.

XX Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;

XX immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;

XX autoimmune disease; inflammation; cancer; nervous system disease;

XX infection; polymorphic protein; ds.

XX Homo sapiens.

XX MO200138586-A2.

XX 31-MAY-2001.

XX 22-NOV-2000; 2000WO-US032311.

XX 24-NOV-1999; 99US-0167383P.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI; 2001-355949/37.

XX Isolated human nucleic acids comprising one or more single nucleotide

XX polymorphisms, useful for treating a subject suffering from a pathology,

XX e.g. autoimmune diseases, ascribed to the presence of a sequence

XX polymorphism.

XX Claim 1; Page 286; 674pp; English.

XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides

XX comprising one or more single nucleotide polymorphisms (SNPs). ABB56531

XX to ABB56903 represent human peptides encoded by some of the SNP

XX oligonucleotides. The sequences from the present invention can have

XX immunosuppressive, cytostatic, antiinflammatory, neuroprotective and

XX antitumor activities. Nucleic acids, polypeptides, oligonucleotides

XX and antibodies from the present invention can be used for treating a

XX subject suffering from, at risk for, or suspected of, suffering from a

XX pathology ascribed to the presence of a sequence polymorphism. The

XX pathology may be autoimmune diseases, inflammation, cancer, diseases of

XX the nervous system, and infection by pathogenic microorganisms. The SNPs

XX are also useful for determining which forms of a characterized

XX polymorphism are present in individuals. The antibodies may be used in

XX the detection, quantitation and/or cellular or tissue localization of a

XX polymorphic protein (e.g., for use in measuring levels of the polymorphic

XX protein within appropriate physiological samples)

XX SQ Sequence 51 BP; 14 A; 12 C; 16 G; 9 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.6; DB 1; Length 51;
Best Local Similarity 91.7%; Pred. No. 2e+02; 4; Indels 0; Gaps 0;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 194 TCTCCATGTTGTCAGGCTGCTCGAATCCCGACCTCAGATGATCC 241
Db 51 TCTCATGTTGTCAGGCTGCTCGAATCCCGACCTCAGATGATCC 4

RESULT 119

AAA77442
ID AAA77442 standard; cDNA; 51 BP.

AC AAA77442;

DT 16-NOV-2000 (first entry)

DE Human Aluubfamily SQ gene polymorphic site, SEQ ID NO:1125.

XX Human; single nucleotide polymorphism; SNP; detection; identification;

KM gene therapy; ss.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT variation replace(26,C) /+tag= a

XX WO200029623-A2.

XX 25-MAY-2000.

XX 17-NOV-1999; 99WO-US027293.

XX 17-NOV-1998; 98US-0109024P.

XX 16-NOV-1999; 99US-00443199.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach MD;

XX WPI; 2000-387826/33.

XX P-PSDB; AAB11761.

XX Claim 1; Page 498; 543pp; English.

XX Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 1112
CC (AAA76318-A77429) are consecutive pairs of nucleotides which contain
CC silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are consecutive
CC pairs of nucleotides containing SNPs which result in changes in the
CC corresponding amino acid sequences (AAB11749-B11828). The SNPs in
CC sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid
CC changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result
CC in non-conservative changes. The SNPs in sequences 1187 to 1192
CC (AAA77504-A77509) generate frameshift mutations. The invention also
CC relates to a method of detecting a polymorphic site in a nucleic acid and
CC a method of determining the relatedness of two nucleic acids. It also
CC encompasses peptides containing polymorphic sites, antibodies raised
CC against such peptides, and a method of detecting polymorphic
CC proteins/peptides using the antibodies. The nucleic acids are useful for
CC gene therapy of an individual having, suspected of having, or at risk of
CC developing a pathological condition due to the presence of a sequence
CC polymorphism. Such treatment would comprise administration of the wild-
CC type nucleic acid sequence. Antibodies raised against polymorphic
CC peptides can also be used in the treatment of such individuals
XX Sequence 51 BP; 8 A; 8 C; 15 G; 20 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2e+02; 6; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1071 TTTTGTATTTTTCATTAGAGCGGGGTTTCACCATATTTGTCAGGCTGCT 1121
Db 1 TTTTGTATTTTTCATTAGAGCGGGGTTTCACCATATTTGTCAGGCTGCT 51

RESULT 120

AAA76988/c
ID AAA76988 standard; cDNA; 51 BP.

AC AAA76988;

DT 16-NOV-2000 (first entry)

DE Human clone cg42924993 polymorphic site, SEQ ID NO:671.

XX Human; single nucleotide polymorphism; SNP; detection; identification;

KM gene therapy; ss.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT variation replace(26,G) /+tag= a

XX WO200029623-A2.

XX 25-MAY-2000.

XX 17-NOV-1999; 99WO-US027293.

XX 17-NOV-1998; 98US-0109024P.

XX 16-NOV-1999; 99US-00443199.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach MD;

XX WPI; 2000-387826/33.

XX Claim 1; Page 360; 543pp; English.

XX Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 1112
CC (AAA76318-A77429) are consecutive pairs of nucleotides which contain
CC silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are consecutive
CC pairs of nucleotides containing SNPs which result in changes in the
CC corresponding amino acid sequences (AAB11749-B11828). The SNPs in
CC sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid
CC changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result
CC in non-conservative changes. The SNPs in sequences 1187 to 1192
CC (AAA77504-A77509) generate frameshift mutations. The invention also
CC relates to a method of detecting a polymorphic site in a nucleic acid and
CC a method of determining the relatedness of two nucleic acids. It also
CC encompasses peptides containing polymorphic sites, antibodies raised
CC against such peptides, and a method of detecting polymorphic
CC proteins/peptides using the antibodies. The nucleic acids are useful for
CC gene therapy of an individual having, suspected of having, or at risk of
CC developing a pathological condition due to the presence of a sequence
CC polymorphism. Such treatment would comprise administration of the wild-
CC type nucleic acid sequence. Antibodies raised against polymorphic
CC peptides can also be used in the treatment of such individuals
XX Sequence 51 BP; 20 A; 15 C; 8 G; 8 T; 0 U; 0 Other;

Query Match	4.2%	Pred	41.4	DB	1	length	51
Similarity	88.2%	Pred	No. 2e+02				
Best local							
Matches	45	Conservative	0	Mismatches	6	Indels	0
Gap							
1071	TTTGTATTTTCATTAGAGCGCGGGTTTCACCATATTTGTACGCGTGCCT						1121
db	51	TTTGTATTTTCATTAGAGACGGGATTTTCACCATGTGTGCGCGGCTGCCT					1

RESULT 121
AAA77021/c
ID AAA77021 standard; cDNA; 51 BP.

DT	16-NOV-2000	(first entry)
XX		
DE	Human clone	cg43089031 polymorphic site, SEQ ID NO:704

KW Human; single nucleotide polymorphism; SNP; detection; identification;
KW gene therapy; ss.

05 Homo sapiens.

	Key variation	Location/Qualifiers replace(26,A)
FH		
FT		

PN WO2000029623-A2.

PD 25-MAY-2000.

PF 17-NOV-1999; 99WO-US027293.

PR 17-NOV-1998; 98US-0109024P.

PR 16-NOV-1999; 99US-00443199.

PA (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach MD;

DR WPI; 2000-387826/33.

PT Human nucleic acids containing single nucleotide polymorphisms, useful for treating a subject suffering, or at risk from a pathology due to the presence of a sequence polymorphism.

PS Claim 1; Page 370; 543pp; English.

CC Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 1112
CC (AAA76318-A77429) are consecutive pairs of nucleotides which contain
CC silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are consecutive
CC pairs of nucleotides containing SNPs which result in changes in the
CC corresponding amino acid sequences (AA411749-B11828). The SNPs in
CC sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid
CC changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result
CC in non-conservative changes. The SNPs in sequences 1187 to 1192
CC (AAA77504-A77509) generate frameshift mutations. The invention also
CC relates to a method of detecting a polymorphic site in a nucleic acid and
CC a method of determining the relatedness of two nucleic acids. It also
CC encompasses peptides containing polymorphic sites, antibodies raised
CC against such peptides, and a method of detecting polymorphic
CC proteins/peptides using the antibodies. The nucleic acids are useful for
CC gene therapy of an individual having, suspected of having, or at risk of
CC developing a pathological condition due to the presence of a sequence
CC polymorphism. Such treatment would comprise administration of the wild-
CC type nucleic acid sequence. Antibodies raised against polymorphic
CC peptides can also be used in the treatment of such individuals
XX
XX Sequence 51 BP; 12 A; 14 C; 16 G; 9 T; 0 U; 0 Other;

SQ Sequence 51 BP; 12 A; 14 C; 16 G; 9 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.4; DB 1; Length 51;

Best Local Similarity	88.2%	Pred. No. 2e+02;	
Matches	45;	Conservative	0; Mismatches
			6; Indels
			0; Gaps
			0.

Qy	853	CCTCCCAAGGCTGGATTACAG3CGTGAACCAACAGCCGGCTTATT	903
Db	51	CCTCCCAAGGCTGGATTATAGCGGTGATCAACGGCGCTGGCCATT	1

RESULT 122
ADCl6930/c
ID ADCl6930 standard; DNA; 51 BP

DT 18-DEC-2003 (first entry)

DE Human single nucleotide polymorphism (SNP) region Seq ID32.

sequence polymorphism analysis; human identity; human relatedness;
single nucleotide polymorphism; SN; genetic disease; cytostatic;
immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
fatty acid metabolism; glycolysis; amino acid metabolism;
paternity analysis; forensic; autoimmune disease; cancer; nervous system
infection; pathogenic microorganism; human; ds.

Os Homo sapiens.

	Key	Location/Qualifiers
FH	variation	replace(26,T)
FT		

13

PN WO2000029622-

PD 25-MAY-2000.

PF 17-NOV-1999; 99WO-US027283.

PR 17-NOV-1998; 98US-0109024P.

XX (CURA-) CURAGEN CORP.
PA

PI Shimkets RA, Leach MD;

DR WPI; 2000-399731/34.

Novel polynucleotide and polypeptide including one or more single nucleotide polymorphisms, useful for diagnosing and treating conditions associated with the presence of sequence polymorphism in humans and animals.

PS Claim 1; SEQ ID NO 32; 187pp; English

This invention relates to novel isolated nucleotide sequences which comprise 217 defined polymorphic sequences. Sequence polymorphism-based analysis of nucleic acid sequences can augment or replace previously known methods for determining the identity and relatedness of individuals. Single nucleotide polymorphisms (SNPs) tend to occur with great frequency throughout the genome and may be located close to loci of interest. Such variations can cause or be closely linked to pathological conditions (genetic diseases). Hence the SNPs of the invention may be useful in the development of compounds with cytostatic, immunosuppressive, antiinflammatory, neuroprotective or antimicrobial activities. Regulators of metabolic pathways such as fatty acid metabolism, glycolysis, and amino acid metabolism may also be developed. The compounds may be useful for treating a subject suffering from or at risk for a pathology associated with the presence of a sequence polymorphism. SNP detection is also useful in paternity analysis and forensic application. Polymorphisms may contribute to the phenotype of an organism and phenotypic traits include genetic diseases such as autoimmune diseases, cancer, diseases of the nervous system and infection by pathogenic microorganisms. The present sequence is the sequence

CC surrounding and including a human SNP of the invention.

XX Sequence 51 BP; 12 A; 15 C; 14 G; 10 T; 0 U; 0 Other;

SO Query Match 4.2%; Score 41.4; DB 1; Length 51;

Best Local Similarity 88.2%; Pred. No. 2e+02;

Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1087 GAGGCGGGGTTTACCATATTGTCAGGCTGTCTCAAACTCCGACCTCA 1137

DB 51 GAGACGGGTTTACCATATTGTCAGGCTGTCTCAAACTCCGACCTCA 1

RESULT 123

AA176193/c ID AA176193 standard; DNA; 51 BP.

AA176193;

09-NOV-2001 (first entry)

Human silent SNP containing nucleic acid SEQ:3134.

Human; single nucleotide polymorphism; SNP; genome; gene therapy;

protein therapy; vaccine; probe; diagnostic assay; detection;

quantitation; restorative therapy; polymorphic; ds.

Homo sapiens.

MO200140521-A2.

07-JUN-2001.

30-NOV-2000; 2000WO-US032758.

30-NOV-1999; 99US-0168138P.

29-NOV-2000; 2000US-00726173.

(CURA-) CURAGEN CORP.

Shimkets RA, Leach M;

WPI; 2001-356160/37.

Polymorphic nucleic acid sequences, useful in genetic testing and

therapy.

Claim 1; Page 1009; 2653pp; English.

AA173060 to AA179867 represent isolated human polymorphic polynucleotide

sequences (I), which contain single nucleotide polymorphisms (SNPs).

AA173060 to AA173329 represent peptides related to human polymorphic

polynucleotide sequences. The sequences can be used in gene and protein

therapy, and in vaccine production. (I) and the polypeptides encoded by

them may be used in the prevention, diagnosis and treatment of diseases

associated with inappropriate expression of polymorphic polypeptides. For

example, (I) may be used to treat disorders by rectifying mutations or

deletions in a patient's genome that affect the activity of polypeptides

by expressing inactive proteins or to supplement the patient's own

production of polypeptide. Additionally, (I) and its complementary

sequences may also be used as DNA probes in diagnostic assays to detect

and quantitate the presence of similar nucleic acids in samples, and

therefore which patients may be in need of restorative therapy. The

polypeptides encoded by (I) may be used as antigens in the production of

antibodies specific for polymorphic polypeptides. The antibodies may also

be used to down regulate expression and activity. The antibodies may also

be used as diagnostic agents for detecting the presence of polymorphic

polypeptides in samples

Sequence 51 BP; 13 A; 16 C; 13 G; 9 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.4; DB 1; Length 51;

Best Local Similarity 88.2%; Pred. No. 2e+02;

Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 177 TTAGTAGAGATGAGTTCCTTCATGTTGTGTGACGCTGTCTCGAATCCCG 227

DB 51 TTAGTAGAGAGGAGGTTTACCATATGTCGCGAGCTGTCTCGAATCTCTG 1

RESULT 124

AA173061/c ID AA173061 standard; DNA; 51 BP.

AA173061;

09-NOV-2001 (first entry)

Human silent SNP containing nucleic acid SEQ:2.

Human; single nucleotide polymorphism; SNP; genome; gene therapy;

protein therapy; vaccine; probe; diagnostic assay; detection;

quantitation; restorative therapy; polymorphic; ds.

Homo sapiens.

MO200140521-A2.

07-JUN-2001.

30-NOV-2000; 2000WO-US032758.

30-NOV-1999; 99US-0168138P.

29-NOV-2000; 2000US-00726173.

(CURA-) CURAGEN CORP.

Shimkets RA, Leach M;

WPI; 2001-356160/37.

Polymorphic nucleic acid sequences, useful in genetic testing and

therapy.

Claim 1; Page 54; 2653pp; English.

AA173060 to AA179867 represent isolated human polymorphic polynucleotide

sequences (I), which contain single nucleotide polymorphisms (SNPs).

AA173060 to AA173329 represent peptides related to human polymorphic

polynucleotide sequences. The sequences can be used in gene and protein

therapy, and in vaccine production. (I) and the polypeptides encoded by

them may be used in the prevention, diagnosis and treatment of diseases

associated with inappropriate expression of polymorphic polypeptides. For

example, (I) may be used to treat disorders by rectifying mutations or

deletions in a patient's genome that affect the activity of polypeptides

by expressing inactive proteins or to supplement the patient's own

production of polypeptide. Additionally, (I) and its complementary

sequences may also be used as DNA probes in diagnostic assays to detect

and quantitate the presence of similar nucleic acids in samples, and

therefore which patients may be in need of restorative therapy. The

polypeptides encoded by (I) may be used as antigens in the production of

antibodies specific for polymorphic polypeptides. The antibodies may also

be used to down regulate expression and activity. The antibodies may also

be used as diagnostic agents for detecting the presence of polymorphic

polypeptides in samples

Sequence 51 BP; 12 A; 11 C; 22 G; 6 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.4; DB 1; Length 51;

Best Local Similarity 88.2%; Pred. No. 2e+02;

Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 684 CTTCTGCTCCGCGTTTCAATTTCTCTGCTCCGCGAGCTCCGAGTAGC 734

DB 51 CTTCTGCTCTCTGCTTCAAGCGATCTCTCTGCTCCGAGCTCCGAGTAGC 1

KM protein therapy; vaccine; probe; diagnostic assay; detection;
KM quantitation; restorative therapy; polymorphic; ds.
XX Homo sapiens.
OS WO200140521-A2.
XX PD 07-JUN-2001.
XX PE 30-NOV-2000; 2000WO-US032758.
XX PR 30-NOV-1999; 99US-0168138P.
XX PR 29-NOV-2000; 2000US-00726173.
XX PA (CURA-) CURAGEN CORP.
XX PI Shinkets RA, Leach M;
XX DR WPI; 2001-356160/37.
XX PT Polymorphic nucleic acid sequences, useful in genetic testing and
XX therapy.
XX PS Claim 1; Page 1007; 2653pp; English.
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA53114 to AA53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 17 A; 16 C; 9 G; 9 T; 0 U; 0 Other;
Query Match 4.2%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 170 TTTTCTTCTAGAGATGAGTTCTCCATGTCGTGAGCTGCTCGA 220
DB 51 TGTATTCTTAGAGACGCGGGTTTCACCATGTCGCCAGGCTGCTCGA 1
RESULT 128
AA174502/C
ID AA174502 standard; DNA; 51 BP.
XX AC AA174502;
XX DT 09-NOV-2001 (first entry)
XX DE Human silent SNP containing nucleic acid SEQ:1443.
XX KM Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KM protein therapy; vaccine; probe; diagnostic assay; detection;
XX quantitation; restorative therapy; polymorphic; ds.
OS Homo sapiens.
XX PR 30-NOV-1999; 99US-0168138P.
XX PR WO200140521-A2.

XX PD 07-JUN-2001.
XX PE 30-NOV-2000; 2000WO-US032758.
XX PR 30-NOV-1999; 99US-0168138P.
XX PR 29-NOV-2000; 2000US-00726173.
XX PA (CURA-) CURAGEN CORP.
XX PI Shinkets RA, Leach M;
XX DR WPI; 2001-356160/37.
XX PT Polymorphic nucleic acid sequences, useful in genetic testing and
XX therapy.
XX PS Claim 1; Page 495; 2653pp; English.
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA53114 to AA53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 13 A; 16 C; 12 G; 10 T; 0 U; 0 Other;
Query Match 4.2%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 178 TAGTAGAGATGAGTTCTCCATGTCGTGAGCTGCTGAACTCCGA 228
DB 51 TAGTAGAGATGAGTTCTCCATGTCGTGAGCTGCTGAACTCCGA 1
RESULT 129
AA176499
ID AA176499 standard; DNA; 51 BP.
XX AC AA176499;
XX DT 09-NOV-2001 (first entry)
XX DE Human silent SNP containing nucleic acid SEQ:1440.
XX KM Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KM protein therapy; vaccine; probe; diagnostic assay; detection;
XX quantitation; restorative therapy; polymorphic; ds.
OS Homo sapiens.
XX PR 30-NOV-1999; 99US-0168138P.
XX PR WO200140521-A2.
XX PD 07-JUN-2001.
XX PE 30-NOV-2000; 2000WO-US032758.
XX PR 30-NOV-1999; 99US-0168138P.

PR 29-NOV-2000; 2000US-00726173.
XX (CURA-) CURAGEN CORP.
XX Shimkets RA, Leach M;
XX WPI; 2001-356160/37.
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
PS Claim 1; Page 1103; 2653pp; English.
XX AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 10 A; 22 C; 11 G; 8 T; 0 U; 0 Other;
Query Match 4.2%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 216 CTCGACTCCGACCTCAGATGATCCCTCCGCTCGGCGCTCCCAAGTGCT 266
DB 1 CTCGAATCTCCGACCTCAGATGATCCGACCGCGCGCTCCCAAGTGCT 51
RESULT 130
AAI79633/C
ID AAI79633 standard; DNA; 51 BP.
XX
AC AAI79633;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ.6574.
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KM protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
OS
XX WO200140521-A2.
PN
XX 07-JUN-2001.
PD
XX 30-NOV-2000; 2000WO-US032758.
PF
XX 30-NOV-1999; 99US-0168138P.
PR 29-NOV-2000; 2000US-00726173.
XX
XX (CURA-) CURAGEN CORP.
PA
XX Shimkets RA, Leach M;
PI
XX

DR WPI; 2001-356160/37.
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
PS Claim 1; Page 2518; 2653pp; English.
XX AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 17 A; 14 C; 11 G; 9 T; 0 U; 0 Other;
Query Match 4.2%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1085 TAGAGCGGGGTTTACCATATTTGTCAGGCTGCTCAACTCTGACT 1135
DB 51 TAGAGCGGGGTTTACCATATTTGTTAGCTGCTTGAATCTCTGACT 1
RESULT 131
AAI79539/C
ID AAI79539 standard; DNA; 51 BP.
XX
AC AAI79539;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ.6480.
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KM protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
OS
XX WO200140521-A2.
PN
XX 07-JUN-2001.
PD
XX 30-NOV-2000; 2000WO-US032758.
PF
XX 30-NOV-1999; 99US-0168138P.
PR 29-NOV-2000; 2000US-00726173.
XX
XX (CURA-) CURAGEN CORP.
PA
XX Shimkets RA, Leach M;
PI
XX WPI; 2001-356160/37.
DR Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
PS Claim 1; Page 2490; 2653pp; English.

XX AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX

SO Sequence 51 BP; 13 A; 10 C; 20 G; 8 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 970 TCGGCTCACTGACACTGCTCCGGGCTCAAGGATTCCTGCTCA 1020
DB 51 TCGGCTCGCTGACAGCTGCTCCCGGGTCAAGCAATCTCTGCTCA 1

RESULT 132
AAI76814
ID AAI76814 standard; DNA; 51 BP.
XX
XX AAI76814;
XX
XX 09-NOV-2001 (first entry)
XX
XX Human silent SNP containing nucleic acid SEQ:3755.
XX
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
XX protein therapy; vaccine; probe; diagnostic assay; detection;
XX quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
XX
XX
XX WO200140521-A2.
XX
XX 07-JUN-2001.
XX
XX 30-NOV-2000; 2000WO-US032758.
XX
XX 30-NOV-1999; 99US-0168138P.
XX PR 29-NOV-2000; 2000US-00726173.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shinkets RA, Leach M;
XX
XX WPI; 2001-356160/37.
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
XX therapy.
XX
XX Claim 1; Page 1200; 2653pp; English.
XX
XX AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary

CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX

SO Sequence 51 BP; 9 A; 9 C; 15 G; 18 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 172 TTTTGTAGTAGAGATGAGTTTCTCCATGTTGTCAGGCTGCTCGAAC 222
DB 1 TTTTGTAGTAGACAGAGGTTTCCCATGTTGCTGACGCTGCTTGAAAC 51

RESULT 133
AAI76092/c
ID AAI76092 standard; DNA; 51 BP.
XX
XX AAI76092;
XX
XX 09-NOV-2001 (first entry)
XX
XX Human silent SNP containing nucleic acid SEQ:3033.
XX
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
XX protein therapy; vaccine; probe; diagnostic assay; detection;
XX quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
XX
XX
XX WO200140521-A2.
XX
XX 07-JUN-2001.
XX
XX 30-NOV-2000; 2000WO-US032758.
XX
XX 30-NOV-1999; 99US-0168138P.
XX PR 29-NOV-2000; 2000US-00726173.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shinkets RA, Leach M;
XX
XX WPI; 2001-356160/37.
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
XX therapy.
XX
XX Claim 1; Page 978; 2653pp; English.
XX
XX AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary

CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples

XX Sequence 51 BP; 12 A; 8 C; 23 G; 8 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.4; DB 1; Length 51;

Best Local Similarity 88.2%; Pred. No. 2e+02;

Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 974 CTCACGCAACCTCTCCGCGGCTCAGGATTCCTCTGCTGAGCCT 1024

DB 51 CTCACGCAACCTCTCCGCGGCTCAGGATTCCTCTGCTGAGCCT 1

RESULT 134

AA179838/c

ID AA179838 standard; DNA; 51 BP.

XX AA179838;

DT 09-NOV-2001 (first entry)

DE Human nonconservative amino acid changing SNP nucleic acid SEQ:6779.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;

KW protein therapy; vaccine; probe; diagnostic assay; detection;

KW quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX WO200140521-A2.

XX 07-JUN-2001.

XX 30-NOV-2000; 2000MO-US032758.

XX 30-NOV-1999; 99US-0168138P.

XX 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and

XX therapy.

XX Claim 1; Page 2579; 2653pp; English.

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA173060 to AA179867 represent peptides related to human polymorphic

CC polynucleotide sequences. The sequences can be used in gene and protein

CC therapy, and in vaccine production. (I) and the polypeptides encoded by

CC them may be used in the prevention, diagnosis and treatment of diseases

CC associated with inappropriate expression of polymorphic polypeptides. For

CC example, (I) may be used to treat disorders by rectifying mutations or

CC deletions in a patient's genome that affect the activity of polypeptides

CC by expressing inactive proteins or to supplement the patient's own

CC production of polypeptide. Additionally, (I) and its complementary

CC sequences may also be used as DNA probes in diagnostic assays to detect

CC and quantitate the presence of similar nucleic acids in samples, and

CC therefore which patients may be in need of restorative therapy. The

CC polypeptides encoded by (I) may be used as antigens in the production of

CC antibodies specific for polymorphic polypeptides. The antibodies may also

CC be used to down regulate expression and activity. The antibodies may also

CC be used as diagnostic agents for detecting the presence of polymorphic

CC polypeptides in samples

XX Sequence 51 BP; 10 A; 13 C; 17 G; 11 T; 0 U; 0 Other;

XX Query Match 4.2%; Score 41.4; DB 1; Length 51;

XX Best Local Similarity 88.2%; Pred. No. 2e+02;

XX Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 835 GTGATCTGCTGCTCTCCGCGCTCCCAAGTCTGAGATTACAGCGCTGAGCC 885

DB 51 GTGATCTGCTGCTCTCCGCGCTCCCAAGTCTGAGATTACAGCGCTGAGCC 1

AA176541/c

ID AA176541 standard; DNA; 51 BP.

XX AA176541;

DT 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ:3482.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;

KW protein therapy; vaccine; probe; diagnostic assay; detection;

KW quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX WO200140521-A2.

XX 07-JUN-2001.

XX 30-NOV-2000; 2000MO-US032758.

XX 30-NOV-1999; 99US-0168138P.

XX 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and

XX therapy.

XX Claim 1; Page 1116; 2653pp; English.

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA173060 to AA179867 represent peptides related to human polymorphic

CC polynucleotide sequences. The sequences can be used in gene and protein

CC therapy, and in vaccine production. (I) and the polypeptides encoded by

CC them may be used in the prevention, diagnosis and treatment of diseases

CC associated with inappropriate expression of polymorphic polypeptides. For

CC example, (I) may be used to treat disorders by rectifying mutations or

CC deletions in a patient's genome that affect the activity of polypeptides

CC by expressing inactive proteins or to supplement the patient's own

CC production of polypeptide. Additionally, (I) and its complementary

CC sequences may also be used as DNA probes in diagnostic assays to detect

CC and quantitate the presence of similar nucleic acids in samples, and

CC therefore which patients may be in need of restorative therapy. The

CC polypeptides encoded by (I) may be used as antigens in the production of

CC antibodies specific for polymorphic polypeptides. The antibodies may also

CC be used to down regulate expression and activity. The antibodies may also

CC be used as diagnostic agents for detecting the presence of polymorphic

CC polypeptides in samples

XX Sequence 51 BP; 14 A; 13 C; 16 G; 8 T; 0 U; 0 Other;

XX Query Match 4.2%; Score 41.4; DB 1; Length 51;

Best Local Similarity 88.2%; Pred. No. 2e+02; Mismatches 6; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
692 TCCGGGGTTGATATTCCTGCGCCGAGCTGAGTAGTGGAGCTA 742
Oy 51 TCTGGGCTCAAGTATCTCTGCTCACTGCTGAGTAGTGGAGCTA 1
Db

RESULT 136
AA179697/c
ID AA179697 standard; DNA; 51 BP.

AA179697;
09-NOV-2001 (first entry)
Human conservative amino acid changing SNP nucleic acid SEQ:6638.
XX
DE Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
PN WO200140521-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US032758.
XX
PR 30-NOV-1999; 99US-0168138P.
PR 29-NOV-2000; 2000US-00726173.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-356160/37.
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.

Claim 1; Page 2537; 2653pp; English.
AA173060 to AA179867 represent isolated human polymorphic polynucleotide
sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA53114 to AA53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX

Sequence 51 BP; 10 A; 12 C; 18 G; 11 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1025 CCCAAGCAGCTGGGATTACGGGCACTGCCACCAACCCCGTATTTTGG 1075
Db 51 CCCAAGTACGCTGGGATTACAGGCGCCGCCACACGACCCCACTATTTTGG 1

RESULT 137
AA174778
ID AA174778 standard; DNA; 51 BP.
XX
AC AA174778;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:1719.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
PN WO200140521-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US032758.
XX
PR 30-NOV-1999; 99US-0168138P.
PR 29-NOV-2000; 2000US-00726173.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-356160/37.
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.

Claim 1; Page 580; 2653pp; English.
AA173060 to AA179867 represent isolated human polymorphic polynucleotide
sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA53114 to AA53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX

Sequence 51 BP; 9 A; 21 C; 13 G; 8 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 847 CCTGGGCTCCCAAGTCTGGGATTACAGGCGTGAAGCCACGCGCGG 897
Db 1 CCTGGGCTCCCAATTCCTGGGACTACAGGCGTGAAGCCACGCGCGG 51

RESULT 138
AA173250/c
ID AA173250 standard; DNA; 51 BP.
XX

AC AA173250;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:191.
XX
KM Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KM quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
PN WO200140521-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US032758.
XX
PR 30-NOV-1999; 99US-0168138P.
XX 29-NOV-2000; 2000US-00726173.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimketa RA, Leach M;
XX
DR WPI; 2001-356160/37.
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX
PS Claim 1; Page 113; 2653pp; English.
XX
CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA53114 to AA53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 11 A; 13 C; 18 G; 9 T; 0 U; 0 Other;
XX
Query Match 4.2%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 956 GCATGGCCAAATCTGCTCACTGCAACCTGCTCCCGGGTCAAGG 1006
DB 51 GCAGTGGCATGATCTGCTCACTGCAACCTGCTCCCGGGTCAAGG 1
XX
RESULT 139
AA179700/C
ID AA179700 standard; DNA; 51 BP.
XX
AC AA179700;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human conservative amino acid changing SNP nucleic acid SEQ:6641.
XX

KM Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KM quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
PN WO200140521-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US032758.
XX
PR 30-NOV-1999; 99US-0168138P.
XX 29-NOV-2000; 2000US-00726173.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimketa RA, Leach M;
XX
DR WPI; 2001-356160/37.
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX
PS Claim 1; Page 2538; 2653pp; English.
XX
CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA53114 to AA53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 10 A; 12 C; 17 G; 12 T; 0 U; 0 Other;
XX
Query Match 4.2%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 836 TGATCGCTGCTGCGCCCAAGTGTGGATTACAGGCGTACGCA 886
DB 51 TGATCGCCCATCTCGGCTCCCAAAATGCTGGATTACAGCATACGCA 1
XX
RESULT 140
AA178386
ID AA178386 standard; DNA; 51 BP.
XX
AC AA178386;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:5327.
XX
AC AA178386;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KM quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX

PN WO200140521-A2.
XX 07-JUN-2001.
PD
XX 30-NOV-2000; 2000WO-US032758.
PF 30-NOV-1999; 99US-0168138P.
XX 29-NOV-2000; 2000US-00726173.
PR (CURA-) CURAGEN CORP.
PA Shimkets RA, Leach M;
PI WPI; 2001-356160/37.
DR
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
PS Claim 1; Page 2140; 2653pp; English.
XX
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA173114 to AA173329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 9 A; 17 C; 16 G; 9 T; 0 U; 0 Other;
Query Match 4.2%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2e+02; 6; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 646 AGGCTGAGTGCAGTGGCGCAATCTTGGCTCACTGCACCTTGCCTCCG 696
DB 1 AGGCTGAGTGCAGTGGCGCAATCTTGGCTCACTGCACCTTGCCTCCG 51
RESULT 141
AA173862
ID AA173862 standard; DNA; 51 BP.
XX
XX AA173862;
XX
DT 09-NOV-2001 (first entry)
XX
XX Human silent SNP containing nucleic acid SEQ:803.
DE
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
OS
XX WO200140521-A2.
PN
XX 07-JUN-2001.
PD
XX 30-NOV-2000; 2000WO-US032758.
PF
XX

PR 30-NOV-1999; 99US-0168138P.
PR 29-NOV-2000; 2000US-00726173.
XX
XX (CURA-) CURAGEN CORP.
PA Shimkets RA, Leach M;
PI WPI; 2001-356160/37.
DR
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
PS Claim 1; Page 300; 2653pp; English.
XX
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA173114 to AA173329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 10 A; 21 C; 8 G; 12 T; 0 U; 0 Other;
Query Match 4.2%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2e+02; 6; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 671 TGGCTCACTGCACCTTGCCTCCCGGTTCAAGTATTCTTCCTGCCAG 721
DB 1 TGGCTCACTGCACCTTGCCTCCCGGTTCAAGTATTCTTCCTGCCAG 51
RESULT 142
AA179783/C
ID AA179783 standard; DNA; 51 BP.
XX
XX AA179783;
XX
DT 09-NOV-2001 (first entry)
XX
XX Human nonconservative amino acid changing SNP nucleic acid SEQ:6724.
DE
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
OS
XX WO200140521-A2.
PN
XX 07-JUN-2001.
PD
XX 30-NOV-2000; 2000WO-US032758.
PF
XX 30-NOV-1999; 99US-0168138P.
PR 29-NOV-2000; 2000US-00726173.
XX
XX (CURA-) CURAGEN CORP.
PA Shimkets RA, Leach M;
PI

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XX DR WPI; 2001-356160/37.
XX PT Polymorphic nucleic acid sequences, useful in genetic testing and
XX PT therapy.
XX PS Claim 1; Page 2563; 2653pp; English.
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
XX CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
XX CC AA173114 to AA175329 represent peptides related to human polymorphic
XX CC polynucleotide sequences. The sequences can be used in gene and protein
XX CC therapy, and in vaccine production. (I) and the polypeptides encoded by
XX CC them may be used in the prevention, diagnosis and treatment of diseases
XX CC associated with inappropriate expression of polymorphic polypeptides. For
XX CC example, (I) may be used to treat disorders by rectifying mutations or
XX CC deletions in a patient's genome that affect the activity of polypeptides
XX CC by expressing inactive proteins or to supplement the patient's own
XX CC production of polypeptide. Additionally, (I) and its complementary
XX CC sequences may also be used as DNA probes in diagnostic assays to detect
XX CC and quantitate the presence of similar nucleic acids in samples, and
XX CC therefore which patients may be in need of restorative therapy. The
XX CC polypeptides encoded by (I) may be used as antigens in the production of
XX CC antibodies specific for polymorphic polypeptides. The antibodies may also
XX CC be used to down regulate expression and activity. The antibodies may also
XX CC be used as diagnostic agents for detecting the presence of polymorphic
XX CC polypeptides in samples
XX SQ Sequence 51 BP; 11 A; 12 C; 19 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 4.2%; Score 41.4; DB 1; Length 51;
XX Best Local Similarity 88.2%; Pred. No. 2e+02;
XX Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 989 GCGTCCCGGCGCTCAAGGATTCTCTGCTCAGCCTTCCAGACGCTGGGA 1039
DB 51 GCGTCCCGGCGCTCAAGGATTCTCTGCTCAGCCTTCCAGACGCTGGGA 1
XX
XX RESULT 143
XX AAH90585/c
XX ID AAH90585 standard; cDNA; 51 BP.
XX AC AAH90585;
XX AC
XX DT 08-OCT-2001 (first entry)
XX DE Human clone CG43080072 SNP site, SEQ ID NO:465.
XX DE
XX KW Human; single nucleotide polymorphism; SNP; detection; identification;
XX KW gene therapy; genetic disorder; ss.
XX OS Homo sapiens.
XX OS
XX FH Key Location/Qualifiers
XX FT replace(26,C)
XX FT /*tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX FT
XX WO200147942-A2.
XX PN
XX PD 05-JUL-2001.
XX PD
XX PF 27-DEC-2000; 2000WO-US035387.
XX PF
XX PR 27-DEC-1999; 99US-00472865.
XX PR
XX PA (CURA-) CURAGEN CORP.
XX PA
XX PI Shimkets RA, Leach M;
XX PI
XX DR WPI; 2001-425617/45.
XX DR
XX XX
```

```
PT PT New polynucleotides containing single nucleotide polymorphisms, for
PT PT detecting the presence of polymorphism, detecting a polymorphic site, and
PT PT treating a patient suffering from a pathology ascribed to the
PT PT polymorphism.
XX PS Claim 1; Page 109; 295pp; English.
XX PS
XX CC Sequences AAH90121-AAH90700 represent 580 human cDNA sequences which
XX CC contain single nucleotide polymorphisms (SNPs). Sequences 1 to 568
XX CC (AAH90121-AAH90688) are consecutive pairs of nucleotides which contain
XX CC silent SNPs. Sequences 569 to 580 (AAH90689-AAH90700) are consecutive
XX CC pairs of nucleotides containing SNPs which result in changes in the
XX CC corresponding amino acid sequences (AAG64751-AAG64762). The SNPs in
XX CC sequences 569 to 574 (AAH90689-AAH90694) lead to conservative amino acid
XX CC changes, while those in sequences 575 to 578 (AAH90695-AAH90698) result
XX CC in non-conservative changes. The SNP in sequences 579 and 580 (AAH90699-
XX CC AAH90700) generates a frameshift mutation. The invention also relates to
XX CC a method of detecting a polymorphic site in a nucleic acid and a method
XX CC of determining the relatedness of two nucleic acids. It also encompasses
XX CC peptides containing polymorphic sites, antibodies raised against such
XX CC peptides, and a method of detecting polymorphic proteins/peptides using
XX CC the antibodies. The nucleic acids are useful for gene therapy of an
XX CC individual having, suspected of having, or at risk of developing a
XX CC pathological condition due to the presence of a sequence polymorphism.
XX CC Such treatment would comprise administration of the wild-type nucleic
XX CC acid sequence. Antibodies raised against polymorphic peptides can also be
XX CC used in the treatment of such individuals
XX SQ Sequence 51 BP; 12 A; 14 C; 15 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 4.2%; Score 41.4; DB 1; Length 51;
XX Best Local Similarity 88.2%; Pred. No. 2e+02;
XX Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 836 TGATCGCTGCGCTGCGCCCAAGTCTGCGATTACAGCGGTAGCCA 886
DB 51 TGATCGCTGCGCTGCGCCCAAGTCTGCGATTACAGCGGTAGCCA 1
XX
XX RESULT 144
XX AAH89405
XX ID AAH89405 standard; DNA; 51 BP.
XX AC AAH89405;
XX AC
XX DT 01-OCT-2001 (first entry)
XX DE Human coding sequence polymorphic site SEQ ID NO: 186.
XX DE
XX KW Human; single nucleotide polymorphism; SNP; paternity test;
XX KW forensic test; aberrant protein expression; ds.
XX OS Homo sapiens.
XX OS
XX PN WO200151670-A2.
XX PN
XX PD 19-JUL-2001.
XX PD
XX PF 05-JAN-2001; 2001WO-US000322.
XX PF
XX PR 07-JAN-2000; 2000US-0174962P.
XX PR
XX PA (CURA-) CURAGEN CORP.
XX PA
XX PI Shimkets RA, Leach MD;
XX PI
XX DR WPI; 2001-451871/48.
XX DR
XX DR P-PSDB; AAM00292.
XX DR
XX PT Isolated human polynucleotides containing single nucleotide
XX PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
XX PT infection and diabetes.
XX PT
XX XX
```

PS Claim 1; Page 159; 475bp; English.
XX
CC The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tubercous
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC autoimmunity. The present sequence is a polymorphism-containing
CC oligonucleotide fragment of the invention
SQ Sequence 51 BP; 9 A; 21 C; 9 G; 12 T; 0 U; 0 Other;
Query Match 4.2%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2e+02; Mismatches 6; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY 663 CGCATCTTGCTCACTGCAACCTCTGCTCCGCGGTTCAAGTATTCCTCC 713
DB 1 CACGATCTTGCTCACTGCAACCTCGCTCCCAAGTTCAAGTATTCCTCC 51
RESULT 145
AAH89485/C
ID AAH89485 standard; DNA; 51 BP.
XX
AC AAH89485;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 266.
XX
KM Human; single nucleotide polymorphism; SNP; paternity test;
KM forensic test; aberrant protein expression; ds.
XX
OS Homo sapiens.
XX
PN WO200151670-A2.
XX
PD 19-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US000322.
XX
PR 07-JAN-2000; 2000US-0174962P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach MD;
XX
PI MPI: 2001-451871/48.
DR P-PSDB; AAM00370.
XX
PT Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
XX infection and diabetes.
XX
PS Claim 1; Page 180; 475bp; English.
XX
CC The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tubercous
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC autoimmunity. The present sequence is a polymorphism-containing
CC oligonucleotide fragment of the invention
SQ

SQ Sequence 51 BP; 15 A; 12 C; 12 G; 12 T; 0 U; 0 Other;
Query Match 4.2%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2e+02; Mismatches 6; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY 1080 TTCAATGAGCGGGGTTTCCACCAATATTTGTGACGCTGTCTCAACTCCT 1130
DB 51 TTGATGAGACAGGAGTTTCCATATTTGCGCAGGCTGTCTCAACTCCT 1
RESULT 146
AAH89514/C
ID AAH89514 standard; DNA; 51 BP.
XX
AC AAH89514;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 295.
XX
KM Human; single nucleotide polymorphism; SNP; paternity test;
KM forensic test; aberrant protein expression; ds.
XX
OS Homo sapiens.
XX
PN WO200151670-A2.
XX
PD 19-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US000322.
XX
PR 07-JAN-2000; 2000US-0174962P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach MD;
XX
PI MPI: 2001-451871/48.
DR P-PSDB; AAM00397.
XX
PT Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
XX infection and diabetes.
XX
PS Claim 1; Page 188; 475bp; English.
XX
CC The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tubercous
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC autoimmunity. The present sequence is a polymorphism-containing
CC oligonucleotide fragment of the invention
SQ
Query Match 4.2%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2e+02; Mismatches 6; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY 844 CTGCTCGGCTCCCAAGTCTGGATTACAGCGTGAGCAGCAGCC 894
DB 51 CTGCTCGGCTCCCAAGTCTGGATTACAGCGTGAGCAGCAGCC 1
RESULT 147
AAH89519/C
ID AAH89519 standard; DNA; 51 BP.

PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT infection and diabetes.
XX
PS Claim 1; Page 198; 475bp; English.
XX
CC The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tubercous
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC autoimmunity. The present sequence is a polymorphism-containing
CC oligonucleotide fragment of the invention
XX
SQ Sequence 51 BP; 14 A; 14 C; 14 G; 9 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1086 AGAGCGGGGTTTACCAATTTGTACGGCTGTCTCAAACTCTGACCTC 1136
Db 51 AGAGCGGGGTTTACCAATTTGTACGGCTGTCTCAAACTCTGACCTC 1

RESULT 150
AAH89472
ID AAH89472 standard; DNA; 51 BP.
XX
AC AAH89472;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 253.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.
XX
OS Homo sapiens.
XX
PN WO200151670-A2.
XX
PD 19-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US000322.
XX
PR 07-JAN-2000; 2000US-0174962P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach MD;
XX
DR WPI; 2001-451871/48.
DR P-Psdb; AAM00357.
XX
PT Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT infection and diabetes.
XX
PS Claim 1; Page 177; 475bp; English.
XX
CC The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tubercous
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or

CC autoimmunity. The present sequence is a polymorphism-containing
CC oligonucleotide fragment of the invention
XX
SQ Sequence 51 BP; 9 A; 17 C; 13 G; 12 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 692 TCCCGGGTTCAAGTATTCCTCCGCCAGCCTCTGAGTAGCTGGGACTA 742
Db 1 TCCCGGGTTCAAGTATTCCTCCGCCAGCCTCTGAGTAGCTGGGACTA 51

RESULT 151
ADK19818/C
ID ADK19818 standard; DNA; 51 BP.
XX
AC ADK19818;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human mannosyl transferase-related SNP region DNA SegID20.
XX
KW human; mannosyl transferase; anti-manic; antidepressant; gene therapy;
KW fusion protein; chromosome 9 fusion protein; chromosome 11 translocation;
KW bipolar disorder; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH replace(26,C)
FT variation /*tag= a
FT /standard_name= "Single nucleotide polymorphism"
XX
PN WO2003012064-A2.
XX
PD 13-FEB-2003.
XX
PE 02-AUG-2002; 2002WO-US024490.
XX
PR 02-AUG-2001; 2001US-00922225.
XX
PA (EGEA-) EGEA BIOSCIENCES INC.
XX
PI Evans GA;
XX
DR WPI; 2003-268116/26.
XX
PT New polypeptide comprising human mannosyl transferase, useful for
PT diagnosing or predicting the susceptibility to a bipolar disorder and for
PT identifying a compound that modulates the activity of a mannosyl
PT transferase.
XX
PS Claim 11; SEQ ID NO 20; 147bp; English.
XX
CC This invention relates to a novel isolated protein which comprises a
CC human mannosyl transferase having the same sequence as the fully defined
CC 611- or 255-amino acid sequence or its fragment. The invention may be
CC useful for the production of compounds with an anti-manic or
CC antidepressant activity whilst the disclosed sequences may be used for
CC gene therapy. The invention also provides a human mannosyl transferase
CC fusion protein and a chromosome 9 fusion protein, both of which result
CC from a chromosome 11 translocation. The human mannosyl transferase and
CC the fusion proteins are useful for diagnosing or predicting the
CC susceptibility to a bipolar disorder and for identifying a compound that
CC modulates the activity of a mannosyl transferase. The present sequence is
CC that of a region of human DNA surrounding a single nucleotide
CC polymorphism within the gene which encodes the human mannosyl transferase
CC of the invention.
XX
SQ Sequence 51 BP; 13 A; 12 C; 16 G; 10 T; 0 U; 0 Other;

XX 09-NOV-2001 (first entry)
XX
XX
DE Human silent SNP containing nucleic acid SEQ:3757.
XX
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
XX WO200140521-A2.
XX
XX
XX 07-JUN-2001.
XX
XX
XX 30-NOV-2000; 2000WO-US032758.
XX
XX
XX 30-NOV-1999; 99US-0168138P.
XX
XX 29-NOV-2000; 2000US-00726173.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach M;
XX
XX WPI; 2001-356160/37.
XX
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
XX therapy.
XX
XX
XX Claim 1; Page 1200; 2653pp; English.
XX
XX
XX AAT73060 to AAT79867 represent isolated human polymorphic polynucleotide
XX sequences (I), which contain single nucleotide polymorphisms (SNPs).
XX AAM53114 to AAM53329 represent peptides related to human polymorphic
XX polynucleotide sequences. The sequences can be used in gene and protein
XX therapy, and in vaccine production. (I) and the polypeptides encoded by
XX them may be used in the prevention, diagnosis and treatment of diseases
XX associated with inappropriate expression of polymorphic polypeptides. For
XX example, (I) may be used to treat disorders by rectifying mutations or
XX deletions in a patient's genome that affect the activity of polypeptides
XX by expressing inactive proteins or to supplement the patients own
XX production of polypeptide. Additionally, (I) and its complementary
XX sequences may also be used as DNA probes in diagnostic assays to detect
XX and quantitate the presence of similar nucleic acids in samples, and
XX therefore which patients may be in need of restorative therapy. The
XX polypeptides encoded by (I) may be used as antigens in the production of
XX antibodies specific for polymorphic polypeptides. The antibodies may also
XX be used to down regulate expression and activity. The antibodies may also
XX be used as diagnostic agents for detecting the presence of polymorphic
XX polypeptides in samples
XX
SQ Sequence 51 BP; 8 A; 16 C; 13 G; 14 T; 0 U; 0 Other;
Query Match 4.1%; Score 41; DB 1; Length 51;
Best Local Similarity 89.8%; Pred. No. 2.1e+02;
Matches 44; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 133 TTCTCCATGTTGTCAGGCTGCTCGAATCCCACTCAATATATCC 241
DB 1 TTTCGCAATGTGGCCAGCGCTGCTTGAATCTCTGACCTCAAGTATCC 49
RESULT 155
AAT79093/C
ID AAT79093 standard; DNA; 51 BP.
XX
XX
XX AAT79093;
XX
XX
XX 09-NOV-2001 (first entry)
XX
XX
XX Human silent SNP containing nucleic acid SEQ:6034.
XX
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;

KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
XX
XX Homo sapiens.
XX
XX
XX WO200140521-A2.
XX
XX
XX 07-JUN-2001.
XX
XX
XX 30-NOV-2000; 2000WO-US032758.
XX
XX
XX 30-NOV-1999; 99US-0168138P.
XX
XX 29-NOV-2000; 2000US-00726173.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach M;
XX
XX WPI; 2001-356160/37.
XX
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
XX therapy.
XX
XX
XX Claim 1; Page 2356; 2653pp; English.
XX
XX
XX AAT73060 to AAT79867 represent isolated human polymorphic polynucleotide
XX sequences (I), which contain single nucleotide polymorphisms (SNPs).
XX AAM53114 to AAM53329 represent peptides related to human polymorphic
XX polynucleotide sequences. The sequences can be used in gene and protein
XX therapy, and in vaccine production. (I) and the polypeptides encoded by
XX them may be used in the prevention, diagnosis and treatment of diseases
XX associated with inappropriate expression of polymorphic polypeptides. For
XX example, (I) may be used to treat disorders by rectifying mutations or
XX deletions in a patient's genome that affect the activity of polypeptides
XX by expressing inactive proteins or to supplement the patients own
XX production of polypeptide. Additionally, (I) and its complementary
XX sequences may also be used as DNA probes in diagnostic assays to detect
XX and quantitate the presence of similar nucleic acids in samples, and
XX therefore which patients may be in need of restorative therapy. The
XX polypeptides encoded by (I) may be used as antigens in the production of
XX antibodies specific for polymorphic polypeptides. The antibodies may also
XX be used to down regulate expression and activity. The antibodies may also
XX be used as diagnostic agents for detecting the presence of polymorphic
XX polypeptides in samples
XX
SQ Sequence 51 BP; 12 A; 15 C; 16 G; 8 T; 0 U; 0 Other;
Query Match 4.1%; Score 41; DB 1; Length 51;
Best Local Similarity 89.8%; Pred. No. 2.1e+02;
Matches 44; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 944 CCAGCTGAGTGCATGCAATTCGCTCACTGCACTGCTGCT 992
DB 49 CCAGCTGAGTGCATGCAATGCTGCTGCTCACTGCACTGCTGCT 1
RESULT 156
AAT73524
ID AAT73524 standard; DNA; 51 BP.
XX
XX
XX AAT73524;
XX
XX
XX 09-NOV-2001 (first entry)
XX
XX
XX Human silent SNP containing nucleic acid SEQ:465.
XX
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
XX
XX Homo sapiens.
XX
XX
XX WO200140521-A2.

XX 07-JUN-2001.
PD 30-NOV-2000; 2000WO-US032758.
XX 30-NOV-1999; 99US-0168138P.
PR 29-NOV-2000; 2000US-00726173.
XX (CURA-) CURAGEN CORP.
XX Shimkets RA, Leach M;
PI WPI; 2001-356160/37.
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX Claim 1; Page 196; 2653pp; English.
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA53114 to AA53329 represent peptide sequences related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
SQ Sequence 51 BP; 10 A; 14 C; 13 G; 14 T; 0 U; 0 Other;
Query Match 4.1%; Score 41; DB 1; Length 51;
Best Local Similarity 89.8%; Pred. No. 2.1e+02;
Matches 44; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1091 CGGGGTTTCCCATTTTGTGCTGCTCAAACTCCGACCTCAGG 1139
DB 2 CGGGGTTTCCCATTTGTTGGCCAGGCTGCTCAAACTCTGACCTCATG 50
RESULT 157
ID AAH89516 standard; DNA; 51 BP.
XX AAH89516;
AC 01-OCT-2001 (first entry)
XX 01-OCT-2001 (first entry)
DE Human coding sequence polymorphic site SEQ ID NO: 297.
XX Human, single nucleotide polymorphism; SNP; paternity test;
KM forensic test; aberrant protein expression; ds.
XX Homo sapiens.
OS WO200151670-A2.
XX 19-JUL-2001.
PD 05-JAN-2001; 2001WO-US000322.
PF 07-JAN-2000; 2000US-0174962P.
PR XX

PA (CURA-) CURAGEN CORP.
XX Shimkets RA, Leach MD;
PI WPI; 2001-451871/48.
DR P-PSDB; AA000399.
XX Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT infection and diabetes.
XX Claim 1; Page 189; 475pp; English.
PS The present invention relates to human nucleic acids containing single
XX nucleotide polymorphisms (SNPs). These can be used in forensic and
XX paternity tests, and to aid in the treatment of diseases associated with
XX aberrant protein expression, including cancer, amyloidosis, diabetes,
XX Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
XX glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
XX meningitis, muscular disorders, dementia, neurological diseases, tubercu
XX sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
XX osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
XX autoimmunity. The present sequence is a polymorphism-containing
CC oligonucleotide fragment of the invention
SQ Sequence 51 BP; 11 A; 10 C; 20 G; 10 T; 0 U; 0 Other;
Query Match 4.1%; Score 41; DB 1; Length 51;
Best Local Similarity 89.8%; Pred. No. 2.1e+02;
Matches 44; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 990 CTTCCCGGGCTCAAGCATTTCTGCTCAGCTTCCCAAGCACTGGG 1038
DB 49 CTTCCCGGGCTCAAGCATTTCTGCTCAGCTTCCCAAGCACTGGG 1
RESULT 158
ID AAH38408 standard; DNA; 51 BP.
XX AAH38408;
AC 14-AUG-2001 (first entry)
XX 14-AUG-2001 (first entry)
DE Human SNP flanking oligonucleotide SEQ ID 1204.
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNPs; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; ds.
OS Homo sapiens.
XX WO200129262-A2.
XX 26-APR-2001.
PD 13-OCT-2000; 2000WO-US028436.
PF 15-OCT-1999; 99US-0160096P.
PR (ORCH-) ORCHID BIOSCIENCES INC.
XX P1 Picoult-Newburg L, Pohl M;
XX WPI; 2001-290930/30.
DR New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX

PS Claim 1; Page 56; 83bp; English.

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNP primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Leach-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC diseases of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a fragment of human
CC DNA flanking the site of a single nucleotide polymorphism
XX

SEQ Sequence 51 BP; 12 A; 11 C; 17 G; 10 T; 0 U; 1 Other;

Query Match 4.1%; Score 41; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.1e+02;
Matches 44; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1024 TCCGACGAGCTGGATTACGGGACCTGCCACACACCCCTAATTTT 1074
DB 51 TCCTAGTAGTGGGATTCAGGACCTGCCACACGCCCGGCTAATTTT 1

RESULT 159

AAH40504/C
ID AAH40504 standard; DNA; 51 BP.

AC AAH40504;

DT 14-AUG-2001 (first entry)

DE Human SNP flanking oligonucleotide SEQ ID 3300.

XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KM SNP; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KM Leach-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KM polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KM acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KM inflammation; forensic investigation; paternity analysis; ds.
XX

OS Homo sapiens.

PN WO200129262-A2.

PD 26-APR-2001.

PF 13-OCT-2000; 2000WO-US028436.

PR 15-OCT-1999; 99US-0160096P.

PA (ORCH-) ORCHID BIOSCIENCES INC.

PI Picoult-Newburg L, Pohl M;

DR WPI; 2001-290930/30.

PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.

XX Claim 1; Page 66; 83bp; English.

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNP primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Leach-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC diseases of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a fragment of human
CC DNA flanking the site of a single nucleotide polymorphism
XX

SEQ Sequence 51 BP; 13 A; 13 C; 15 G; 9 T; 0 U; 1 Other;

Query Match 4.1%; Score 41; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.1e+02;
Matches 44; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1003 AGGATTCCTGTCAGGCTCCGACGAGCTGGATTACGGGACCTGC 1053
DB 51 AGGATTCCTGTCAGGCTCCGACGAGCTGGATTACGGGACCTGC 1

RESULT 160

ABL00045/C
ID ABL00045 standard; DNA; 51 BP.

AC ABL00045;

DT 05-MAR-2002 (first entry)

DE Human silent noncoding SNP oligonucleotide SEQ ID NO:36.

XX Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KM immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
KM autoimmune disease; inflammation; cancer; nervous system disease;
KM infection; polymorphic protein; ds.
XX

OS Homo sapiens.

PN WO200138586-A2.

PD 31-MAY-2001.

PF 22-NOV-2000; 2000WO-US032311.

PR 24-NOV-1999; 99US-0167383P.

PA (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach M;

DR WPI; 2001-355949/37.

PT Isolated human nucleic acids comprising one or more single nucleotide
PT polymorphisms, useful for treating a subject suffering from a pathology,
PT e.g. autoimmune diseases, ascribed to the presence of a sequence
PT polymorphism.

Query Match 4.1%; Score 40.4; DB 1; Length 50;
 Best Local Similarity 88.0%; Pred. No. 2.2e+02;
 Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1052 GGCACACACCCCGCAATTTTGTATTTTATTTAGAGGCGGTTTCAC 1101
 DB 50 GGCACACACCCCGCAATTTTGTATTTTATTTAGAGAGAGCGGTTTCAC 1

RESULT 165
 AAV19044/c
 ID AAV19044 standard; DNA; 40 BP.
 AC AAV19044;
 XX
 DT 28-JUL-1998 (first entry)
 XX
 DE Alu PCR primer 1.
 XX
 KM PCR; primer; amplification; Alu repeat sequence; vector;
 KM circular yeast artificial chromosome; YAC; ss.
 OS Synthetic.
 OS Saccharomyces sp.
 XX
 PN WO9801573-A1.
 XX
 PD 15-JAN-1998.
 XX
 PF 09-JUL-1996; 96WO-US011478.
 PF
 PR 09-JUL-1996; 96WO-US011478.
 PR
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Resnick MA, Larionov VL, Kouprina NY, Perkins EL;
 PI WPI; 1998-110234/10.
 DR
 XX
 PT Preparation of yeast artificial chromosomes - by in vivo recombination
 PT using vector comprising yeast centromere, marker, yeast telomere and
 PT nucleic acid for recombination.
 PT
 PS Example 1; Page 45; 117pp; English.
 XX
 CC This is the nucleotide sequence for the PCR primer used in the
 CC amplification of the Alu repeat sequence, which is used to demonstrate
 CC the processes described in the invention. It involves the creation and
 CC use of circular yeast artificial chromosome (YAC) to selectively clone
 CC specific nucleic acids from a background of mixed nucleic acids by
 CC introducing the vector(s) into E. coli cells. They can be used to rapidly
 CC isolate human DNA where only a part of the sequence of DNA is known.
 CC Using the methods large fragments of DNA can be easily cloned and
 CC analysed
 CC
 SQ Sequence 40 BP; 7 A; 12 C; 13 G; 8 T; 0 U; 0 Other;
 QY Query Match 4.0%; Score 40; DB 1; Length 40;
 ID Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 849 TCGGCTCCCAAGTGTGGATTACAGAGCGTGAGCCACC 888
 DB 40 TCGGCTCCCAAGTGTGGATTACAGAGCGTGAGCCACC 1

XX
 DE Nucleotide sequence of an Alu PCR primer.
 XX
 KM Yeast artificial chromosome; YAC; inter-Alu PCR.
 KM transformation-associated recombination; PCR; primer; ss.
 OS Synthetic.
 XX
 PN US6391642-B1.
 PN
 PD 21-MAY-2002.
 PD
 PF 14-APR-1998; 98US-00060023.
 PF
 PR 09-JUL-1996; 96WO-US011478.
 PR
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Resnick MA, Larionov VL, Kouprina NY, Perkins EL;
 PI WPI; 2002-49877/53.
 DR
 XX
 PT Preparing yeast artificial chromosomes, useful e.g. for cloning specific
 PT human nucleic acid, comprises recombination in yeast cells between a
 PT nucleic acid and a yeast vector.
 PT
 PS Example 1; Col 27; 50pp; English.
 XX
 CC The specification describes a method for making a yeast artificial
 CC chromosome (YAC) that includes an origin of replication (ori). The method
 CC comprises incorporating into yeast cells: a population of mammalian
 CC nucleic acid; and a vector that comprises a yeast centromere, selection
 CC marker, yeast telomere and a sequence that recombines with a region of
 CC the nucleic acid, so that in vivo recombination to a YAC occurs. This
 CC method, designated transformation-associated recombination, eliminates
 CC the need for an in vitro ligation step, and makes possible selective
 CC cloning of cDNAs for which only the 3'-sequence is known. The method is
 CC used for making a YAC. The method is also used for selective cloning of
 CC mammalian, specifically human, nucleic acid from a population.
 CC particularly radiation hybrids that contain only a small fragment of a
 CC human chromosome. The present sequence represents an Alu PCR primer. It
 CC was used for inter-Alu PCR, to produce Alu profiles of YACs produced
 CC using the method of the invention
 CC
 SQ Sequence 40 BP; 7 A; 12 C; 13 G; 8 T; 0 U; 0 Other;
 QY Query Match 4.0%; Score 40; DB 1; Length 40;
 ID Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 849 TCGGCTCCCAAGTGTGGATTACAGAGCGTGAGCCACC 888
 DB 40 TCGGCTCCCAAGTGTGGATTACAGAGCGTGAGCCACC 1

RESULT 167
 ABZ49631/c
 ID ABZ49631 standard; DNA; 41 BP.
 AC ABZ49631;
 XX
 DT 26-JUN-2003 (first entry)
 XX
 DE Human sulphotransferase SULF1C1 gene polymorphic site, #6413.
 XX
 KM Human; drug metabolising enzyme; gene; drug metabolism; chromosome 2;
 KM polymorphic site; drug evaluation; drug screening; genotyping;
 KM genetic profiling; therapeutic customisation; adverse reaction;
 KM clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
 OS Homo sapiens.
 OS
 FH Key Location/Qualifiers

```
FT variation replace(21,C)
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX WO200252044-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-JP011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
XX 02-MAY-2001; 2001JP-00135256.
XX 27-AUG-2001; 2001JP-00256862.
XX
XX (RIKE ) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Saito S;
XX
XX WPI, 2002-583571/62.
XX
XX Identifying individuals having a polymorphism, useful for determining the
XX effectiveness or side effect of a drug or treatment protocol, comprises
XX detecting at least one polymorphism in the drug metabolizing enzyme
XX nucleic acid.
XX
XX Claim 23; Page 194; 2785bp; English.
XX
XX Sequences AB243217-AB250887 represent polymorphic sites within genes
XX encoding enzymes associated with drug metabolism. The invention relates
XX to methods and compositions for identifying individuals who have at least
XX one polymorphism in such drug metabolizing enzyme-encoding genes. The
XX polymorphisms may be identified in a nucleic acid sample using probes or
XX primers specific for a sequence selected from AB243217-AB250887 using a
XX variety of detection assays, including hybridisation assays, nucleic acid
XX arrays and PCR-based methods. The invention also encompasses methods of
XX evaluating and screening drugs using genetic polymorphism data. Genetic
XX polymorphism data, particularly that relating to single nucleotide
XX polymorphisms (SNPs), may be used in studying the relationship between
XX DNA sequence variations and human diseases, conditions, and responses to
XX drugs. SNPs are also useful as polymorphism markers for discovering genes
XX that cause or exacerbate certain diseases. SNPs are particularly useful
XX in the above respects as they are stable in populations, occur
XX frequently, and have lower mutation rates than other genome variations
XX such as repeating sequences. The detection and analysis of polymorphisms
XX in genes encoding drug metabolising enzymes allows the customisation of
XX drug therapies based upon the genetic profile of individual patients.
XX This would not only take the guesswork out of selecting the drug with the
XX greatest therapeutic effect for a particular patient, but would also
XX reduce the likelihood of adverse reactions, thereby increasing safety.
XX Methods of the invention are also useful in the drug discovery and
XX approval processes. For example, individuals could be selected for
XX clinical trials only if their genetic profiles indicate that they are
XX capable of responding to a particular drug or drug class, and previously
XX failed drug candidates could be revived if they were matched with more
XX appropriate patient populations. The methods, data and compositions of
XX the invention may therefore lead to an increase in the range of
XX possible drug targets and decreases in the number of adverse drug
XX reactions, failed drug trials, the time taken for a drug to be approved,
XX the length of time patients are on medication and the number of different
XX medications a patient needs to take before finding an effective therapy
XX
XX Sequence 41 BP; 7 A; 13 C; 14 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 4.0%; Score 40; DB 1; Length 41;
XX Best Local Similarity 100.0%; Freq. No. 2e+02;
XX Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 846 GCCTCGGCTCCCAAGTCTGGGATTACAGCGGTGAGCC 885
XX |||||
XX 40 GCCTCGGCTCCCAAGTCTGGGATTACAGCGGTGAGCC 1
```

```
AB243598/C
ID AB243598 standard; DNA; 41 BP.
XX
XX AC AB243598;
XX
XX 26-JUN-2003 (first entry)
XX
XX Human sulphotransferase SULT1C1 gene polymorphic site, #382.
XX
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 2;
XX polymorphic site; drug evaluation; drug screening; genotyping;
XX clinical profiling; therapeutic customisation; adverse reaction;
XX clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Variation replace(21,C)
XX /*tag= a
XX /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX WO200252044-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-JP011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
XX 02-MAY-2001; 2001JP-00135256.
XX 27-AUG-2001; 2001JP-00256862.
XX
XX (RIKE ) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Saito S;
XX
XX WPI, 2002-583571/62.
XX
XX Identifying individuals having a polymorphism, useful for determining the
XX effectiveness or side effect of a drug or treatment protocol, comprises
XX detecting at least one polymorphism in the drug metabolizing enzyme
XX nucleic acid.
XX
XX Claim 23; Page 70; 2785bp; English.
XX
XX Sequences AB243217-AB250887 represent polymorphic sites within genes
XX encoding enzymes associated with drug metabolism. The invention relates
XX to methods and compositions for identifying individuals who have at least
XX one polymorphism in such drug metabolizing enzyme-encoding genes. The
XX polymorphisms may be identified in a nucleic acid sample using probes or
XX primers specific for a sequence selected from AB243217-AB250887 using a
XX variety of detection assays, including hybridisation assays, nucleic acid
XX arrays and PCR-based methods. The invention also encompasses methods of
XX evaluating and screening drugs using genetic polymorphism data. Genetic
XX polymorphism data, particularly that relating to single nucleotide
XX polymorphisms (SNPs), may be used in studying the relationship between
XX DNA sequence variations and human diseases, conditions, and responses to
XX drugs. SNPs are also useful as polymorphism markers for discovering genes
XX that cause or exacerbate certain diseases. SNPs are particularly useful
XX in the above respects as they are stable in populations, occur
XX frequently, and have lower mutation rates than other genome variations
XX such as repeating sequences. The detection and analysis of polymorphisms
XX in genes encoding drug metabolising enzymes allows the customisation of
XX drug therapies based upon the genetic profile of individual patients.
XX This would not only take the guesswork out of selecting the drug with the
XX greatest therapeutic effect for a particular patient, but would also
XX reduce the likelihood of adverse reactions, thereby increasing safety.
XX Methods of the invention are also useful in the drug discovery and
XX approval processes. For example, individuals could be selected for
XX clinical trials only if their genetic profiles indicate that they are
XX capable of responding to a particular drug or drug class, and previously
XX failed drug candidates could be revived if they were matched with more
XX appropriate patient populations. The methods, data and compositions of
XX the invention may therefore lead to an increase in the range of
```

CC possible drug targets and decreases in the number of adverse drug
CC reactions, failed drug trials, the time taken for a drug to be approved,
CC the length of time patients are on medication and the number of different
CC medications a patient needs to take before finding an effective therapy
XX
SQ Sequence 41 BP; 7 A; 13 C; 14 G; 7 T; 0 U; 0 Other;

Query Match 4.0%; Score 40; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 846 GCTCGGCTCCCAAGTGTGGATTACAGCGCTGAGCC 885
DB 40 GCTCGGCTCCCAAGTGTGGATTACAGCGCTGAGCC 1

RESULT 169
AAH89819
ID AAH89819 standard; DNA; 50 BP.

XX AAH89819;

DT 01-OCT-2001 (first entry)

XX Human coding sequence polymorphic site SEQ ID NO: 600.

DE Human; single nucleotide polymorphism; SNP; paternity test;

KM forensic test; aberrant protein expression; ds.

XX Homo sapiens.

XX WO200151670-A2.

PN 19-JUL-2001;

PD 05-JAN-2001; 2001WO-US000322.

XX 07-JAN-2000; 2000US-0174962P.

PR (CUPA-) CUPAGEN CORP.

XX Shinketsu RA, Leach MD;

PI WPI; 2001-451871/48.

XX P-PSDB; AAM00700.

PT Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT infection and diabetes.

XX Claim 1; Page 277; 475pp; English.

XX The present invention relates to human nucleic acids containing single
XX nucleotide polymorphisms (SNPs). These can be used in forensic and
XX paternity tests, and to aid in the treatment of diseases associated with
XX aberrant protein expression, including cancer, amyloidosis, diabetes,
XX Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
XX glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
XX meningitis, muscular disorders, dementia, neurological diseases, tuberculous
XX sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
XX osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
XX autoimmunity. The present sequence is a polymorphism-containing
XX oligonucleotide fragment of the invention

XX Sequence 50 BP; 14 A; 12 C; 9 G; 15 T; 0 U; 0 Other;

Query Match 4.0%; Score 40; DB 1; Length 50;
Best Local Similarity 89.6%; Pred. No. 2.4e+02;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1052 GCCACCGACCCGCTAATTTGTATTTCATTAGAGGGGTTTC 1099
DB 3 GCCACCGACCCGCTAATTTGTATTTCATTAGAGAGCGGATTTC 50

RESULT 170
ACC84472
ID ACC84472 standard; DNA; 39 BP.

XX ACC84472;

DT 28-AUG-2003 (first entry)

XX NTP peptide encoding sequence #19.

DE NTP peptide encoding sequence #19.

KM Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;

XX neutral thread protein; NTP; tumour; ds.

XX Unidentified.

XX WO2003008443-A2.

PN 30-JAN-2003.

PD 19-JUL-2002; 2002WO-CA001105.

PF 19-JUL-2001; 2001US-0306150P.

PR 19-JUL-2001; 2001US-0306151P.

XX 16-NOV-2001; 2001US-0331477P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA;

PI WPI; 2003-247999/24.

XX P-PSDB; ABR63267.

PT Novel neural thread protein peptide, referred as cell death peptide,
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.

XX Disclosure; Page 19; 77pp; English.

XX The present invention relates to a neural thread protein (NTP) peptide
XX referred to as cell death peptide. Thought to be cytostatic,
XX antibacterial, immunosuppressive and antiinflammatory. It is useful for
XX treating a condition in a patient requiring removal or destruction of
XX cells, for treating a condition such as benign or malignant tumor,
XX inflammatory disease, autoimmune disease and infectious disease. The
XX peptide useful for treatment is derived from the amino acid sequence for
XX a pancreatic thread protein. The peptide is conjugated, linked or bound
XX to a molecule chosen from antibody or its fragment, antibody-like binding
XX molecule, where the molecule has a higher affinity for binding to a tumor
XX or other target than binding to other cells. Treatment using NTP peptides
XX can remove benign tumors with less risk and fewer of the undesirable side
XX effects of surgery. The present sequence is an NTP encoding sequence

XX Sequence 39 BP; 6 A; 13 C; 12 G; 8 T; 0 U; 0 Other;

Query Match 3.9%; Score 39; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 843 CTTGCTCGGCTCCCAAGTGTGGATTACAGCGCTG 881
DB 1 CTTGCTCGGCTCCCAAGTGTGGATTACAGCGCTG 39

RESULT 171

ACC84471
ID ACC84471 standard; DNA; 39 BP.

XX ACC84471;

DT 28-AUG-2003 (first entry)

XX

DE NTP peptide encoding sequence #18.
XX
XX Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
KW neural thread protein; NTP; tumour; ds.
XX
XX Unidentified.
XX
XX WO200308443-A2.
XX
XX 30-JAN-2003.
XX
XX 19-JUL-2002; 2002WO-CA001105.
XX
XX 19-JUL-2001; 2001US-0306150P.
XX 19-JUL-2001; 2001US-0306150P.
XX 16-NOV-2001; 2001US-0331477P.
XX
XX (NTMO-) NYMOX CORP.
XX
XX Averbach PA;
XX
XX WPI; 2003-247999/24.
XX
XX P-PSDB; ABR63266.
XX
XX Novel neural thread protein peptide, referred as cell death peptide,
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.
XX
XX Disclosure; Page 19; 77pp; English.
XX
XX The present invention relates to a neural thread protein (NTP) peptide
CC referred to as cell death peptide. Thought to be cytostatic,
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for
CC treating a condition in a patient requiring removal or destruction of
CC cells, for treating a condition such as benign or malignant tumor,
CC inflammatory disease, autoimmune disease and infectious disease. The
CC peptide useful for treatment is derived from the amino acid sequence for
CC a pancreatic thread protein. The peptide is conjugated, linked or bound
CC to a molecule chosen from antibody or its fragment, antibody-like binding
CC molecule, where the molecule has a higher affinity for binding to a tumor
CC or other target than binding to other cells. Treatment using NTP peptides
CC can remove benign tumors with less risk and fewer of the undesirable side
CC effects of surgery. The present sequence is an NTP encoding sequence
CC
XX
SQ Sequence 39 BP; 10 A; 14 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 3.9%; Score 39; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 537 CCTGCTCAGCTCCCAAGTAGCTGGACCAAGCATG 575
DB 1 CCTGCTCAGCTCCCAAGTAGCTGGACCAAGCATG 39

RESULT 172
ABA96813
ID ABA96813 standard; DNA; 41 BP.
XX
XX ABA96813;
XX
XX 30-APR-2002 (first entry)
XX
XX Human uteroglobin 9 probe, SEQ ID NO:9.
XX
XX Human; uteroglobin 9; recombinant production; malignant tumour; cancer;
KW blood disease; HIV infection; gene therapy; human immunodeficiency virus;
KW immune disorder; inflammatory condition; cytostatic; anti-HIV;
KW antiinflammatory; immunomodulator; probe; ss.
XX
XX Homo sapiens.
XX
XX WO200198337-A1.
XX
XX

XX
XX 27-DEC-2001.
XX
XX 14-MAY-2001; 2001WO-CN000756.
XX
XX 16-MAY-2000; 2000CN-00115717.
XX
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-090430/12.
XX
XX Human uteroglobin 9 and encoding polynucleotide, used in diagnosis and
PT treatment of malignant tumors, hemopathy, human immunodeficiency virus
PT infection, immunological diseases and inflammation.
XX
XX Example 6; Page 19; 35pp; Chinese.
XX
XX The invention relates to human uteroglobin 9 (AAM549078), nucleic acids
CC encoding it (ABA96807), and a method for the recombinant production of
CC uteroglobin 9. The protein has a molecular weight of 9 KD. The present
CC invention additionally discloses an antagonist of uteroglobin 9 for
CC therapeutic use, and an antibody which specifically binds to uteroglobin
CC 9. Uteroglobin 9, and nucleotides which encode it may be used for
CC treating a variety of diseases, such as malignant tumours, blood
CC diseases, HIV (human immunodeficiency virus) infection, immune disorders
CC and inflammatory conditions. The protein may also be used to screen for
CC modulators of its activity or for peptide fingerprinting identification.
CC The polynucleotide can be used as a primer for nucleic acid amplification
CC reactions or as a probe for hybridisation reactions, or in producing gene
CC chips or microarrays. Sequences ABA96812-ABA96813 represent human
CC uteroglobin 9 probes used in an exemplification of the invention
XX
SQ Sequence 41 BP; 4 A; 10 C; 13 G; 14 T; 0 U; 0 Other;

Query Match 3.8%; Score 37.8; DB 1; Length 41;
Best Local Similarity 95.1%; Pred. No. 2.6e+02;
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 187 TGGAGTTTCCATGTTGTCAGGCTGCTCCAACTCCG 227
DB 1 TGGAGTTTCCATGTTGTCAGGCTGCTCCAACTCCG 41

RESULT 173
ABA96812
ID ABA96812 standard; DNA; 41 BP.
XX
XX ABA96812;
XX
XX 30-APR-2002 (first entry)
XX
XX Human uteroglobin 9 probe, SEQ ID NO:8.
XX
XX Human; uteroglobin 9; recombinant production; malignant tumour; cancer;
KW blood disease; HIV infection; gene therapy; human immunodeficiency virus;
KW immune disorder; inflammatory condition; cytostatic; anti-HIV;
KW antiinflammatory; immunomodulator; probe; ss.
XX
XX Homo sapiens.
XX
XX WO200198337-A1.
XX
XX 27-DEC-2001.
XX
XX 14-MAY-2001; 2001WO-CN000756.
XX
XX 16-MAY-2000; 2000CN-00115717.
XX
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
XX Mao Y, Xie Y;
XX
XX

XX WPI; 2002-090430/12.
DR Human uteroglobin 9 and encoding polynucleotide, used in diagnosis and
XX treatment of malignant tumors, hemopathy, human immunodeficiency virus
PT infection, immunological diseases and inflammation.
PS Example 6; Page 19; 35pp; Chinese.
XX The invention relates to human uteroglobin 9 (AA0549078), nucleic acids
CC encoding it (AB096807), and a method for the recombinant production of
CC uteroglobin 9. The protein has a molecular weight of 9 kD. The present
CC invention additionally discloses an antagonist of uteroglobin 9 for
CC therapeutic use, and an antibody which specifically binds to uteroglobin
CC 9. Uteroglobin 9, and nucleotides which encode it may be used for
CC treating a variety of diseases, such as malignant tumours, blood
CC diseases, HIV (human immunodeficiency virus) infection, immune disorders
CC and inflammatory conditions. The protein may also be used to screen for
CC modulators of its activity or for peptide fingerprinting identification.
CC The polynucleotide can be used as a primer for nucleic acid amplification
CC reactions or as a probe for hybridisation reactions, or in producing gene
CC chips or microarrays. Sequences AB096812-AB096813 represent human
CC uteroglobin 9 probes used in an exemplification of the invention
XX
SQ Sequence 41 BP; 4 A; 10 C; 13 G; 14 T; 0 U; 0 Other;
Query Match 3.8%; Score 37.8; DB 1; Length 41;
Best Local Similarity 95.1%; Pred. No. 2.6e+02;
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 187 TGGAGTTTCCATGTTGTGTCAGGCTGCTCGAAGTCCCG 227
Db 1 TGGGGTTTCCATGTTGTGTCAGGCTGCTCGAAGTCTCG 41
RESULT 174
AB244526
ID AB244526 standard; DNA; 41 BP.
XX
AC AB244526;
XX
DT 26-JUN-2003 (first entry)
XX
DE Human neuropathy target esterase NTE gene polymorphic site, #1310.
XX
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 19;
KW polymorphic site; drug evaluation; drug screening; genotyping;
KW genetic profiling; therapeutic customisation; adverse reaction;
KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(21,G)
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN WO200252044-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-JP011592.
XX
PR 27-DEC-2000; 2000JP-00399443.
PR 02-MAY-2001; 2001JP-00135256.
PR 27-AUG-2001; 2001JP-00256862.
XX
XX (RIKEN) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Saito S;
XX
DR WPI; 2002-583571/62.
XX

PT Identifying individuals having a polymorphism, useful for determining the
PT effectiveness or side effect of a drug or treatment protocol, comprises
PT detecting at least one polymorphism in the drug metabolizing enzyme
XX nucleic acid.
PS Claim 23; Page 85; 2785pp; English.
XX
XX Sequences AB243217-AB250887 represent polymorphic sites within genes
CC encoding enzymes associated with drug metabolism. The invention relates
CC to methods and compositions for identifying individuals who have at least
CC one polymorphism in such drug metabolising enzyme-encoding genes. The
CC polymorphisms may be identified in a nucleic acid sample using probes or
CC primers specific for a sequence selected from AB243217-AB250887 using a
CC variety of detection assays, including hybridisation assays, nucleic acid
CC arrays and PCR-based methods. The invention also encompasses methods of
CC evaluating and screening drugs using genetic polymorphism data. Genetic
CC polymorphisms (SNPs) may be used in studying the relationship between
CC DNA sequence variations and human diseases, conditions, and responses to
CC drugs. SNPs are also useful as polymorphism markers for discovering genes
CC that cause or exacerbate certain diseases. SNPs are particularly useful
CC in the above respects as they are stable in populations, occur
CC frequently, and have lower mutation rates than other genome variations
CC such as repeating sequences. The detection and analysis of polymorphisms
CC in genes encoding drug metabolising enzymes allows the customisation of
CC drug therapies based upon the genetic profile of individual patients.
CC This would not only take the guesswork out of selecting the drug with the
CC greatest therapeutic effect for a particular patient, but would also
CC reduce the likelihood of adverse reactions, thereby increasing safety.
CC Methods of the invention are also useful in the drug discovery and
CC approval processes. For example, individuals could be selected for
CC clinical trials only if their genetic profiles indicate that they are
CC capable of responding to a particular drug or drug class, and previously
CC failed drug candidates could be revived if they were matched with more
CC appropriate patient populations. The methods, data and compositions of
CC the invention may therefore lead to an increase in the range of
CC possible drug targets and decreases in the number of adverse drug
CC reactions, failed drug trials, the time taken for a drug to be approved,
CC the length of time patients are on medication and the number of different
CC medications a patient needs to take before finding an effective therapy
XX
SQ Sequence 41 BP; 7 A; 16 C; 7 G; 11 T; 0 U; 0 Other;
Query Match 3.8%; Score 37.8; DB 1; Length 41;
Best Local Similarity 95.1%; Pred. No. 2.6e+02;
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 676 CACTGCAACCTGCGCTCCCGGTTCAAGTTATTCCTCGC 716
Db 1 CACTGCAACCTGCGCTCCCGGTTCAAGTTATTCCTCGC 41
RESULT 175
AB250785
ID AB250785 standard; DNA; 41 BP.
XX
AC AB250785;
XX
DT 26-JUN-2003 (first entry)
XX
DE Human neuropathy target esterase NTE gene polymorphic site, #7567.
XX
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 19;
KW polymorphic site; drug evaluation; drug screening; genotyping;
KW genetic profiling; therapeutic customisation; adverse reaction;
KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(21,G)
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX

XX MO20025044-A2.
 XX
 XX 04-JUN-2002.
 XX
 XX 27-DEC-2001; 2001WO-JP011592.
 XX
 XX 27-DEC-2000; 2000JP-00399443.
 XX PR 02-MAY-2001; 2001JP-00135256.
 XX PR 27-AUG-2001; 2001JP-00256862.
 XX
 XX (RIKEN) RIKEN KK.
 XX
 XX Nakamura Y, Sekine A, Iida A, Satto S;
 XX PI
 XX WPI; 2002-583571/62.
 XX
 XX Identifying individuals having a polymorphism, useful for determining the
 XX PT effectiveness or side effect of a drug or treatment protocol, comprises
 XX PT detecting at least one polymorphism in the drug metabolizing enzyme
 XX PT nucleic acid.
 XX
 XX
 XX Claim 23; Page 221; 2785pp; English.
 XX
 XX Sequences AB243217-AB250887 represent polymorphic sites within genes
 XX CC encoding enzymes associated with drug metabolism. The invention relates
 XX CC to methods and compositions for identifying individuals who have at least
 XX CC one polymorphism in such drug metabolizing enzyme-encoding genes. The
 XX CC polymorphisms may be identified in a nucleic acid sample using probes or
 XX CC primers specific for a sequence selected from AB243217-AB250887 using a
 XX CC variety of detection assays, including hybridization assays, nucleic acid
 XX CC arrays and PCR-based methods. The invention also encompasses methods of
 XX CC evaluating and screening drugs using genetic polymorphism data. Genetic
 XX CC polymorphism data, particularly that relating to single nucleotide
 XX CC polymorphisms (SNPs), may be used in studying the relationship between
 XX CC DNA sequence variations and human diseases, conditions, and responses to
 XX CC drugs. SNPs are also useful as polymorphism markers for discovering genes
 XX CC that cause or exacerbate certain diseases. SNPs are particularly useful
 XX CC in the above respects as they are stable in populations, occur
 XX CC frequently, and have lower mutation rates than other genome variations
 XX CC such as repeating sequences. The detection and analysis of polymorphisms
 XX CC in genes encoding drug metabolizing enzymes allows the customization of
 XX CC drug therapies based upon the genetic profile of individual patients.
 XX CC This would not only take the guesswork out of selecting the drug with the
 XX CC greatest therapeutic effect for a particular patient, but would also
 XX CC reduce the likelihood of adverse reactions, thereby increasing safety.
 XX CC Methods of the invention are also useful in the drug discovery and
 XX CC approval processes. For example, individuals could be selected for
 XX CC clinical trials only if their genetic profiles indicate that they are
 XX CC capable of responding to a particular drug or drug class, and previously
 XX CC failed drug candidates could be revived if they were matched with more
 XX CC appropriate patient populations. The methods, data and compositions of
 XX CC the invention may therefore lead to an increase in the range of
 XX CC possible drug targets and decreases in the number of adverse drug
 XX CC reactions, failed drug trials, the time taken for a drug to be approved,
 XX CC the length of time patients are on medication and the number of different
 XX CC medications a patient needs to take before finding an effective therapy
 XX
 XX
 XX Sequence 41 BP; 7 A; 16 C; 7 G; 11 T; 0 U; 0 Other;
 SQ
 Query Match 3.8%; Score 37.8; DB 1; Length 41;
 Best Local Similarity 95.1%; Pred. No. 2.6e+02;
 Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 676 CACTGCAACCTGCTCCCGGTTCAAGTTATTTCTCTGC 716
 DB 1 CACTGCAACCTGCTCCCGGTTCAAGTTATTTCTCTGC 41
 RESULT 176
 AD112521
 ID AD112521 standard; DNA; 42 BP.
 XX

AC AD112521;
 XX
 XX 22-APR-2004 (first entry)
 XX
 XX Human BRCA1 DNA junction sequence comprising large deletion Segid 1.
 DE
 XX
 XX ds; cancer; human; tumour suppressor;
 XX KW breast cancer susceptibility gene 1; BRCA1; repetitive Alu;
 XX KW ovarian cancer; junction sequence; recombination; mutant.
 XX
 XX Homo sapiens.
 XX
 XX WO2003104474-A2.
 XX
 XX 18-DEC-2003.
 XX
 XX 09-JUN-2003; 2003WO-US018098.
 XX
 XX 07-JUN-2002; 2002US-0387132P.
 XX PR 09-AUG-2002; 2002US-0402430P.
 XX
 XX (MYRI-) MYRIAD GENETICS INC.
 XX
 XX Scholl T, Hendrickson BC, Ward B, Pruss D;
 XX PI
 XX WPI; 2004-062369/06.
 XX
 XX Predicting a predisposition to cancer in a patient comprising detecting a
 XX PT deletion in the BRCA1 gene that results from the unequal crossover
 XX PT between a pair of repetitive sequences in the BRCA1 gene.
 XX
 XX
 XX Claim 16; SEQ ID NO 1; 59pp; English.
 XX
 XX This invention relates to a novel method for predicting a predisposition
 XX CC to cancer in a patient by detecting large deletions in the human tumour
 XX CC suppressor gene identified as the breast cancer susceptibility gene 1
 XX CC (BRCA1). Specifically, it refers to deletions that result from the
 XX CC unequal crossover between a pair of repetitive Alu sequences in the
 XX CC gene, such that the recombined nucleotide sequence containing the
 XX CC deletion indicates a predisposition to breast and ovarian cancer. The
 XX CC present invention describes newly discovered deletion mutations that are
 XX CC believed to be deleterious and cause significant alterations in the
 XX CC structure or biochemical function of BRCA1. Accordingly, it provides
 XX CC methods for detecting such mutants, as well as identifying and screening
 XX CC for cytostatic compounds useful for treating or preventing cancers
 XX CC associated with a BRCA1 genetic variant. This polynucleotide is a DNA
 XX CC fragment representing a junction sequence that arises as a result of a
 XX CC recombination event in human BRCA1 that causes the omission of exons 16
 XX CC and 17, given in an exemplification of the invention.
 XX
 XX
 XX Sequence 42 BP; 8 A; 12 C; 12 G; 10 T; 0 U; 0 Other;
 SQ
 Query Match 3.8%; Score 37.8; DB 1; Length 42;
 Best Local Similarity 95.1%; Pred. No. 2.6e+02;
 Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 848 CTCGGCCTCCCAAGTGCTGGATTACAGGCTGAGCCACC 888
 DB 2 CTCGGCCTCCCAAGTGCTGGATTACAGGCTGAGCCACC 42
 RESULT 177
 AA268006
 ID AA268006 standard; DNA; 47 BP.
 XX
 XX AA268006;
 XX
 XX 10-SEP-2001 (first entry)
 XX
 XX Human map-related biallelic marker SEQ ID NO:2353.
 XX
 XX Human genome; biallelic marker; high density disequilibrium map;
 XX KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW

KW haplotyping; hybridisation; identification; characterisation; diagnosis;
KM single nucleotide polymorphism; SNP; ds.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT variation replace(24,A)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX WO954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-1B000822.
XX
XX 21-APR-1998; 98US-0082614P.
XX 23-NOV-1998; 98US-0109732P.
XX
XX (GEST) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome.
XX
XX Claim 3; Page 732; 2745pp; English.
XX
XX AA265654 to AA269578 represent human biallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences. AA269579 to AA277440 represent amplification
XX primers for the biallelic markers. The biallelic markers of the invention
XX have a variety of uses: they can be used for high density mapping of the
XX human genome, and in complex association studies and haplotyping studies
XX which are useful in determining the genetic basis for disease states.
XX Compositions and methods of the invention can also be useful for the
XX identification of the targets for the development of pharmaceutical
XX agents and diagnostic methods, as well as the characterisation of the
XX differential efficacious responses to and side effects from
XX pharmaceutical agents acting on a disease as well as other treatment.
XX N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
XX 3367, are not actually given a sequence in the Sequence Listing from the
XX present invention
XX
XX Sequence 47 BP; 9 A; 16 C; 11 G; 11 T; 0 U; 0 Other;
XX
XX
XX Query Match 3.8%; Score 37.6; DB 1; Length 47;
XX Best Local Similarity 90.9%; Pred. No. 2.9e+02;
XX Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX
XX 1006 GATTCTCTCTCTCAGCTCCCAAGCGCTGGATTACGGGCAC 1049
XX 2 GATTCTCTCTCTCAGCTCCCAAGCGCTGGATTACGGGCAC 45
XX
XX
XX RESULT 178
XX AB243589/C
XX ID AB243589 standard; DNA; 41 BP.
XX
XX AC AB243589;
XX
XX
XX 26-JUN-2003 (first entry)
XX
XX Human cerebroside transferase CST gene polymorphic site, #373.
XX
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;
XX polymorphic site; drug evaluation; drug screening; genotyping;
XX genetic profiling; therapeutic customisation; adverse reaction;
XX clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
XX
OS

XX
XX Key Location/Qualifiers
XX FT variation replace(21,A)
XX FT /*tag= a
XX FT /standard_name= "single nucleotide polymorphism (SNP)"
XX
XX
XX MO200252044-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-0P011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
XX 02-MAY-2001; 2001JP-00135256.
XX 27-AUG-2001; 2001JP-00256862.
XX
XX (RIKE) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Saito S;
XX WPI; 2002-583571/62.
XX
XX
XX Identifying individuals having a polymorphism, useful for determining the
XX effectiveness or side effect of a drug or treatment protocol, comprises
XX detecting at least one polymorphism in the drug metabolizing enzyme
XX nucleic acid.
XX
XX Claim 23; Page 70; 2785pp; English.
XX
XX
XX Sequences AB243217-AB250887 represent polymorphic sites within genes
XX encoding enzymes associated with drug metabolism. The invention relates
XX to methods and compositions for identifying individuals who have at least
XX one polymorphism in such drug metabolising enzyme-encoding genes. The
XX polymorphisms may be identified in a nucleic acid sample using probes or
XX primers specific for a sequence selected from AB243217-AB250887 using a
XX variety of detection assays, including hybridisation assays, nucleic acid
XX arrays and PCR-based methods. The invention also encompasses methods of
XX evaluating and screening drugs using genetic polymorphism data. Genetic
XX polymorphisms (SNPs), may be used in studying the relationship between
XX DNA sequence variations and human diseases, conditions, and responses to
XX drugs. SNPs are also useful as polymorphism markers for discovering genes
XX that cause or exacerbate certain diseases. SNPs are particularly useful
XX in the above respects as they are stable in populations, occur
XX frequently, and have lower mutation rates than other genome variations
XX such as repeating sequences. The detection and analysis of polymorphisms
XX in genes encoding drug metabolising enzymes allows the customisation of
XX drug therapies based upon the genetic profile of individual patients.
XX This would not only take the guesswork out of selecting the drug with the
XX greatest therapeutic effect for a particular patient, but would also
XX reduce the likelihood of adverse reactions, thereby increasing safety.
XX Methods of the invention are also useful in the drug discovery and
XX approval processes. For example, individuals could be selected for
XX clinical trials only if their genetic profiles indicate that they are
XX capable of responding to a particular drug or drug class, and previously
XX failed drug candidates could be revived if they were matched with more
XX appropriate patient populations. The methods, data and compositions of
XX the invention may therefore lead to an increase in the range of
XX possible drug targets and decreases in the number of adverse drug
XX reactions, failed drug trials, the time taken for a drug to be approved,
XX the length of time patients are on medication and the number of different
XX medications a patient needs to take before finding an effective therapy
XX
XX
XX Sequence 41 BP; 9 A; 11 C; 13 G; 8 T; 0 U; 0 Other;
XX
XX
XX Query Match 3.7%; Score 36.2; DB 1; Length 41;
XX Best Local Similarity 92.7%; Pred. No. 3.1e+02;
XX Matches 38; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX
XX 198 CATGTTGGCCAGGCTGCTCTCGAATCCGACCTCGAGTCA 238
XX 41 CATGTTGGCCAGGCTGCTCTCGAATCCGACCTCGAGTCA 1
XX
XX
XX

RESULT 179
 ABZ4509
 ID ABZ4509 standard; DNA; 41 BP.
 AC ABZ4509;
 XX
 XX 26-JUN-2003 (first entry)
 DE Human ATP-binding cassette ABCA7 gene polymorphic site, #2293.
 XX
 XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 19;
 KM polymorphic site; drug evaluation; drug screening; genotyping;
 KM genetic profiling; therapeutic customisation; adverse reaction;
 KM clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT variation replace(21,T)
 FT /*tag= a
 FT /standard_name= "Single nucleotide polymorphism (SNP)"
 XX
 XX WO200252044-A2.
 XX
 XX 04-JUL-2002.
 XX
 XX 27-DEC-2001; 2001WO-JP011592.
 XX
 XX 27-DEC-2000; 2000JP-00399443.
 PR 02-MAY-2001; 2001JP-00135256.
 PR 27-AUG-2001; 2001JP-00256862.
 XX
 XX (RIKE) RIKEN KK.
 XX
 XX Nakamura Y, Sekine A, Iida A, Saito S;
 PI WPI; 2002-583571/62.
 DR
 XX
 XX Identifying individuals having a polymorphism, useful for determining the
 PT effectiveness or side effect of a drug or treatment protocol, comprises
 PT detecting at least one polymorphism in the drug metabolizing enzyme
 PT nucleic acid.
 XX
 XX
 XX Claim 23; Page 102; 2785pp; English.
 XX
 XX Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes
 CC encoding enzymes associated with drug metabolism. The invention relates
 CC to methods and compositions for identifying individuals who have at least
 CC one polymorphism in such drug metabolising enzyme-encoding genes. The
 CC polymorphisms may be identified in a nucleic acid sample using probes or
 CC primers specific for a sequence selected from ABZ43217-ABZ50887 using a
 CC variety of detection assays, including hybridisation assays, nucleic acid
 CC arrays and PCR-based methods. The invention also encompasses methods of
 CC evaluating and screening drugs using genetic polymorphism data. Genetic
 CC polymorphism data, particularly that relating to single nucleotide
 CC polymorphisms (SNPs), may be used in studying the relationship between
 CC DNA sequence variations and human diseases, conditions, and responses to
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes
 CC that cause or exacerbate certain diseases. SNPs are particularly useful
 CC in the above respects as they are stable in populations, occur
 CC frequently, and have lower mutation rates than other genome variations
 CC such as repeating sequences. The detection and analysis of polymorphisms
 CC in genes encoding drug metabolising enzymes allows the customisation of
 CC drug therapies based upon the genetic profile of individual patients.
 CC This would not only take the guesswork out of selecting the drug with the
 CC greatest therapeutic effect for a particular patient, but would also
 CC reduce the likelihood of adverse reactions, thereby increasing safety.
 CC Methods of the invention are also useful in the drug discovery and
 CC approval processes. For example, individuals could be selected for
 CC clinical trials only if their genetic profiles indicate that they are
 CC capable of responding to a particular drug or drug class, and previously
 CC failed drug candidates could be revived if they were matched with more

CC appropriate patient populations. The methods, data and compositions of
 CC the invention may therefore lead to an increase in the range of
 CC possible drug targets and decreases in the number of adverse drug
 CC reactions, failed drug trials, the time taken for a drug to be approved,
 CC the length of time patients are on medication and the number of different
 CC medications a patient needs to take before finding an effective therapy
 XX
 XX SQ Sequence 41 BP; 8 A; 12 C; 13 G; 8 T; 0 U; 0 Other;
 XX
 XX Query Match 3.7%; Score 36.2; DB 1; Length 41;
 XX Best local similarity 92.7%; Pred. No. 3.1e+02;
 XX Matches 38; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 XX QY 643 CCCAGCTGAGTGCAGTGGCGCAATCTTGGCTCATGCAA 683
 XX |||||
 DB 1 CCCAGCTGAGTGCAGTGGCGAGATCTTGGCTCATGCAA 41
 XX
 XX
 XX RESULT 180
 XX ABZ46915
 XX ID ABZ46915 standard; DNA; 41 BP.
 XX
 XX AC ABZ46915;
 XX
 XX 26-JUN-2003 (first entry)
 DE Human ATP-binding cassette ABCA7 gene polymorphic site, #3699.
 XX
 XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 19;
 KM polymorphic site; drug evaluation; drug screening; genotyping;
 KM genetic profiling; therapeutic customisation; adverse reaction;
 KM clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT variation replace(17,A)
 FT /*tag= a
 FT /standard_name= "Single nucleotide polymorphism (SNP)"
 FT variation replace(21,T)
 FT /*tag= b
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 XX
 XX WO200252044-A2.
 XX
 XX 04-JUL-2002.
 XX
 XX 27-DEC-2001; 2001WO-JP011592.
 XX
 XX 27-DEC-2000; 2000JP-00399443.
 PR 02-MAY-2001; 2001JP-00135256.
 PR 27-AUG-2001; 2001JP-00256862.
 XX
 XX (RIKE) RIKEN KK.
 XX
 XX Nakamura Y, Sekine A, Iida A, Saito S;
 PI WPI; 2002-583571/62.
 DR
 XX
 XX Identifying individuals having a polymorphism, useful for determining the
 PT effectiveness or side effect of a drug or treatment protocol, comprises
 PT detecting at least one polymorphism in the drug metabolizing enzyme
 PT nucleic acid.
 XX
 XX
 XX Claim 23; Page 129; 2785pp; English.
 XX
 XX Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes
 CC encoding enzymes associated with drug metabolism. The invention relates
 CC to methods and compositions for identifying individuals who have at least
 CC one polymorphism in such drug metabolising enzyme-encoding genes. The
 CC polymorphisms may be identified in a nucleic acid sample using probes or
 CC primers specific for a sequence selected from ABZ43217-ABZ50887 using a
 CC variety of detection assays, including hybridisation assays, nucleic acid

arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data. Genetic polymorphism data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolising enzymes allows the customisation of drug therapies based upon the genetic profile of individual patients. This would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety. Methods of the invention are also useful in the drug discovery and approval processes. For example, individuals could be selected for clinical trials only if their genetic profiles indicate that they are capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to an increase in the range of possible drug targets and decreases in the number of adverse drug reactions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy

Sequence 41 BP; 8 A; 12 C; 13 G; 8 T; 0 U; 0 Other;

Query Match
Best Local Similarity 92.7%; Score 36.2; DB 1; Length 41;
Matches 38; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

643 CCCAGGCTGAGTCAGTCAGTCGCAATTTGGCTCAGTCGCA 683
1 CCCAGGCTGAGTCAGTCAGTCGCAATTTGGCTCAGTCGCA 41

RESULT 181
AB249741/C
ID AB249741 standard; DNA; 41 BP.
AC AB249741;
XX
DT 26-JUN-2003 (first entry)
XX
DE Human cerebroside transferase CST gene polymorphic site, #6523.
XX
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;
KM polymorphic site; drug evaluation; drug screening; genotyping;
KM genetic profiling; therapeutic customisation; adverse reaction;
KM clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH replace(21,A)
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX MO200252044-A2.
XX
XX PD 04-JUL-2002.
XX
XX PF 27-DEC-2001; 2001WO-JP011592.
XX
XX PR 27-DEC-2000; 2000JP-0039443.
XX
XX PR 02-MAY-2001; 2001JP-00135256.
XX
XX PR 27-AUG-2001; 2001JP-00256862.
XX
XX PA (RIKE) RIKEN KK.
XX
XX PI Nakamura Y, Sekine A, Iida A, Saito S;

WP1; 2002-583571/62.
Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolising enzyme nucleic acid.

Claim 23; Page 197; 2785pp; English.

Sequences AB243217-AB250887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism in such drug metabolising enzyme-encoding genes. The polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from AB243217-AB250887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data. Genetic polymorphism data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolising enzymes allows the customisation of drug therapies based upon the genetic profile of individual patients. This would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety. Methods of the invention are also useful in the drug discovery and approval processes. For example, individuals could be selected for clinical trials only if their genetic profiles indicate that they are capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to an increase in the range of possible drug targets and decreases in the number of adverse drug reactions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy

Sequence 41 BP; 9 A; 11 C; 13 G; 8 T; 0 U; 0 Other;

Query Match
Best Local Similarity 92.7%; Score 36.2; DB 1; Length 41;
Matches 38; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

198 CATGTTGCTCAGGCTGTGCTCGAATCCGACCTCAGATGA 238
41 CATGTTGCTCAGGCTGTGCTCGAATCCGACCTCAGATGA 1

RESULT 182
AAH91207/C
ID AAH91207 standard; DNA; 40 BP.
AC AAH91207;
XX
XX DT 09-OCT-2001 (first entry)
XX
XX DE Human inflammatory bowel disease associated polymorphic site #282.
XX
XX KM Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KM single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
KM chromosome 5q31-33; forensic test; gene therapy; ds.
XX
XX OS Homo sapiens.
XX
XX XX Key Location/Qualifiers
FH m18c_feature 13
FT

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FT      /note= "SNP, optionally T or C at this position"
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XX
XX      WO200142511-A2.
XX
XX      14-JUN-2001.
XX
XX      11-DEC-2000; 2000WO-US033632.
XX
XX      10-DEC-1999; 99US-0170257P.
XX      10-APR-2000; 2000US-0196046P.
XX
XX      (WHEED ) WHITEHEAD INST BIOMEDICAL RES.
XX      (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX
XX      Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
XX      WPI; 2001-367874/38.
XX
XX      Testing for the presence of polymorphisms associated with inflammatory
XX      bowel disease, using a hybridization assay.
XX
XX      Claim 1; Page 50; 463pp; English.
XX
XX      The present invention describes a method for detecting the presence of
XX      polymorphisms associated with inflammatory bowel diseases such as
XX      ulcerative colitis and Crohn's disease. The methods can be used to detect
XX      the presence of genetic polymorphisms associated with inflammatory bowel
XX      disease and correlating their occurrence with disease states. They may be
XX      used in this way for phenotypic correlations, forensics, paternity
XX      testing, medicine and genetic analysis. The present sequence is a
XX      polymorphic site described in the exemplification of the invention
XX
XX      Sequence 40 BP; 13 A; 7 C; 12 G; 7 T; 0 U; 1 Other:
XX
XX      Query Match      3.6%; Score 35.8; DB 1; Length 40;
XX      Best Local Similarity 92.5%; Pred. No. 3.2e+02;
XX      Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX      1096 TTTCACCATATTTCGAGGCTGCTCCAAACCTCGACCT 1135
XX      Db      40 TTTCACCATGTTAGTCAGGCTGCTCCNAACCTCGACCT 1
XX
XX      RESULT 183
XX      ID      ABZ50133 standard; DNA; 41 BP.
XX
XX      AC      ABZ50133;
XX
XX      DT      26-JUN-2003 (first entry)
XX
XX      DE      Human NDUF51 gene polymorphic site, #6915.
XX
XX      KW      Human; drug metabolising enzyme; gene; drug metabolism; chromosome 2;
XX      polymorphic site; drug evaluation; drug screening; genotyping;
XX      genetic profiling; therapeutic customisation; adverse reaction;
XX      clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX
XX      OS      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      FT      variation      /tag= a
XX      FT      /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX      PN      WO200252044-A2.
XX
XX      PD      04-JUL-2002.
XX
XX      PP      27-DEC-2001; 2001WO-JP011592.
XX
XX      PR      27-DEC-2000; 2000JP-00399443.

```

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PR      02-MAY-2001; 2001JP-00135256.
PR      27-AUG-2001; 2001JP-00256862.
XX
XX      (RIKE ) RIKEN KK.
XX
XX      Nakamura Y, Sekine A, Iida A, Saito S;
XX      WPI; 2002-583571/62.
XX
XX      Identifying individuals having a polymorphism, useful for determining the
XX      effectiveness or side effect of a drug or treatment protocol, comprises
XX      detecting at least one polymorphism in the drug metabolizing enzyme
XX      nucleic acid.
XX
XX      Claim 23; Page 206; 2785pp; English.
XX
XX      Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes
XX      encoding enzymes associated with drug metabolism. The invention relates
XX      to methods and compositions for identifying individuals who have at least
XX      one polymorphism in such drug metabolising enzyme-encoding genes. The
XX      polymorphisms may be identified in a nucleic acid sample using probes or
XX      primers specific for a sequence selected from ABZ43217-ABZ50887 using a
XX      variety of detection assays, including hybridisation assays, nucleic acid
XX      arrays and PCR-based methods. The invention also encompasses methods of
XX      evaluating and screening drugs using genetic polymorphism data. Genetic
XX      polymorphism data, particularly that relating to single nucleotide
XX      polymorphisms (SNPs), may be used in studying the relationship between
XX      DNA sequence variations and human diseases, conditions, and responses to
XX      drugs. SNPs are also useful as polymorphism markers for discovering genes
XX      that cause or exacerbate certain diseases. SNPs are particularly useful
XX      in the above respects as they are stable in populations, occur
XX      frequently, and have lower mutation rates than other genome variations
XX      such as repeating sequences. The detection and analysis of polymorphisms
XX      in genes encoding drug metabolising enzymes allows the customisation of
XX      drug therapies based upon the genetic profile of individual patients.
XX      This would not only take the guesswork out of selecting the drug with the
XX      greatest therapeutic effect for a particular patient, but would also
XX      reduce the likelihood of adverse reactions, thereby increasing safety.
XX      Methods of the invention are also useful in the drug discovery and
XX      approval processes. For example, individuals could be selected for
XX      clinical trials only if their genetic profiles indicate that they are
XX      capable of responding to a particular drug or drug class, and previously
XX      failed drug candidates could be revived if they were matched with more
XX      appropriate patient populations. The methods, data and compositions of
XX      the invention may therefore lead to an increase in the range of
XX      possible drug targets and decreases in the number of adverse drug
XX      reactions, failed drug trials, the time taken for a drug to be approved,
XX      the length of time patients are on medication and the number of different
XX      medications a patient needs to take before finding an effective therapy
XX
XX      Sequence 41 BP; 12 A; 7 C; 12 G; 10 T; 0 U; 0 Other:
XX
XX      Query Match      3.6%; Score 35.8; DB 1; Length 41;
XX      Best Local Similarity 94.9%; Pred. No. 3.3e+02;
XX      Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX      1045 GGACATGCGCACGACCCGCTAATTTTGTATTTCCTCA 1083
XX      Db      40 GGACATGCGCACGACCCGCTAATTTTGTATTTCCTCA 2
XX
XX      RESULT 184
XX      ID      ABZ44123/C
XX
XX      AC      ABZ44123;
XX
XX      DT      26-JUN-2003 (first entry)
XX
XX      DE      Human NDUF51 gene polymorphic site, #907.
XX
XX      KW      Human; drug metabolising enzyme; gene; drug metabolism; chromosome 2;
XX      polymorphic site; drug evaluation; drug screening; genotyping;
XX

```

```
KW genetic profiling; therapeutic customisation; adverse reaction;
KM clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(21,T)
FT /*tag=a
FT /standard_name="Single nucleotide polymorphism (SNP)"
XX
EN WO200252044-A2.
XX
PD 04-JUL-2002.
XX
PD 27-DEC-2001; 2001WO-JP011592.
XX
PF 27-DEC-2000; 2000JP-00399443.
XX
PR 02-MAY-2001; 2001JP-00135256.
XX
PR 27-AUG-2001; 2001JP-00256862.
XX
XX (RIKE ) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Saito S;
XX
XX WPI; 2002-583571/62.
XX
XX Identifying individuals having a polymorphism, useful for determining the
XX effectivenss or side effect of a drug or treatment protocol, comprises
XX detecting at least one polymorphism in the drug metabolizing enzyme
XX nucleic acid.
XX
PS Claim 23; Page 79; 2785pp; English.
XX
CC Sequences AB243217-AB250887 represent polymorphic sites within genes
CC encoding enzymes associated with drug metabolism. The invention relates
CC to methods and compositions for identifying individuals who have at least
CC one polymorphism in such drug metabolizing enzyme-encoding genes. The
CC polymorphisms may be identified in a nucleic acid sample using probes or
CC primers specific for a sequence selected from AB243217-AB250887 using a
CC variety of detection assays, including hybridisation assays, nucleic acid
CC arrays and PCR-based methods. The invention also encompasses methods of
CC evaluating and screening drugs using genetic polymorphism data. Genetic
CC polymorphism data, particularly that relating to single nucleotide
CC polymorphisms (SNPs), may be used in studying the relationship between
CC DNA sequence variations and human diseases, conditions, and responses to
CC drug. SNPs are also useful as polymorphism markers for discovering genes
CC that cause or exacerbate certain diseases. SNPs are particularly useful
CC in the above respects as they are stable in populations, occur
CC frequently, and have lower mutation rates than other genome variations
CC such as repeating sequences. The detection and analysis of polymorphisms
CC in genes encoding drug metabolizing enzymes allows the customisation of
CC drug therapies based upon the genetic profile of individual patients.
CC This would not only take the guesswork out of selecting the drug with the
CC greatest therapeutic effect for a particular patient, but would also
CC reduce the likelihood of adverse reactions, thereby increasing safety.
CC Methods of the invention are also useful in the drug discovery and
CC approval processes. For example, individuals could be selected for
CC clinical trials only if their genetic profiles indicate that they are
CC capable of responding to a particular drug or drug class, and previously
CC failed drug candidates could be revived if they were matched with more
CC appropriate patient populations. The methods, data and compositions of
CC the invention may therefore lead to an increase in the range of
CC possible drug targets and decreases in the number of adverse drug
CC reactions, failed drug trials, the time taken for a drug to be approved,
CC the length of time patients are on medication and the number of different
CC medications a patient needs to take before finding an effective therapy
XX
SQ Sequence 41 BP; 12 A; 7 C; 12 G; 10 T; 0 U; 0 Other;
```

```
Query Match 3.6%; Score 35.8; DB 1; Length 41;
Best Local Similarity 94.9%; Pred. No. 3.3e+02;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1045 GGACCTGCACACACACCCCGCTAATTTTGTATTTTCA 1083
DB 40 GGACATGCGACACACCCCGCTAATTTTGTATTTTCA 2
XX
XX RESULT 185
XX AAT97407/C
XX ID AAT97407 standard; DNA; 40 BP.
XX
XX AAT97407;
XX
XX 14-APR-1998 (first entry)
XX
XX Synthetic oligomer D1868 Allele G from WO9722719 Example 2.
XX
XX Detection; target site; nucleic acid; fluorophore; labelled; fluorescent;
XX inherited disease; tissue typing; PCR; ss.
XX
XX Synthetic.
XX
XX WO9722719-A1.
XX
XX 26-JUN-1997.
XX
XX 17-DEC-1996; 96WO-US020379.
XX
XX 18-DEC-1995; 95US-0008743P.
XX
XX (UNITW ) UNIT WASHINGTON.
XX
XX Kwok P, Chen X;
XX
XX WPI; 1997-341707/31.
XX
XX Detecting target site in nucleic acid by forming a fluorophore-labelled
XX oligonucleotide at the site - and detecting fluorescent energy following
XX denaturation, used e.g. to detect inherited diseases, in tissue typing
XX etc.
XX
XX Example 2; Page 27; 68pp; English.
XX
XX A method has been developed for detecting the presence of a target site
XX (TS), of at least one nucleotide (nt) in a nucleic acid (NA). The method
XX comprises: (a) forming an oligonucleotide (ON), consisting of two
XX fluorophores (F1, F2) each covalently linked to separate nt, bound to TS;
XX and (b) detecting fluorescence energy transfer (FET) between F1 and F2
XX when ON is released from TS. The present sequence represents a synthetic
XX polynucleotide used in an example of the present invention. The method is
XX used to diagnose hereditary and other diseases; to determine infectious
XX agents; in tissue typing for histocompatibility; in forensic
XX identification and paternity testing, and in monitoring the genetic make
XX up of plants and animals. Specifically it is used to detect single nt
XX polymorphisms. The method provides inexpensive, simple, accurate and
XX automatable nucleic acid analyses
XX
XX Sequence 40 BP; 11 A; 7 C; 15 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 3.6%; Score 35.2; DB 1; Length 40;
XX Best Local Similarity 92.5%; Pred. No. 3.4e+02;
XX Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 675 TCACGTGCAACCTCTGCTCCCGGGTTCAAGTTATTTCTCT 714
DB 40 TCACGTGCAAGCTCTGCTCCCGGGTTCAAGCAATTTCTCT 1
XX
XX RESULT 186
XX AAV19045/C
XX ID AAV19045 standard; DNA; 40 BP.
XX
XX AAV19045;
XX
XX 28-JUL-1998 (first entry)
```

```

XX Alu PCR primer 2.
DE
XX PCR; primer; amplification; Alu repeat sequence; vector;
KM circular yeast artificial chromosome; YAC; ss.
XX
XX Synthetic.
OS Saccharomyces sp.
XX
XX WO9801573-A1.
XX
XX 15-JAN-1998.
XX
XX 09-JUL-1996; 96WO-US011478.
XX
XX 09-JUL-1996; 96WO-US011478.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Resnick MA, Laktionov VL, Kouprina NY, Perkins EL;
PI WPI; 1998-110234/10.
XX
XX Preparation of yeast artificial chromosomes - by in vivo recombination
PT using vector comprising yeast centromere, marker, yeast telomere and
XX nucleic acid for recombination.
XX
XX Example 1; Page 45; 117pp; English.
XX
XX This is the nucleotide sequence for the PCR primer used in the
CC amplification of the Alu repeat sequence, which is used to demonstrate
CC the processes described in the invention. It involves the creation and
CC use of circular yeast artificial chromosome (YAC) to selectively clone
CC specific nucleic acids from a background of mixed nucleic acids by
CC introducing the vector(s) into E. coli cells. They can be used to rapidly
CC isolate human DNA where only a part of the sequence of DNA is known.
CC Using the methods large fragments of DNA can be easily cloned and
CC analysed
XX
XX Sequence 40 BP; 9 A; 8 C; 19 G; 4 T; 0 U; 0 Other;
SQ
Query Match 3.6%; Score 35.2; DB 1; Length 40;
Best Local Similarity 92.5%; Pred. No. 3.4e+02;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 987 CTGCTCCCGGGCTCAGCGATTCTCTGTCTCAGCTCC 1026
DB 40 CCGCTCCCGGGTCAAGCGATTCTCTGTCTCAGCTCC 1

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PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Resnick MA, Laktionov VL, Kouprina NY, Perkins EL;
XX WPI; 2002-498777/53.
XX
XX Preparing yeast artificial chromosomes, useful e.g. for cloning specific
PT human nucleic acid, comprises recombination in yeast cells between a
PT nucleic acid and a yeast vector.
XX
XX Example 1; Col 27; 50pp; English.
XX
XX The specification describes a method for making a yeast artificial
CC chromosome (YAC) that includes an origin of replication (ori). The method
CC comprises incorporating into yeast cells a population of mammalian
CC nucleic acid; and a vector that comprises a yeast centromere, selection
CC marker, yeast telomere and a sequence that recombines with a region of
CC the nucleic acid, so that in vivo recombination to a YAC occurs. This
CC method, designated transformation-associated recombination, eliminates
CC the need for an in vitro ligation step, and makes possible selective
CC cloning of cDNAs for which only the 3'-sequence is known. The method is
CC used for making a YAC. The method is also used for selective cloning of
CC mammalian, specifically human, nucleic acid from a population.
CC particularly radiation hybrids that contain only a small fragment of a
CC human chromosome. The present sequence represents an Alu PCR primer. It
CC was used for inter-Alu PCR, to produce Alu profiles of YACs produced
XX using the method of the invention
XX
XX Sequence 40 BP; 9 A; 8 C; 19 G; 4 T; 0 U; 0 Other;
SQ
Query Match 3.6%; Score 35.2; DB 1; Length 40;
Best Local Similarity 92.5%; Pred. No. 3.4e+02;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 987 CTGCTCCCGGGCTCAGCGATTCTCTGTCTCAGCTCC 1026
DB 40 CCGCTCCCGGGTCAAGCGATTCTCTGTCTCAGCTCC 1

```

Db 41 TTCTCCTGCTCAACCTCCCGAGTAGCTGGACTACAGGC 2

XX

```
XX CN1345751-A.
PN
XX
XX 24-APR-2002.
PD
XX
XX 26-SEP-2000; 2000CN-00125456.
PF
XX 26-SEP-2000; 2000CN-00125456.
PR
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
PA
XX Mao Y, Xie Y;
PI
XX WPI; 2002-675773/73.
DR
XX Novel polypeptide-human G protein subunit 9.01.
PT
XX Example 6; Page 22(Disclosure); 34pp; Chinese.
PS
XX The present invention provides the protein and coding sequences of human
CC G protein subunit 9.02. The sequences can be used in the treatment of
CC cancers, coughs, cardiac asthma, diarrhoea, constipation, colic, psychic
CC disease and morphine analgesic acute poisoning. The present sequence is
CC a probe used to isolate the coding sequence of the invention
XX
SQ Sequence 41 BP; 7 A; 9 C; 16 G; 9 T; 0 U; 0 Other;

Query Match          3.6%; Score 35.2; DB 1; Length 41;
Best Local Similarity 92.5%; Pred. No. 3.5e+02;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 369 TCCACCTGCTCAGCTCCCAAGTGTGGATTACAGGC 408
DB 41 TCCACCCACCTCGGCTCCCAAGTGTGGATTACAGGC 2

RESULT 192
ABQ77547
ID ABQ77547 standard; DNA; 41 BP.
XX
XX ABQ77547;
AC
XX 01-OCT-2002 (first entry)
DT
XX Human red blood cell cytoplasmic protein 15.29 probe, SEQ ID:8.
DE
XX Human; red blood cell cytoplasmic protein 15.29; erythrocyte;
KM recombinant production; gene therapy; cerebral anoxia;
KM respiratory adynamia; arrhythmia; intestinal palsy; anaemia; haemostatic;
KM cardiac; probe; ss.
XX
XX Homo sapiens.
OS
XX CN139497-A.
PN
XX 13-MAR-2002.
PD
XX 23-AUG-2000; 2000CN-00119732.
PF
XX 23-AUG-2000; 2000CN-00119732.
PR
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
PA
XX Mao Y, Xie Y;
PI
XX WPI; 2002-472206/51.
DR
XX New polypeptide-human red blood cell cytoplasmic protein 15.29 for
PT treating anaerobic cerebral disease, respiratory adynamia, arrhythmia,
PT intestinal palsy, and anemia.
XX
XX Example 6; Page 19 (Disclosure); 32pp; Chinese.
```

```
CC The invention relates to human red blood cell cytoplasmic protein 15.29
CC (AAM49384) and nucleic acids encoding it (ABQ77542). The protein has a
CC molecular weight of 15 kD. The invention also relates to a method for the
CC recombinant production of the protein, an antagonist of the protein, and
CC the use of the protein, gene and antagonist in therapeutic applications
CC Red blood cell cytoplasmic protein 15.29 can be used in the treatment of
CC a variety of diseases such as cerebral anoxia, respiratory adynamia,
CC arrhythmia, intestinal palsy and anaemia. The present sequence represents
CC a human red blood cell cytoplasmic protein 15.29 probe used in an
CC exemplification of the invention
XX
SQ Sequence 41 BP; 8 A; 9 C; 11 G; 13 T; 0 U; 0 Other;

Query Match          3.6%; Score 35.2; DB 1; Length 41;
Best Local Similarity 92.5%; Pred. No. 3.5e+02;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1092 GGGGTTTCCCAATTTTGTCAAGCTGCTTCACAACTCCTG 1131
DB 2 GAGGTTTCCACCATATGTGTGTCAGCTGCTGCTCAACTGCTG 41

RESULT 193
ABV77328
ID ABV77328 standard; DNA; 41 BP.
XX
XX ABV77328;
AC
XX 07-FEB-2003 (first entry)
DT
XX Human protein 10.01 related probe 1.
DE
XX Human; 10.01; aminolase active site; arrhythmia; diabetes; probe; ss.
XX
XX Homo sapiens.
OS
XX CN1342770-A.
PN
XX 03-APR-2002.
PD
XX 12-SEP-2000; 2000CN-00125186.
PF
XX 12-SEP-2000; 2000CN-00125186.
PR
XX 12-SEP-2000; 2000CN-00125186.
XX
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
PA
XX Mao Y, Xie Y;
PI
XX WPI; 2002-529811/57.
DR
XX New human protein 10.01 containing Phe-His aminolase active site and
PT encoding polynucleotide, useful for treating arrhythmia and diabetes.
XX
XX Example 7; Page 21 (disclosure); 33pp; Chinese.
PS
XX The invention relates to a human protein designated 10.01, containing the
CC Phe-His aminolase active site. Also disclosed are the encoding
CC polynucleotide, and a method for preparing the polypeptide by DNA
CC recombination. The application of the polypeptide is in treating
CC arrhythmia and diabetes. Also disclosed are the antagonist against this
CC polypeptide and its therapeutic action, and the application of the
CC polynucleotide. The current sequence represents a human protein 10.01
CC related probe sequence
XX
SQ Sequence 41 BP; 6 A; 16 C; 9 G; 10 T; 0 U; 0 Other;

Query Match          3.6%; Score 35.2; DB 1; Length 41;
Best Local Similarity 92.5%; Pred. No. 3.5e+02;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 655 TGCAGTGGCCGCAATCTTGCTCACTGCACACTCTGCTCC 694
DB 1 TGCAGTGGCCGCAATCTTGCTCACTGCACACCCCGCCTCC 40
```

RESULT 194
ACC00156
ID ACC00156 standard; DNA; 41 BP.
XX
XX
AC ACC00156;
XX
XX
DT 14-JUL-2003 (first entry)
XX
XX
DE Probe #1 for guanosine triphosphate activator 10.01.
XX
XX
KM Guanosine triphosphatase activator 10.01; squamabaal cell;
XX
KM carcinoma of skin; osteosarcoma; leukemia; teratoma; probe; ss.
XX
OS Unidentified.
XX
XX
PN CN1380320-A.
XX
XX
PD 20-NOV-2002.
XX
XX
PF 10-APR-2001; 2001CN-00105912.
XX
XX
PR 10-APR-2001; 2001CN-00105912.
XX
XX
PA (SHAN-) SHANGHAI BIOWINDOM GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2003-222552/22.
XX
PT A polypeptide-guanosine triphosphatase activator protein -10.01 and
XX
XX polynucleotide for coding this polypeptide.
XX
PS Example 7; Page 23; 33pp; Chinese.
XX
XX
CC The present invention discloses a polypeptide-guanosine triphosphatase
XX
XX activator protein-10.01. The invention also discloses the method for
XX
XX curing several diseases, such as squamabaal cell carcinoma of skin,
XX
XX osteosarcoma, leukemia and teratoma by using said polypeptide. The
XX
XX present sequence represents a probe for guanosine triphosphatase activator
XX
XX protein 10.01
XX
SQ Sequence 41 BP; 6 A; 16 C; 10 G; 9 T; 0 U; 0 Other;
XX
XX
Query Match 3.6%; Score 35.2; DB 1; Length 41;
Best Local Similarity 92.5%; Pred. No. 3.5e+02;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 655 TGCAGTGGCGCATCTTGCTCACTGCAACCTCTGCCTCC 694
DB 1 TGCAGTGGCGCATCTTGCTCACTGCAACCTCTGCCTCC 40
XX
XX
RESULT 195
AAQ27391
ID AAQ27391 standard; DNA; 35 BP.
XX
XX
AC AAQ27391;
XX
XX
DT 25-MAR-2003 (revised)
XX
XX
DT 27-JAN-1993 (first entry)
XX
XX
DE Inter-Alu specific primer PDJ33.
XX
XX
KM Polymerase chain reaction; PCR; repetitive element; ss.
XX
XX
OS Synthetic.
XX
XX
PN WO9213101-A1.
XX
XX
PD 06-AUG-1992.
XX
XX

PF 24-JAN-1992; 92MO-NL000018.
XX
XX
PR 25-JAN-1991; 91NL-00000132.
XX
XX
XX
PA (INGE-) INGENY BV.
XX
XX
PI Uitterlinden AG, Vrijg J;
XX
XX
DR WPI; 1992-284683/34.
XX
XX
PT Detection of genetic variation by 2-D electrophoresis of fragments - and
XX
XX hybridisation with labelled probes, carried out on fragments consisting
XX
XX of inter-repeat sequences generated by PCR.
XX
XX
PS Claim 6; Page 6; 31pp; English.
XX
XX
CC Primer PDJ33 is one of several primers which are preferred for use in
XX
XX amplifying inter-Alu regions of DNA. The amplified fragments are then
XX
XX subjected to 2-D electrophoresis on the basis of length and differences
XX
XX in base sequence. The resulting separation pattern is transferred to a
XX
XX filter for screening with a probe. The method can be used to detect
XX
XX genetic variation. See AAQ27389-Q27404 and AAQ31141-Q31144. (Updated on
XX
XX 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 35 BP; 8 A; 10 C; 11 G; 6 T; 0 U; 0 Other;
XX
XX
Query Match 3.5%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 852 GCCTCCCAAGTCTGGATTACAGCCGTGAGCCA 886
DB 1 GCCTCCCAAGTCTGGATTACAGCCGTGAGCCA 35
XX
XX
RESULT 196
ABQ83633
ID ABQ83633 standard; DNA; 41 BP.
XX
XX
AC ABQ83633;
XX
XX
DT 26-JAN-2003 (first entry)
XX
XX
DE Human mPer3-10.01 probe 1 SEQ ID NO:8.
XX
XX
XX Human; mPer3-10.01; vegetative nervous dysfunction; psychic disease;
XX
XX endocrinopathy; growth development disturbance disease; tumour; probe;
XX
XX ss.
XX
OS Homo sapiens.
XX
XX
PN CN1345805-A.
XX
XX
PD 24-APR-2002.
XX
XX
PF 26-SEP-2000; 2000CN-00125425.
XX
XX
PR 26-SEP-2000; 2000CN-00125425.
XX
XX
PA (SHAN-) SHANGHAI BIOWINDOM GENE DEV INC.
XX
XX
PI Mao Y, Xie Y;
XX
XX
DR WPI; 2002-539321/58.
XX
XX
PT Novel polypeptide-human mPer 3-10.01 and polynucleotide for encoding the
XX
XX polypeptide.
XX
XX
PS Example 6; Page 20 (Disclosure); 33pp; Chinese.
XX
XX
CC The present invention describes human mPer3-10.01 (1). Also described is
XX
XX a method for producing (1) using DNA recombination technology. (1) can be
XX
XX used in the treatment of several diseases, such as vegetative nervous

CC dysfunction, psychic disease, endocrinopathy, growth development
CC disturbance disease and tumours. The present sequence represents a probe
CC for (I), which is used in an example from the present invention
XX
SO Sequence 41 BP; 5 A; 10 C; 14 G; 12 T; 0 U; 0 Other;

Query Match 3.5%; Score 34.6; DB 1; Length 41;
Best Local Similarity 90.2%; Pred. No. 3.7e+02;
Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 187 TGGAGTTTCTCCATGTGCTGAGCTGCTGCTGCAACTCCG 227
DB 1 TGGGGTTTCACCATGTGGGCGAGCTGCTGCTGCAACTCCTG 41

RESULT 197

ABQ83634
ID ABQ83634 standard; DNA; 41 BP.

XX AC ABQ83634;

XX DT 26-JAN-2003 (first entry)

XX DE Human mPer3-10.01 probe 2 SEQ ID NO:9.

XX KW Human; mPer3-10.01; vegetative nervous dysfunction; psychic disease;
XX endocrinopathy; growth development disturbance disease; tumour; probe;
XX ss.

XX OS Homo sapiens.

XX PN CN1345805-A.

XX PD 24-APR-2002.

XX PF 26-SEP-2000; 2000CN-00125425.

XX PR 26-SEP-2000; 2000CN-00125425.

XX PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX PI Mao Y, Xie Y;

XX DR WPI; 2002-539321/58.

XX PT Novel polypeptide-human mPer 3-10.01 and polynucleotide for encoding the
XX PT polypeptide.

XX PS Example 6; Page 20 (Disclosure); 33pp; Chinese.

XX CC The present invention describes human mPer3-10.01 (I). Also described is
XX CC a method for producing (I) using DNA recombination technology. (I) can be
XX CC used in the treatment of several diseases, such as vegetative nervous
XX CC dysfunction, psychic disease, endocrinopathy, growth development
XX CC disturbance disease and tumours. The present sequence represents a probe
XX CC for (I), which is used in an example from the present invention

XX SQ Sequence 41 BP; 5 A; 10 C; 14 G; 12 T; 0 U; 0 Other;

Query Match 3.5%; Score 34.6; DB 1; Length 41;
Best Local Similarity 90.2%; Pred. No. 3.7e+02;
Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 187 TGGAGTTTCTCCATGTGCTGAGCTGCTGCTGCAACTCCG 227
DB 1 TGGGGTTTCACCATGTGGGCGAGCTGCTGCTGCAACTCCTG 41

RESULT 198

ABL52955/C
ID ABL52955 standard; DNA; 41 BP.

XX AC ABL52955;

XX XX 24-MAY-2002 (first entry)

XX DE Serine proteinase 10 probe #1.

XX KW Serine proteinase 10; enzyme; cancer; HIV infection; anti-HIV;

XX KW cytosolic; probe; ss.

XX OS Unidentified.

XX PN CN1325996-A.

XX PD 12-DEC-2001.

XX PF 31-MAY-2000; 2000CN-00116278.

XX PR 31-MAY-2000; 2000CN-00116278.

XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX PI Mao Y, Xie Y;

XX DR WPI; 2002-196715/26.

XX PT Polypeptide-serine proteinase 10 and polynucleotide encoding it.

XX PS Example 6; Page 19 (Disclosure); 32pp; Chinese.

XX CC The present invention relates to serine proteinase 10 (AAM48453). Serine
XX CC proteinase 10 and its coding sequence can be used for treating diseases
XX CC such as cancer and HIV infection. The present sequence is a probe, which
XX CC was used in an example from the invention

XX SQ Sequence 41 BP; 9 A; 14 C; 13 G; 5 T; 0 U; 0 Other;

Query Match 3.5%; Score 34.6; DB 1; Length 41;
Best Local Similarity 90.2%; Pred. No. 3.7e+02;
Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 637 CTGTACCCAGAGCTGAGTGCAGTGGCGCATCTTGCTCA 677
DB 41 CTGTGCCCGAGCTGAGTGCAGTGTGCCATCTCGCTCA 1

RESULT 199

ABZ49715
ID ABZ49715 standard; DNA; 41 BP.

XX AC ABZ49715;

XX DT 26-JUN-2003 (first entry)

XX DE Human sulphotransferase TPST2 gene polymorphic site, #6497.

XX KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;

XX KW polymorphic site; drug evaluation; drug screening; genotyping;

XX KW genetic profiling; therapeutic customisation; adverse reaction;

XX KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.

XX OS Homo sapiens.

XX PN WO200252044-A2.

XX PD 04-JUL-2002.

XX PF 27-DEC-2001; 2001WO-JP011592.

XX PR 27-DEC-2000; 2000JP-00399443.

XX AC ABL52955;

QY 831 CCTGTGATCTGCTCGGCTCCCAAGTCTGGAT 871
DB 1 CCTGTGATTTGCCACCTCGGCTCCCAAGTCTGGAT 41

RESULT 201
ABZ49550
ID ABZ49550 standard; DNA; 41 BP.
AC ABZ49550;
XX 26-JUN-2003 (first entry)
XX Human glucathione-S-transferase MGST2 gene polymorphic site, #6333.
XX
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 4;
XX polymorphic site; drug evaluation; drug screening; genotyping;
XX genetic profiling; therapeutic customisation; adverse reaction;
XX clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX variation replace(21,A)
XX /*tag= a
XX /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX MO200252044-A2.
XX
XX 04-JUN-2002.
XX
XX 27-DEC-2001; 2001WO-JP011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
XX PR 02-MAY-2001; 2001JP-00135256.
XX PR 27-AUG-2001; 2001JP-00256862.
XX
XX (RIKEN) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Saito S;
XX
XX WPI: 2002-583571/62.
XX
XX Identifying individuals having a polymorphism, useful for determining the
XX effectiveness or side effect of a drug or treatment protocol, comprises
XX detecting at least one polymorphism in the drug metabolizing enzyme
XX nucleic acid.
XX
XX
XX Claim 23; Page 192; 2785pp; English.
XX
XX Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes
XX encoding enzymes associated with drug metabolism. The invention relates
XX to methods and compositions for identifying individuals who have at least
XX one polymorphism in such drug metabolising enzyme-encoding genes. The
XX polymorphisms may be identified in a nucleic acid sample using probes or
XX primers specific for a sequence selected from ABZ43217-ABZ50887 using a
XX variety of detection assays, including hybridisation assays, nucleic acid
XX arrays and PCR-based methods. The invention also encompasses methods of
XX evaluating and screening drugs using genetic polymorphism data. Genetic
XX polymorphism data, particularly that relating to single nucleotide
XX polymorphisms (SNPs), may be used in studying the relationship between
XX DNA sequence variations and human diseases, conditions, and responses to
XX drug therapies based upon the genetic profile of individual patients.
XX This would not only take the guesswork out of selecting the drug with the
XX greatest therapeutic effect for a particular patient, but would also
XX reduce the likelihood of adverse reactions, thereby increasing safety.
XX Methods of the invention are also useful in the drug discovery and

CC approval processes. For example, individuals could be selected for
CC clinical trials only if their genetic profiles indicate that they are
CC capable of responding to a particular drug or drug class, and previously
CC failed drug candidates could be revived if they were matched with more
CC appropriate patient populations. The methods, data and compositions of
CC the invention may therefore lead to an increase in the range of
CC possible drug targets and decreases in the number of adverse drug
CC reactions, failed drug trials, the time taken for a drug to be approved,
CC the length of time patients are on medication and the number of different
CC medications a patient needs to take before finding an effective therapy
XX
XX SQ Sequence 41 BP; 6 A; 15 C; 10 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 3.5%; Score 34.6; DB 1; Length 41;
XX Best Local Similarity 90.2%; Pred. No. 3.7e+02;
XX Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX

QY 831 CCTGTGATCTGCTCGGCTCCCAAGTCTGGAT 871
DB 1 CCTGTGATTTGCCACCTCGGCTCCCAAGTCTGGAT 41

RESULT 202
ABZ49230
ID ABZ49230 standard; DNA; 41 BP.
XX
XX AC ABZ49230;
XX
XX 26-JUN-2003 (first entry)
XX
XX Human aldehyde dehydrogenase ALDH6A1 gene polymorphic site, #6013.
XX
XX Human; drug metabolising enzyme; gene; drug metabolism; polymorphic site;
XX drug evaluation; drug screening; genotyping; genetic profiling;
XX therapeutic customisation; adverse reaction; clinical trial;
XX drug approval; single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX variation replace(21,A)
XX /*tag= a
XX /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX MO200252044-A2.
XX
XX 04-JUN-2002.
XX
XX 27-DEC-2001; 2001WO-JP011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
XX PR 02-MAY-2001; 2001JP-00135256.
XX PR 27-AUG-2001; 2001JP-00256862.
XX
XX (RIKEN) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Saito S;
XX
XX WPI: 2002-583571/62.
XX
XX Identifying individuals having a polymorphism, useful for determining the
XX effectiveness or side effect of a drug or treatment protocol, comprises
XX detecting at least one polymorphism in the drug metabolizing enzyme
XX nucleic acid.
XX
XX
XX Claim 23; Page 184; 2785pp; English.
XX
XX Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes
XX encoding enzymes associated with drug metabolism. The invention relates
XX to methods and compositions for identifying individuals who have at least
XX one polymorphism in such drug metabolising enzyme-encoding genes. The
XX polymorphisms may be identified in a nucleic acid sample using probes or
XX primers specific for a sequence selected from ABZ43217-ABZ50887 using a

CC variety of detection assays, including hybridisation assays, nucleic acid
CC arrays and PCR-based methods. The invention also encompasses methods of
CC evaluating and screening drugs using genetic polymorphism data. Genetic
CC polymorphism data, particularly that relating to single nucleotide
CC polymorphisms (SNPs), may be used in studying the relationship between
CC DNA sequence variations and human diseases, conditions, and responses to
CC drugs. SNPs are also useful as polymorphism markers for discovering genes
CC that cause or exacerbate certain diseases. SNPs are particularly useful
CC in the above respects as they are stable in populations, occur
CC frequently, and have lower mutation rates than other genome variations
CC such as repeating sequences. The detection and analysis of polymorphisms
CC in genes encoding drug metabolising enzymes allows the customisation of
CC drug therapies based upon the genetic profile of individual patients.
CC This would not only take the guesswork out of selecting the drug with the
CC greatest therapeutic effect for a particular patient, but would also
CC reduce the likelihood of adverse reactions, thereby increasing safety.
CC Methods of the invention are also useful in the drug discovery and
CC approval processes. For example, individuals could be selected for
CC clinical trials only if their genetic profiles indicate that they are
CC capable of responding to a particular drug or drug class, and previously
CC failed drug candidates could be revived if they were matched with more
CC appropriate patient populations. The methods, data and compositions of
CC the invention may therefore lead to an increase in the range of
CC possible drug targets and decreases in the number of adverse drug
CC reactions, failed drug trials, the time taken for a drug to be approved,
CC the length of time patients are on medication and the number of different
CC medications a patient needs to take before finding an effective therapy

Sequence 41 BP; 6 A; 16 C; 9 G; 10 T; 0 U; 0 Other;

Query Match 3.5%; Score 34.6; DB 1; Length 41;

Best Local Similarity 90.2%; Pred. No. 3.7e+02; Mismatches 4; Indels 0; Gaps 0;

Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 992 TCCCGGGCTCAAGCGATTCTCTGTCTCAGCTCCCAAGA 1032
DB 1 TCCCGGGCTCAAGCGATTCTCTGTCTCAGCTCCCAAGA 41

RESULT 203

ABZ49236
ID ABZ49236 standard; DNA; 41 BP.

XX AC ABZ49236;

XX DT 26-JUN-2003 (first entry)

DE Human aldehyde dehydrogenase ALDH6A1 gene polymorphic site, #6019.

XX Human; drug metabolising enzyme; gene; drug metabolism; polymorphic site;
KM drug evaluation; drug screening; genotyping; genetic profiling;
KW therapeutic customisation; adverse reaction; clinical trial;
XX drug approval; single nucleotide polymorphism; SNP; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
FT variation replace(21,C)
FT /tag= a
FT /standard_name= "Single nucleotide polymorphism (SNP) "

PN WO200252044-A2.

PD 04-JUL-2002.

XX 27-DEC-2001; 2001WO-JP011592.

XX 27-DEC-2000; 2000JP-00399443.

PR 02-MAY-2001; 2001JP-00135256.

XX 27-AUG-2001; 2001JP-00256862.

XX (RIKE) RIKEN KK.

PI Nakamura Y, Sekine A, Iida A, Saito S;
XX WPI; 2002-583571/62.
XX
PT Identifying individuals having a polymorphism, useful for determining the
PT effectiveness or side effect of a drug or treatment protocol, comprises
PT detecting at least one polymorphism in the drug metabolizing enzyme
PT nucleic acid.

PS Claim 23; Page 184; 27855P; English.

XX Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes
CC encoding enzymes associated with drug metabolism. The invention relates
CC to methods and compositions for identifying individuals who have at least
CC one polymorphism in such drug metabolising enzyme-encoding genes. The
CC polymorphisms may be identified in a nucleic acid sample using probes or
CC primers specific for a sequence selected from ABZ43217-ABZ50887 using a
CC variety of detection assays, including hybridisation assays, nucleic acid
CC arrays and PCR-based methods. The invention also encompasses methods of
CC evaluating and screening drugs using genetic polymorphism data. Genetic
CC polymorphism data, particularly that relating to single nucleotide
CC DNA sequence variations and human diseases, conditions, and responses to
CC drugs. SNPs are also useful as polymorphism markers for discovering genes
CC that cause or exacerbate certain diseases. SNPs are particularly useful
CC in the above respects as they are stable in populations, occur
CC frequently, and have lower mutation rates than other genome variations
CC such as repeating sequences. The detection and analysis of polymorphisms
CC in genes encoding drug metabolising enzymes allows the customisation of
CC drug therapies based upon the genetic profile of individual patients.
CC This would not only take the guesswork out of selecting the drug with the
CC greatest therapeutic effect for a particular patient, but would also
CC reduce the likelihood of adverse reactions, thereby increasing safety.
CC Methods of the invention are also useful in the drug discovery and
CC approval processes. For example, individuals could be selected for
CC clinical trials only if their genetic profiles indicate that they are
CC capable of responding to a particular drug or drug class, and previously
CC failed drug candidates could be revived if they were matched with more
CC appropriate patient populations. The methods, data and compositions of
CC the invention may therefore lead to an increase in the range of
CC possible drug targets and decreases in the number of adverse drug
CC reactions, failed drug trials, the time taken for a drug to be approved,
CC the length of time patients are on medication and the number of different
CC medications a patient needs to take before finding an effective therapy

Sequence 41 BP; 6 A; 10 C; 13 G; 12 T; 0 U; 0 Other;

Query Match 3.5%; Score 34.6; DB 1; Length 41;

Best Local Similarity 90.2%; Pred. No. 3.7e+02; Mismatches 4; Indels 0; Gaps 0;

Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 198 CATGTTGTCAGGCTGTCTCGAAGTCCGACCTCAGATGA 238
DB 1 CGTGTGTCAGGCTGTCTCGAAGTCCGACCTCAGATGA 41

RESULT 204

ABZ43562
ID ABZ43562 standard; DNA; 41 BP.

XX AC ABZ43562;

XX DT 26-JUN-2003 (first entry)

DE Human sulphotransferase TPST2 gene polymorphic site, #346.

XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;
KM polymorphic site; drug evaluation; drug screening; genotyping;
KW genetic profiling; therapeutic customisation; adverse reaction;
XX clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.

XX Homo sapiens.

```

FH Key Location/Qualifiers
FT variation replace(21,A)
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX WO200252044-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-JP011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
XX
XX 02-MAY-2001; 2001JP-00135256.
XX
XX 27-AUG-2001; 2001JP-00256862.
XX
XX (RIKEN ) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Satoh S;
XX
XX WPI, 2002-583571/62.
XX
XX Identifying individuals having a polymorphism, useful for determining the
XX effectiveness or side effect of a drug or treatment protocol, comprises
XX detecting at least one polymorphism in the drug metabolizing enzyme
XX nucleic acid.
XX
XX Claim 23; Page 69; 2785pp; English.
XX
XX Sequences AB243217-AB250887 represent polymorphic sites within genes
XX encoding enzymes associated with drug metabolism. The invention relates
XX to methods and compositions for identifying individuals who have at least
XX one polymorphism in such drug metabolizing enzyme-encoding genes. The
XX polymorphisms may be identified in a nucleic acid sample using probes or
XX primers specific for a sequence selected from AB243217-AB250887 using a
XX variety of detection assays, including hybridisation assays, nucleic acid
XX arrays and PCR-based methods. The invention also encompasses methods of
XX evaluating and screening drugs using genetic polymorphism data. Genetic
XX polymorphisms (SNPs), particularly that relating to single nucleotide
XX DNA sequence variations and human diseases, conditions, and responses to
XX drugs. SNPs are also useful as polymorphism markers for discovering genes
XX that cause or exacerbate certain diseases. SNPs are particularly useful
XX in the above respects as they are stable in populations, occur
XX frequently, and have lower mutation rates than other genome variations
XX such as repeating sequences. The detection and analysis of polymorphisms
XX in genes encoding drug metabolising enzymes allows the customisation of
XX drug therapies based upon the genetic profile of individual patients.
XX This would not only take the guesswork out of selecting the drug with the
XX greatest therapeutic effect for a particular patient, but would also
XX reduce the likelihood of adverse reactions, thereby increasing safety.
XX Methods of the invention are also useful in the drug discovery and
XX approval processes. For example, individuals could be selected for
XX clinical trials only if their genetic profiles indicate that they are
XX capable of responding to a particular drug or drug class, and previously
XX failed drug candidates could be revived if they were matched with more
XX appropriate patient populations. The methods, data and compositions of
XX the invention may therefore lead to an increase in the range of
XX possible drug targets and decreases in the number of adverse drug
XX reactions, failed drug trials, the time taken for a drug to be approved,
XX the length of time patients are on medication and the number of different
XX medications a patient needs to take before finding an effective therapy
XX
XX Sequence 41 BP; 6 A; 17 C; 9 G; 9 T; 0 U; 0 Other:
XX
XX Query Match 3.5%; Score 34.6; DB 1; Length 41;
XX Best Local Similarity 90.2%; Pied. No. 3.7e+02;
XX Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 969 CTCGGCTACATGCAACCTCTGCTCCCGGGGCTCAGGCAATT 1009
XX 1 CTCGGCTACATGCAACCTCTGCTCCCGGGGCTCAGGCAATT 41

```

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RESULT 205
ADP75520/C
ID ADP75520 standard; DNA; 41 BP.
XX
XX ADP75520;
XX
XX 12-AUG-2004 (first entry)
XX
XX Human ADAM19 gene, sequence surrounding SNP 16.
XX
XX DE
XX
XX Human; ds; ADAM19; Endophilin 1; Endophilin 2; NRG2; ADAMTS2;
XX a disintegrin and metalloprotease; neuroregulin 2; SNP;
XX single nucleotide polymorphism;
XX a disintegrin and metalloprotease with thrombospondin type1 motif 2;
XX asthma; atopy; obesity; inflammatory bowel disease; respiratory disorder.
XX
XX OS
XX Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT variation replace(21,G)
XX FT /*tag= a
XX FT /standard_name= "Single nucleotide polymorphism"
XX
XX WO2003031594-A2.
XX
XX 17-APR-2003.
XX
XX 11-OCT-2002; 2002WO-US032700.
XX
XX 11-OCT-2001; 2001US-0328424P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Keith T, Little RD, Van Berdewegh P, Dupuis J, Del Mastro RG;
XX Allen K;
XX WPI, 2003-381712/36.
XX
XX New isolated nucleic acid or alternate splice variant, useful for
XX diagnosing and treating a disintegrin and metalloprotease (ADAM) or
XX interactor gene-associated disorder, e.g. asthma, atopy, obesity or
XX inflammatory bowel disease.
XX
XX Claim 2; Page 135; 338pp; English.
XX
XX The invention relates to an isolated nucleic acid or alternate splice
XX variant comprising a nucleotide sequence containing at least one of the
XX single nucleotide polymorphisms given in the specification, a nucleotide
XX sequence having at least 15 contiguous nucleotides of them, or
XX complements of them. The genes are ADAM19 (a disintegrin and
XX metalloprotease 19, also known as gene 845), NRG2 (neuroregulin 2, also
XX known as gene 847), endophilin 1 (also known as gene 874), endophilin 2
XX (also known as gene 803) and ADAMTS2 (a disintegrin and metalloprotease
XX with thrombospondin type1 motif 2, also known as gene 962). Also included
XX are a vector comprising the isolated nucleic acid (or alternate splice
XX variant), a host cell containing the vector, an isolated polypeptide
XX encoded by the novel nucleic acid (or alternate splice variant), an
XX antibody or antibody fragment that binds to the polypeptide,
XX pharmaceutical compositions (comprising the nucleic acid or alternate
XX splice variant, vector, polypeptide or antibody, and a carrier,
XX excipient or diluent), a kit for detecting a disintegrin and
XX metalloprotease (ADAM) gene nucleotide sequence (comprising the isolated
XX nucleic acid or alternate splice variant, antibody or antibody fragment,
XX and at least one component to detect the hybridisation of the variant or
XX the binding of the antibody to an ADAM gene amino acid sequence), a kit
XX for detecting an interactor gene amino acid sequence (comprising the
XX antibody or antibody fragment, and at least one component to detect the
XX binding of the antibody to the interactor gene amino acid sequence),
XX diagnosing an ADAM or interactor gene-associated disorder or a
XX respiratory disorder in a human subject, determining an ADAM or
XX interactor gene pharmacogenetic profile in a human subject, identifying
XX an orthologue of a human ADAM or interactor gene, treating an ADAM or
XX interactor gene-associated disorder (or a respiratory disorder) by

```

CC administering the pharmaceutical composition, a transgenic mouse (whose
CC genome comprises an introduced null mutation in an endogenous gene that
CC is orthologous to a human ADAM gene), making a homozygous transgenic
CC knockout mouse, forming a crystal of the isolated polypeptide, a cell
CC line comprising the isolated nucleic acid or alternate splice variant, a
CC biochip comprising the isolated nucleic acid or alternate splice variant,
CC an isolated nucleic acid probe or primer comprising at least 8 contiguous
CC nucleotides of the nucleic acid, an isolated antisense nucleic acid,
CC identifying an ADAM or interactor gene ligand and an isolated nucleic
CC acid variant of Gene 803, 845, 847, 874 or 962. The nucleic acid or
CC alternate splice variants, methods, kits and antibody/antibody fragment
CC are useful for diagnosing and treating an ADAM or interactor gene-
CC associated disorder, e.g. asthma, atopy, obesity or inflammatory bowel
CC disease. The present sequence is a SNP (single nucleotide polymorphism)
CC containing region from one of the above mentioned genes.

SQ Sequence 41 BP; 7 A; 12 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 3.5%; Score 34.6; DB 1; Length 41;

Best Local Similarity 90.2%; Pred. No. 3.7e+02; Mismatches 4; Indels 0; Gaps 0;

Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 844 CTGCTCGGCTTCCCAAGTCTGGATTACAGGCGCTGAGC 884
DB 41 CCGCTTGGCCACCCCAAGTCTGGATTACAGGCGCTGAGC 1

RESULT 206

ADL64137/C
ID ADL64137 standard; DNA; 41 BP.

AC ADL64137;

DT 20-MAY-2004 (first entry)

DE Human single nucleotide polymorphism (SNP) #60.

XX ss; human; single nucleotide polymorphism; SNP;
KW C1 S subcomponent protein; C1S; alanyl aminopeptidase protein; ANPEP;
KW tissue kallikrein protein; KLK1; aminopeptidase P protein; MEPIB;
KW soluble guanylate cyclase 1 alpha-2 subunit protein; GUCY1A2; haplotype;
KW angioedema; angioedema-like disorder; paternity testing;
KW cardiovascular diseases; angina pectoris; hypertension; heart failure;
KW myocardial infarction; aneurysm; stroke; embolism; thrombosis;
KW coronary artery disease; arteriosclerosis; hypersensitivity;
KW haemodialysis; sepsis; inflammatory disease; inflammatory arthritis;
KW asthma; chronic obstructive pulmonary disease; cough reflex; allergy;
KW cancer; ANPEP.

OS Homo sapiens.

PN US2004033582-A1.

PD 19-FEB-2004.

PF 03-JUN-2003; 2003US-00453827.

PR 03-JUN-2002; 2002US-0384980P.

XX (EDMO/) EDMONDS M.

PA (HUI/) HUI L.

PA (PERR/) PERRONE M.

PA (POWE/) POWELL J R.

PA (RAMA/) RAMANATHAN C S.

PA (SWAN/) SWANSON B.

PA (TSUC/) TSUCHIHASHI Z.

PA (ZERB/) ZERBA K.

PI Edmunds M, Hui L, Perrone M, Powell JR, Ramanathan CS, Swanson B;

PI Tsuchihashi Z, Zerba K;

XX WPI; 2004-180052/17.

XX New nucleic acid comprising a single nucleotide polymorphism at a
PT specific location, useful in paternity testing, genetic analysis or
PT diagnosing, preventing or treating cardiovascular diseases e.g.
PT angioedema or angina pectoris.

PS Claim 3; SEQ ID NO 60; 376pp; English.

XX The invention relates to an isolated nucleic acid (I) derived from a
XX human gene encoding a protein, such as the C1 S subcomponent protein
XX (C1S) the alanyl aminopeptidase protein (ANPEP), the meprin A, beta
XX protein (MEPIB), the aminopeptidase P-like protein (XPN-PEP), the tissue
XX kallikrein protein (KLK1), the membrane bound aminopeptidase P protein
XX (XPNPEP2), or the soluble guanylate cyclase 1, alpha-2 subunit protein
XX (GUCY1A2). The nucleic acid comprises at least one polymorphic position,
XX including the alleles, reference alleles and alternate alleles of the
XX single nucleotide polymorphisms, listed in the specification. The
XX polymorphic position resides in a (non) coding position within the genomic
XX sequence of the gene. The polymorphic position residing in a coding
XX position results in a missense or silent mutation of the translated
XX product of the gene. The polymorphic position residing in a non-coding
XX position resides within the untranslated region or an intronic region of
XX the gene. Constructing haplotypes using the nucleic acids above further
XX comprises using the haplotypes to identify an individual for the presence
XX of a disease phenotype, and correlating the presence of the disease
XX phenotype with the haplotype. The disease phenotype is angioedema or an
XX angioedema-like disorder. The nucleic acids, primers and probes are
XX useful in phenotype correlations, paternity testing, medicine and genetic
XX analysis. The nucleic acids and polypeptides can be used in diagnosing,
XX preventing or treating cardiovascular diseases, e.g. angioedema, angina
XX pectoris, hypertension, heart failure, myocardial infarction, aneurysm,
XX stroke, embolism, thrombosis, coronary artery disease or
XX arteriosclerosis, hypersensitivity reactions during haemodialysis,
XX sepsis, inflammatory diseases, inflammatory arthritis, asthma, chronic
XX obstructive pulmonary disease, cough reflex, allergies, or cancer. The
XX present sequence represents a human single nucleotide polymorphism (SNP)
XX of the invention.

SQ Sequence 41 BP; 8 A; 13 C; 12 G; 8 T; 0 U; 0 Other;

Query Match 3.5%; Score 34.6; DB 1; Length 41;

Best Local Similarity 90.2%; Pred. No. 3.7e+02; Mismatches 4; Indels 0; Gaps 0;

Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 643 CCCAGGCTGAGTGCAGTGCAGTGCCTCAATCTTGGCTCACTGCA 683
DB 41 CCCAGGCTGAGTGCAGTGCAGTGCCTCAATCTTGGCTCACTGCA 1

RESULT 207

ADL64139
ID ADL64139 standard; DNA; 41 BP.

AC ADL64139;

DT 20-MAY-2004 (first entry)

DE Human single nucleotide polymorphism (SNP) #62.

XX ss; human; single nucleotide polymorphism; SNP;
KW C1 S subcomponent protein; C1S; alanyl aminopeptidase protein; ANPEP;
KW meprin A beta protein; aminopeptidase P-like protein; XPN-PEP;
KW tissue kallikrein protein; KLK1; aminopeptidase P protein; MEPIB;
KW soluble guanylate cyclase 1 alpha-2 subunit protein; GUCY1A2; haplotype;
KW angioedema; angioedema-like disorder; paternity testing;
KW cardiovascular diseases; angina pectoris; hypertension; heart failure;
KW myocardial infarction; aneurysm; stroke; embolism; thrombosis;
KW coronary artery disease; arteriosclerosis; hypersensitivity;
KW haemodialysis; sepsis; inflammatory disease; inflammatory arthritis;
KW asthma; chronic obstructive pulmonary disease; cough reflex; allergy;
KW cancer; ANPEP.

OS Homo sapiens.

XX US2004033582-A1.
 XX 19-FEB-2004.
 PD 03-JUN-2003; 2003US-00453827.
 XX 03-JUN-2002; 2002US-0384980P.
 XX (EDMO/) EDMONDS M.
 PA (HUI/) HUI L.
 PA (PERR/) PERRONE M.
 PA (POWE/) POWELL J R.
 PA (RAMA/) RAMANATHAN C S.
 PA (SWAN/) SWANSON B.
 PA (TSUC/) TSUCHIHASHI Z.
 PA (ZERB/) ZERBA K.
 XX Edmonds M, Hui L, Perrone M, Powell JR, Ramanathan CS, Swanson B;
 P1 Tsuchihashi Z, Zerba K;
 P1 MPI; 2004-180052/17.
 XX New nucleic acid comprising a single nucleotide polymorphism at a
 PT specific location, useful in paternity testing, genetic analysis or
 PT diagnosing, preventing or treating cardiovascular diseases e.g.
 PT angioedema or angina pectoris.
 XX Claim 3; SEQ ID NO 62; 376pp; English.
 XX The invention relates to an isolated nucleic acid (I) derived from a
 CC human gene encoding a protein, such as the C1, S subcomponent protein
 CC (C1S), the alanyl aminopeptidase protein (ANPEP), the meprin A, beta
 CC protein (MEP1B), the aminopeptidase P-like protein (XPN-PEPL), the tissue
 CC kallikrein protein (KLK1), the membrane bound aminopeptidase P protein
 CC (XPNPEP2), or the soluble guanylate cyclase 1, alpha-2 subunit protein
 CC (GUCY1A2). The nucleic acid comprises at least one polymorphic position,
 CC including the alleles, reference alleles and alternate alleles of the
 CC single nucleotide polymorphisms, listed in the specification. The
 CC polymorphic position resides in a (non) coding position within the genomic
 CC sequence of the gene. The polymorphic position residing in a coding
 CC position results in a missense or silent mutation of the translated
 CC product of the gene. The polymorphic position residing in a non-coding
 CC position resides within the untranslated region or an intronic region of
 CC the gene. Constructing haplotypes using the nucleic acids above further
 CC comprises using the haplotypes to identify an individual for the presence
 CC of a disease phenotype, and correlating the presence of the disease
 CC phenotype with the haplotype. The disease phenotype is angioedema or an
 CC angioedema-like disorder. The nucleic acids, primers and probes are
 CC useful in phenotype correlations, paternity testing, medicine and genetic
 CC analysis. The nucleic acids and polypeptides can be used in diagnosing,
 CC preventing or treating cardiovascular diseases, e.g. angioedema, angina
 CC pectoris, hypertension, heart failure, myocardial infarction, aneurysm,
 CC stroke, embolism, thrombosis, coronary artery disease or
 CC arteriosclerosis, hypersensitivity reactions during haemodialysis, chronic
 CC sepsis, inflammatory diseases, inflammatory arthritis, asthma, chronic
 CC obstructive pulmonary disease, cough reflex, allergies, or cancer. The
 CC present sequence represents a human single nucleotide polymorphism (SNP)
 CC of the invention.
 XX
 CC Sequence 41 BP; 12 A; 12 C; 8 G; 9 T; 0 U; 0 Other;
 SQ
 Query Match 3.5%; Score 34.6; DB 1; Length 41;
 Best Local Similarity 90.2%; Pred. No. 3.7e+02;
 Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 557 AGCTGGGACCAAGACATGACCACTACACCTGGCTAATTT 597
 Db 1 AGCTGGGATTAAGACATGACCACTACACCTGGCTAATTT 41

RESULT 208
 ADL64284/c

ID ADL64284 standard; DNA; 41 BP.
 XX ADL64284;
 AC 20-MAY-2004 (first entry)
 XX Human single nucleotide polymorphism (SNP) #207.
 DE CS; human; single nucleotide polymorphism; SNP;
 XX C1 S subcomponent protein; C1S; alanyl aminopeptidase protein; ANPEP;
 KW meprin A beta protein; aminopeptidase P-like protein; XPN-PEPL;
 KW tissue kallikrein protein; KLK1; aminopeptidase P protein; MEP1B;
 KW soluble guanylate cyclase 1 alpha-2 subunit protein; GUCY1A2; haplotype;
 KW angioedema; angioedema-like disorder; paternity testing;
 KW cardiovascular diseases; angina pectoris; hypertension; heart failure;
 KW myocardial infarction; aneurysm; stroke; embolism; thrombosis;
 KW coronary artery disease; arteriosclerosis; hypersensitivity;
 KW haemodialysis; sepsis; inflammatory diseases; inflammatory arthritis;
 KW asthma; chronic obstructive pulmonary disease; cough reflex; allergy;
 KW cancer; ANPEP.
 XX Homo sapiens.
 OS
 XX US2004033582-A1.
 XX 19-FEB-2004.
 XX 03-JUN-2003; 2003US-00453827.
 XX 03-JUN-2002; 2002US-0384980P.
 XX (EDMO/) EDMONDS M.
 PA (HUI/) HUI L.
 PA (PERR/) PERRONE M.
 PA (POWE/) POWELL J R.
 PA (RAMA/) RAMANATHAN C S.
 PA (SWAN/) SWANSON B.
 PA (TSUC/) TSUCHIHASHI Z.
 PA (ZERB/) ZERBA K.
 XX Edmonds M, Hui L, Perrone M, Powell JR, Ramanathan CS, Swanson B;
 P1 Tsuchihashi Z, Zerba K;
 P1 MPI; 2004-180052/17.
 XX New nucleic acid comprising a single nucleotide polymorphism at a
 PT specific location, useful in paternity testing, genetic analysis or
 PT diagnosing, preventing or treating cardiovascular diseases e.g.
 PT angioedema or angina pectoris.
 XX Claim 3; SEQ ID NO 207; 376pp; English.
 XX The invention relates to an isolated nucleic acid (I) derived from a
 CC human gene encoding a protein, such as the C1, S subcomponent protein
 CC (C1S), the alanyl aminopeptidase protein (ANPEP), the meprin A, beta
 CC protein (MEP1B), the aminopeptidase P-like protein (XPN-PEPL), the tissue
 CC kallikrein protein (KLK1), the membrane bound aminopeptidase P protein
 CC (XPNPEP2), or the soluble guanylate cyclase 1, alpha-2 subunit protein
 CC (GUCY1A2). The nucleic acid comprises at least one polymorphic position,
 CC including the alleles, reference alleles and alternate alleles of the
 CC single nucleotide polymorphisms, listed in the specification. The
 CC polymorphic position resides in a (non) coding position within the genomic
 CC sequence of the gene. The polymorphic position residing in a coding
 CC position results in a missense or silent mutation of the translated
 CC product of the gene. The polymorphic position residing in a non-coding
 CC position resides within the untranslated region or an intronic region of
 CC the gene. Constructing haplotypes using the nucleic acids above further
 CC comprises using the haplotypes to identify an individual for the presence
 CC of a disease phenotype, and correlating the presence of the disease
 CC phenotype with the haplotype. The disease phenotype is angioedema or an
 CC angioedema-like disorder. The nucleic acids, primers and probes are
 CC useful in phenotype correlations, paternity testing, medicine and genetic
 CC analysis. The nucleic acids and polypeptides can be used in diagnosing,

CC preventing or treating cardiovascular diseases, e.g. angioedema, angina
CC pectoris, hypertension, heart failure, myocardial infarction, aneurysm,
CC stroke, embolism, thrombosis, coronary artery disease or
CC arteriosclerosis, hypersensitivity reactions during haemodialysis,
CC sepsis, inflammatory diseases, inflammatory arthritis, asthma, chronic
CC obstructive pulmonary disease, cough reflex, allergies, or cancer. The
CC present sequence represents a human single nucleotide polymorphism (SNP)
CC of the invention.

XX Sequence 41 BP; 7 A; 14 C; 12 G; 8 T; 0 U; 0 Other;

XX Query Match 3.5%; Score 34.6; DB 1; Length 41;

XX Best Local Similarity 90.2%; Pred. No. 3.7e+02;

XX Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

XX Db 643 CCAGGCTGAGTGCAGTGGCGCATCTGGCTCAGTGCNA 683

XX 41 CCAGGCTGAGTGCAGTGGCGCATCTGGCTCAGTGCNA 1

XX RESULT 209

XX AAT97406/C

XX AAT97406 standard; DNA; 40 BP.

XX AAT97406;

XX 14-APR-1998 (first entry)

XX Synthetic oligomer D188 Allele A from WO9722719 Example 2.

XX Detection; target site; nucleic acid; fluorophore; labelled; fluorescent;

XX inherited disease; tissue typing; PCR; ss.

XX Synthetic.

XX WO9722719-A1.

XX 26-JUN-1997.

XX 17-DEC-1996; 96WO-US020379.

XX 18-DEC-1995; 95US-0008743P.

XX (UNIW) UNIV WASHINGTON.

XX Kwok P, Chen X;

XX WPI; 1997-341707/31.

XX Detecting target site in nucleic acid by forming a fluorophore-labelled

XX oligonucleotide at the site - and detecting fluorescent energy following

XX denaturation, used e.g. to detect inherited diseases, in tissue typing

XX etc.

XX Example 2; Page 27; 68pp; English.

XX A method has been developed for detecting the presence of a target site

XX (TS), of at least one nucleotide (nt) in a nucleic acid (NA). The method

XX comprises: (a) forming an oligonucleotide (ON), consisting of two

XX fluorophores (F1, F2) each covalently linked to separate nt, bound to TS;

XX and (b) detecting fluorescence energy transfer (FET) between F1 and F2

XX when ON is released from TS. The present sequence represents a synthetic

XX polynucleotide used in an example of the present invention. The method is

XX used to diagnose hereditary and other diseases; to determine infectious

XX agents; in tissue typing for histocompatibility; in forensic

XX identification and paternity testing; and in monitoring the genetic make

XX up of plants and animals. Specifically it is used to detect single nt

XX polymorphisms. The method provides inexpensive, simple, accurate and

XX automatable nucleic acid analyses

XX Sequence 40 BP; 12 A; 7 C; 14 G; 7 T; 0 U; 0 Other;

XX Query Match 3.4%; Score 33.6; DB 1; Length 40;

Best Local Similarity 90.0%; Pred. No. 4.1e+02;

XX Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

XX Db 675 TCACGCAACCTCTGCTCCCGGGTTCAAGTATTCTCT 714

XX 40 TCACGCAACCTCTGCTCCCGGGTTCAAGTATTCTCT 1

XX RESULT 210

XX ADK41334/C

XX ADK41334 standard; DNA; 40 BP.

XX ADK41334;

XX 06-MAY-2004 (first entry)

XX Human chromosome 19 single nucleotide polymorphism detecting probe #22.

XX sequence polymorphism analysis; human; chromosome 19q; cancer; RAI; ss;

XX single nucleotide polymorphism; SNP; probe.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

XX variation replace(20,G)

XX /*tag= a

XX /standard_name= "single nucleotide polymorphism"

XX MO2004003229-A2.

XX 08-JAN-2004.

XX 27-JUN-2003; 2003WO-DK000448.

XX 27-JUN-2002; 2002DK-00001005.

XX 07-OCT-2002; 2002DK-00001500.

XX 25-FEB-2003; 2003DK-0000288.

XX 29-APR-2003; 2003DK-0000639.

XX (UYAA-) UNIV AARHUS.

XX (ARBE-) ARBEJDSMILJO INST NAT INST OCCUPA.

XX Nexo BA, Vogel U, Rockenbauer E, Bukowy ZK;

XX WPI; 2004-142878/14.

XX Estimating the disease risk or prognosis of an individual by sequence

XX polymorphism analysis.

XX Claim 18; SEQ ID NO 92; 145pp; English.

XX The invention relates to a novel method of estimating disease risk or

XX prognosis of an individual by sequence polymorphism analysis, especially

XX to: estimating a treatment response of an individual suffering from

XX cancer to a disease treatment; a primer or probe for use in the method of

XX estimating the disease risk or prognosis of an individual or for

XX estimating a treatment response of an individual suffering from cancer to

XX a disease treatment; an antibody directed to an epitope of a RAI gene

XX product; and a kit for use in the method of estimating the disease risk

XX or prognosis of an individual or for estimating a treatment response of

XX at least one primer or probe and optionally amplifying means for nucleic

XX acid amplification. The novel method is useful for estimating the disease

XX risk or prognosis of an individual or for estimating a treatment response

XX of an individual suffering from cancer to a disease treatment. This

XX polynucleotide sequence represents a probe used for detecting single

XX nucleotide polymorphisms in the DNA of human chromosome 19 of the

XX invention.

XX Sequence 40 BP; 8 A; 13 C; 12 G; 7 T; 0 U; 0 Other;

Query Match 3.4%; Score 33.6; DB 1; Length 40;
Best Local Similarity 90.0%; Pred. No. 4.1e+02;
Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 469 CCCAGGATGAGTGTGTGTATCATCAGCTCACTGCA 508
DB 40 CCCAGGCTGAGTGCAGTGTGCTCATCTCACTGCA 1

RESULT 211

AAH49728/C
ID AAH49728 standard; DNA; 41 BP.

AC AAH49728;

DT 25-SEP-2001 (first entry)

XX Human DNA mismatch repair protein 11 coding sequence probe #2.

XX Human; DNA repair mismatch protein 11; cancer; haemopathy; HIV infection;
XX immunological disease; inflammation; gene therapy; probe; ss.

OS Homo sapiens.

PN WO200147988-A1.

PD 05-JUL-2001.

PF 18-DEC-2000; 2000MO-CN0000627.

PR 23-DEC-1999; 99CN-00125733.

PA (UYFU-) UNIV FUDAN.

PI (SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD.

PI Mao Y, Xie Y;

DR WPI; 2001-425639/45.

XX DNA mismatch repair protein 11 and encoded polynucleotide, applicable in
XX diagnosis and treatment of malignant tumor, hemopathy, HIV infection,
XX immunological diseases and various inflammation.

PS Example 7; Page 20; 36pp; Chinese.

XX The present invention provides the protein and coding sequences of human
XX DNA mismatch repair protein 11. The sequences are useful in the treatment
XX of cancer, haemopathy, HIV infection, immunological diseases and
XX inflammation. The present sequence is a probe for the coding sequence of
XX the invention

SQ Sequence 41 BP; 9 A; 11 C; 15 G; 6 T; 0 U; 0 Other;

Query Match 3.4%; Score 33.6; DB 1; Length 41;

Best Local Similarity 90.0%; Pred. No. 4.2e+02;
Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 839 TCTGCTGCTGCGCTCCCAAGTCTGGGATTACAGGC 878
DB 41 TCTTCTGCTGCGGCTCCCAAGTCTGGGATTACAGGC 2

RESULT 212

ABL49776
ID ABL49776 standard; DNA; 41 BP.

AC ABL49776;

DT 29-MAY-2002 (first entry)

XX Human tyrosinase 10.34 probe 2 SEQ ID NO:9.

XX Human; tyrosinase; enzyme; human immunodeficiency virus infection;

KW HIV infection; cancer; probe; ss.

XX Homo sapiens.

OS Homo sapiens.

PN CN1325972-A.

PD 12-DEC-2001.

PF 31-MAY-2000; 2000CN-00116261.

PR 31-MAY-2000; 2000CN-00116261.

PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

PI Mao Y, Xie Y;

DR WPI; 2002-196693/26.

XX New polypeptide-tyrosinase 10.34 for treating diseases such as cancer and
XX human immunodeficiency virus infection.

PS Example 6; Page 19 (Disclosure); 32pp; Chinese.

XX The present invention describes human tyrosinase 10.34 (I). The present
XX invention also described a method for preparing (I) using DNA
XX recombination techniques. (I) and the polynucleotide encoding it can be
XX used in the treatment of diseases such as cancer and human
XX immunodeficiency virus (HIV) infection. The present sequence represents a
XX probe for human tyrosinase 10.34, which is used in an example from the
XX present invention

SQ Sequence 41 BP; 5 A; 12 C; 13 G; 11 T; 0 U; 0 Other;

Query Match 3.4%; Score 33.6; DB 1; Length 41;
Best Local Similarity 90.0%; Pred. No. 4.2e+02;
Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 187 TGGAGTTCTCCATGTTGTCAGGCTGCTCGAATCCC 226
DB 1 TGGGCTTTCACCATGTTGCGCGGCTGCTCGAATCCC 40

RESULT 213

ABL49775
ID ABL49775 standard; DNA; 41 BP.

AC ABL49775;

DT 29-MAY-2002 (first entry)

XX Human tyrosinase 10.34 probe 1 SEQ ID NO:8.

XX Human; tyrosinase; enzyme; human immunodeficiency virus infection;

XX HIV infection; cancer; probe; ss.

OS Homo sapiens.

PN CN1325972-A.

PD 12-DEC-2001.

PF 31-MAY-2000; 2000CN-00116261.

PR 31-MAY-2000; 2000CN-00116261.

PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

PI Mao Y, Xie Y;

DR WPI; 2002-196693/26.

XX New polypeptide-tyrosinase 10.34 for treating diseases such as cancer and
XX human immunodeficiency virus infection.

XX Example 6; Page 19 (Disclosure); 32pp; Chinese.
 PS
 XX
 CC The present invention describes human tyrosinase 10.34 (I). The present
 CC invention also described a method for preparing (II) using DNA
 CC recombination techniques. (I) and the polynucleotide encoding it can be
 CC used in the treatment of diseases such as cancer and human
 CC immunodeficiency virus (HIV) infection. The present sequence represents a
 CC probe for human tyrosinase 10.34, which is used in an example from the
 CC present invention
 CC
 SQ Sequence 41 BP; 5 A; 12 C; 13 G; 11 T; 0 U; 0 Other;
 Query Match 3.4%; Score 33.6; DB 1; Length 41;
 Best Local Similarity 90.0%; Pred. No. 4.2e+02;
 Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 187 TGGAGTTTCTCCATGTTGTCAGGCTGGTCTCGAACTCCC 226
 DB 1 TGGGGTTTCACCATGTTGGCCGGGCTGCTCGAACTCCC 40
 RESULT 214
 ABZ20667/c
 ID ABZ20667 standard; DNA; 41 BP.
 XX
 AC ABZ20667;
 XX
 DT 03-MAR-2003 (first entry)
 XX
 DE Human G protein subunit 9-02 coding sequence probe #2.
 XX
 KW Human; G protein subunit 9.02; cancer; constipation; diarrhoea; cough;
 KW cardiac asthma; colic; psychic disease; probe;
 KW morphinic analgesic acute poisoning; ss.
 XX
 OS Homo sapiens.
 XX
 PS CN1345751-A.
 XX
 PD 24-APR-2002.
 XX
 PF 26-SEP-2000; 2000CN-00125456.
 XX
 PR 26-SEP-2000; 2000CN-00125456.
 XX
 PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-675773/73.
 XX
 PT Novel polypeptide-human G protein subunit 9.01.
 XX
 PS Example 6; Page 22(Disclosure); 34pp; Chinese.
 XX
 CC The present invention provides the protein and coding sequences of human
 CC G protein subunit 9.02. The sequences can be used in the treatment of
 CC cancers, coughs, cardiac asthma, diarrhoea, constipation, colic, psychic
 CC disease and morphinic analgesic acute poisoning. The present sequence is
 CC a probe used to isolate the coding sequence of the invention
 CC
 SQ Sequence 41 BP; 7 A; 10 C; 16 G; 8 T; 0 U; 0 Other;
 Query Match 3.4%; Score 33.6; DB 1; Length 41;
 Best Local Similarity 90.0%; Pred. No. 4.2e+02;
 Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 369 TCCACCTGCTCAGCTCCCAAGTGGTGGATTACAGGC 408
 DB 41 TCCACCTCAGCTCAGCTCCCAAGTGGTGGATTACAGGC 2
 OS

RESULT 215
 ABA94091/c
 ID ABA94091 standard; DNA; 41 BP.
 XX
 AC ABA94091;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human tumour suppressor factor 11.77 probe 1 SEQ ID NO:8.
 XX
 KW Human; tumour suppressor factor 11.77; cytostatic; haemostatic; virucide;
 KW immunomodulatory; antiinflammatory; gene therapy; malignant tumour;
 KW haemopathy; human immunodeficiency virus infection; HIV infection;
 KW immunological disease; inflammation; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200196526-A2.
 XX
 PD 20-DEC-2001.
 XX
 PF 04-JUN-2001; 2001WO-CN000906.
 XX
 PR 07-JUN-2000; 2000CN-00116365.
 XX
 PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-075588/10.
 XX
 PT Human tumor suppressor factor 11.77 and encoding polynucleotide, used in
 PT diagnosis and treatment of malignant tumors, hemopathy, human
 PT immunodeficiency virus infection, immunological diseases and
 PT inflammation.
 XX
 PS Example 6; Page 20; 33pp; Chinese.
 XX
 CC The present invention describes human tumour suppressor factor 11.77 (I).
 CC (I) has cytostatic, haemostatic, virucide, immunomodulatory and
 CC antiinflammatory activities. The polynucleotide (II) encoding (I) can be
 CC used in gene therapy. (I) and (II) can be used in the diagnosis and
 CC treatment of malignant tumour, haemopathy, human immunodeficiency virus
 CC (HIV) infection, immunological diseases and various inflammations. The
 CC present sequence represents a probe for human tumour suppressor factor
 CC 11.77, which is used in an example from the present invention
 CC
 SQ Sequence 41 BP; 9 A; 11 C; 14 G; 7 T; 0 U; 0 Other;
 Query Match 3.4%; Score 33.6; DB 1; Length 41;
 Best Local Similarity 90.0%; Pred. No. 4.2e+02;
 Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 839 TCTGCTGCTCGGCTCCCAAGTGGTGGATTACAGGC 878
 DB 41 TCCGCCGCTCTGGCTCCCAAGTGGTGGATTACAGGC 2
 RESULT 216
 AAL43826
 ID AAL43826 standard; DNA; 41 BP.
 XX
 AC AAL43826;
 XX
 DT 19-SEP-2002 (first entry)
 XX
 DE Human oncogene protein 11-66 nucleotide probe 1.
 XX
 KW Human; ss; gene therapy; oncogene protein 11.66; malignant tumour;
 KW haemopathy; development disturbance; HIV; immunological disease;
 KW inflammation; probe.
 XX
 OS Homo sapiens.

XX CN1333235-A.
XX 30-JAN-2002.
XX 07-JUL-2000; 2000CN-00119427.
XX 07-JUL-2000; 2000CN-00119427.
XX (SHAN-) SHANGHAI BIODOR GENE DEV CO LTD.
XX Mao Y, Xie Y;
XX WPI; 2002-305565/35.
XX Novel polypeptide-oncoprotein 11.66 and polynucleotide for encoding said
XX polypeptide.
XX Example 6; Page 21 (Disclosure); 33pp; Chinese.
XX The invention comprises the amino acid and coding sequence of the human
XX oncoprotein 11.66. The oncoprotein 11.66 DNA and protein
XX sequences are useful for treating malignant tumour, haemopathy,
XX development disturbance, HIV infection, immunological disease and various
XX inflammations. The present DNA sequence represents a probe that is
XX specific for the gene sequence of the human oncoprotein 11.66
SQ Sequence 41 BP; 6 A; 13 C; 12 G; 10 T; 0 U; 0 Other;

Query Match 3.4%; Score 33.6; DB 1; Length 41;
Best Local Similarity 90.0%; Pred. No. 4.2e+02;
Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 187 TGGAGTTCTCCATGTTGTCAGGCTGTCGTAACCTCCC 226
DB 1 TGGAGTTCTCCATGTTGTCAGGCTGTCGTAACCTCCC 40

RESULT 217

AA143827
ID AA143827 standard; DNA; 41 BP.

XX AC AA143827;

XX DT 19-SEP-2002 (first entry)

XX DE Human oncogene protein 11-66 nucleotide probe 2.

XX KW Human; ss; gene therapy; oncogene protein 11.66; malignant tumour;
XX haemopathy; development disturbance; HIV; immunological disease;
XX inflammation; probe.

XX OS Homo sapiens.

XX PN CN1333235-A.

XX PD 30-JAN-2002.

XX PF 07-JUL-2000; 2000CN-00119427.

XX PR 07-JUL-2000; 2000CN-00119427.

XX PA (SHAN-) SHANGHAI BIODOR GENE DEV CO LTD.

XX PI Mao Y, Xie Y;

XX DR WPI; 2002-305565/35.

XX PT Novel polypeptide-oncoprotein 11.66 and polynucleotide for encoding said
XX polypeptide.

XX Example 6; Page 21 (Disclosure); 33pp; Chinese.

CC The invention comprises the amino acid and coding sequence of the human
CC oncoprotein 11.66. The oncoprotein 11.66 DNA and protein
CC sequences are useful for treating malignant tumour, haemopathy,
CC development disturbance, HIV infection, immunological disease and various
CC inflammations. The present DNA sequence represents a probe that is
CC specific for the gene sequence of the human oncoprotein 11.66
SQ Sequence 41 BP; 6 A; 13 C; 12 G; 10 T; 0 U; 0 Other;

Query Match 3.4%; Score 33.6; DB 1; Length 41;
Best Local Similarity 90.0%; Pred. No. 4.2e+02;
Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 187 TGGAGTTCTCCATGTTGTCAGGCTGTCGTAACCTCCC 226
DB 1 TGGAGTTCTCCATGTTGTCAGGCTGTCGTAACCTCCC 40

RESULT 218

AB244551/C
ID AB244551 standard; DNA; 41 BP.

XX AC AB244551;

XX DT 26-JUN-2003 (first entry)

XX DE Human glycosyltransferase DOST gene polymorphic site, #1335.

XX KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 1;
XX polymorphic site; drug evaluation; drug screening; genotyping;
XX genetic profiling; therapeutic customisation; adverse reaction;
XX clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT variation replace(21,A)
XX FT /*tag= a
XX FT /standard_name= "Single nucleotide polymorphism (SNP)"

XX PN WO200252044-A2.

XX PD 04-JUL-2002.

XX PF 27-DEC-2001; 2001WO-JP011592.

XX PR 27-DEC-2000; 2000JP-00399443.

XX PR 02-MAY-2001; 2001JP-00135256.

XX PR 27-AUG-2001; 2001JP-00256862.

XX PA (RIKE) RIKEN KK.

XX PI Nakamura Y, Sekine A, Iida A, Saito S;

XX DR WPI; 2002-583571/62.

XX PT Identifying individuals having a polymorphism, useful for determining the
XX effectiveness or side effect of a drug or treatment protocol, comprises
XX detecting at least one polymorphism in the drug metabolising enzyme
XX nucleic acid.

XX PS Claim 23; Page 86; 2785pp; English.

XX CC Sequences AB243217-AB250887 represent polymorphic sites within genes
XX encoding enzymes associated with drug metabolism. The invention relates
XX to methods and compositions for identifying individuals who have at least
XX one polymorphism in such drug metabolising enzyme-encoding genes. The
XX polymorphisms may be identified in a nucleic acid sample using probes or
XX primers specific for a sequence selected from AB243217-AB250887 using a
XX variety of detection assays, including hybridisation assays, nucleic acid
XX arrays and PCR-based methods. The invention also encompasses methods of
XX evaluating and screening drugs using genetic polymorphism data. Genetic
XX polymorphism data, particularly that relating to single nucleotide

CC polymorphisms (SNPs), may be used in studying the relationship between
CC DNA sequence variations and human diseases, conditions, and responses to
CC drugs. SNPs are also useful as polymorphism markers for discovering genes
CC that cause or exacerbate certain diseases. SNPs are particularly useful
CC in the above respects as they are stable in populations, occur
CC frequently, and have lower mutation rates than other genome variations
CC such as repeating sequences. The detection and analysis of polymorphisms
CC in genes encoding drug metabolising enzymes allows the customisation of
CC drug therapies based upon the genetic profile of individual patients.
CC This would not only take the guesswork out of selecting the drug with the
CC greatest therapeutic effect for a particular patient, but would also
CC reduce the likelihood of adverse reactions, thereby increasing safety.
CC Methods of the invention are also useful in the drug discovery and
CC approval processes. For example, individuals could be selected for
CC clinical trials only if their genetic profiles indicate that they are
CC capable of responding to a particular drug or drug class, and previously
CC failed drug candidates could be revived if they were matched with more
CC appropriate patient populations. The methods, data and compositions of
CC the invention may therefore lead to an increase in the range of
CC possible drug targets and decreases in the number of adverse drug
CC reactions, failed drug trials, the time taken for a drug to be approved,
CC the length of time patients are on medication and the number of different
CC medications a patient needs to take before finding an effective therapy

Query Match	3.4%	Score 33.6	DB 1	Length 41
Best Local Similarity	90.0%	Pred. No. 4.2e+02		
Matches 36; Conservative	0	Mismatches 4	Indels 0	Gaps 0

```
QY      669 CTTGGCTCACTGCAACCTTGCCCTCCCGGTTCAAGTTAT 708
        |||||
Db      40  CTTGGCTCACTGCAACCTCCGCCTCCTGGGTTCAAGAAT 1
```

RESULT 219
ABZ50761/c
ID ABZ50761 standard; DNA; 41 BP

AC ABZ50761;

DT 26-JUN-2003 (first entry)

DE Human glycosyltransferase DDOST gene polymorphic site, #7543.

KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 1.

KW genetic profiling; therapeutic customisation; adverse reaction

XX

XX

FT variation

13

PN W0200252044-A2

PD 04-JUL-2002.

PF 27-DEC-2001;

PR 27-DEC-2000;

PR 27-AUG-2001;

PA (RIKE) RIKE

PI Nakamura Y,
yv

DR WPI; 2002-58
xx

PR Identifying individuals having a polymorphism, useful for determining the
 PR effectiveness or side effect of a drug or treatment protocol, comprises
 PR detecting at least one polymorphism in the drug metabolizing enzyme
 PR nucleic acid.
 XX
 XX Claim 23; Page 221; 2785pp; English.
 XX

Claim 23; Page 221; 2785pp; English.

Sequence ABZ431217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism in such drug metabolising enzyme-encoding genes. The polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43211-ABZ50887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data. Genetic polymorphism data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolising enzymes allows the customisation of drug therapies based upon the genetic profile of individual patients. This would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety. Methods of the invention are also useful in the drug discovery and approval processes. For example, individuals could be selected for clinical trials only if their genetic profiles indicate that they are capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to an increase in the range of possible drug targets and decreases in the number of adverse drug reactions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy

Query Match	3.4%	Score	36.6	DB	1	length	41
Best Local Similarity	90.0%	Pred	No. 4.2e+02				
Matches	36	Conservative	0	Mismatches	4	Indels	0
						Gaps	0

```

QY      669 CTGGCTCACTGCAACTCTGCTCCGGGTTCAAGTTAT 708
          |||||
Db      40  CTGGCTCACTGCAACTCCGGCTCTGGGTTCAAGCAAT 1

```

RESULT 220
ABV77329
ID ABV77329 standard; DNA; 41 BP.

AC ABV77329

DT 07-FEB-2003 (first entry)

Human protein 10.01 related probe 2.

Human; 10.01; aminolysase active site; arrhythmia; diabetes; probe; ss.

OS Homo sapiens

PN CN1342770-A.

PD 03-APR-2002.

PF 12-SEP-2000;

PR 12-SEP-2000;

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 PA
 XX Mao Y, Xie Y;
 PI
 XX WPI; 2002-529811/57.
 DR
 XX New human protein 10.01 containing Phe-His aminolysase active site and
 PT encoding polynucleotide, useful for treating arrhythmia and diabetes.
 XX
 PS Example 7; Page 22 (disclosure); 33pp; Chinese.
 XX
 XX The invention relates to a human protein designated 10.01, containing the
 CC Phe-His aminolysase active site. Also disclosed are the encoding
 CC polynucleotide, and a method for preparing the polypeptide by DNA
 CC recombination. The application of the polypeptide is in treating
 CC arrhythmia and diabetes. Also disclosed are the antagonist against this
 CC polypeptide and its therapeutic action, and the application of the
 CC polynucleotide. The current sequence represents a human protein 10.01
 CC related probe sequence
 XX
 SQ Sequence 41 BP; 6 A; 17 C; 9 G; 9 T; 0 U; 0 Other;
 XX
 Query Match 3.4%; Score 33.6; DB 1; Length 41;
 Best Local Similarity 90.0%; Pred. No. 4.2e+02;
 Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 655 TGCAGTGGCGCAATCTTGGCTCACTGCAACCTTGCTCC 694
 DB 1 TGCAGTGGCGCAATCTTGGCTCACTGCAACCTTGCTCC 40
 RESULT 221
 ACC00157
 ID ACC00157 standard; DNA; 41 BP.
 XX
 AC ACC00157;
 XX
 DT 14-JUL-2003 (first entry)
 XX
 DE Probe #2 for guanosine triphosphate activator 10.01.
 XX
 XX Guanosine triphosphatase activator 10.01; squamobasal cell;
 KW carcinoma of skin; osteosarcoma; leukemia; teratoma; probe; ss.
 XX
 OS Unidentified.
 XX
 XX CN1380320-A.
 PN
 XX 20-NOV-2002.
 PD
 XX 10-APR-2001; 2001CN-00105912.
 PF
 XX 10-APR-2001; 2001CN-00105912.
 PR
 XX 10-APR-2001; 2001CN-00105912.
 PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2003-222552/22.
 XX
 PT A polypeptide-guanosine triphosphatase activator protein -10.01 and
 PT polynucleotide for coding this polypeptide.
 XX
 PS Example 7; Page 23; 33pp; Chinese.
 XX
 XX The present invention discloses a polypeptide-guanosine triphosphatase
 CC activator protein-10.01. The invention also discloses the method for
 CC curing several diseases, such as squamobasal cell carcinoma of skin,
 CC osteosarcoma, leukemia and teratoma by using said polypeptide. The
 CC present sequence represents a probe for guanosine triphosphatase activator
 CC protein 10.01
 XX

SQ Sequence 41 BP; 6 A; 16 C; 11 G; 8 T; 0 U; 0 Other;
 XX
 Query Match 3.4%; Score 33.6; DB 1; Length 41;
 Best Local Similarity 90.0%; Pred. No. 4.2e+02;
 Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 655 TGCAGTGGCGCAATCTTGGCTCACTGCAACCTTGCTCC 694
 DB 1 TGCAGTGGCGCAATCTTGGCTCACTGCAACCTTGCTCC 40
 RESULT 222
 AB257114
 ID AB257114 standard; DNA; 41 BP.
 XX
 AC AB257114;
 XX
 DT 24-MAR-2003 (first entry)
 XX
 DE Human KIAA0608 protein 10.12 probe, SEQ ID NO:9.
 XX
 XX Human; KIAA0608 protein 10.12; recombinant production; gene therapy;
 KW peptic ulcer; diabetes; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN CN1355220-A.
 XX
 PD 26-JUN-2002.
 XX
 PF 24-NOV-2000; 2000CN-00127565.
 XX
 PR 24-NOV-2000; 2000CN-00127565.
 XX
 XX (UYFU-) UNIV FUDAN.
 PA
 XX Mao Y, Xie Y;
 XX
 DR WPI; 2003-000145/01.
 XX
 PT Polypeptide-human KIAA0608 protein 10.12 and polynucleotide encoding it.
 XX
 PS Example 6; Page 22 (Disclosure); 35pp; Chinese.
 XX
 CC The invention relates to human KIAA0608 protein 10.12 (ABP58674) and
 CC nucleic acids encoding it (AB257108). The protein has a molecular weight
 CC of 10 KD. The invention also relates to a method for the recombinant
 CC production of the protein, an antagonist in therapeutic applications. KIAA0608
 CC protein 10.12 can be used in the treatment of a variety of diseases such
 CC as peptic ulcers and diabetes. Sequences AB257113-AB257114 represent
 CC human KIAA0608 protein 10.12 probes used in an exemplification of the
 CC invention
 XX
 SQ Sequence 41 BP; 6 A; 11 C; 14 G; 10 T; 0 U; 0 Other;
 XX
 Query Match 3.4%; Score 33.6; DB 1; Length 41;
 Best Local Similarity 90.0%; Pred. No. 4.2e+02;
 Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 648 GCTGAGTGCAGTGGCGCAATCTTGGCTCACTGCAACCTC 687
 DB 2 GCTGAGTGCAGTGGCGCAATCTTGGCTCACTGCAACCTC 41
 RESULT 223
 ADL64136/C
 ID ADL64136 standard; DNA; 41 BP.
 XX
 AC ADL64136;
 XX
 DT 20-MAY-2004 (first entry)
 XX

DE Human single nucleotide polymorphism (SNP) #59.
 XX
 KW ss; human; single nucleotide polymorphism; SNP;
 KW C1 S subcomponent protein; C1S; alanyl aminopeptidase protein; ANPEP;
 KW mepirin A beta protein; aminopeptidase P-like protein; XPN-PEP;
 KW tissue kallikrein protein; KLK1; aminopeptidase P protein; MEPIB;
 KW soluble guanylate cyclase 1 alpha-2 subunit protein; GUCY1A2; haplotype;
 KW angioedema; angioedema-like disorder; paternity testing;
 KW cardiovascular diseases; angina pectoris; hypertension; heart failure;
 KW myocardial infarction; aneurysm; stroke; embolism; thrombosis;
 KW coronary artery disease; arteriosclerosis; hypersensitivity;
 KW haemodialysis; sepsis; inflammatory disease; inflammatory arthritis;
 KW asthma; chronic obstructive pulmonary disease; cough reflex; allergy;
 KW cancer; ANPEP.
 XX
 OS Homo sapiens.
 XX
 PN US200403582-A1.
 XX
 PD 19-FEB-2004.
 XX
 PF 03-JUN-2003; 2003US-00453827.
 XX
 PR 03-JUN-2002; 2002US-0384980P.
 XX
 PA (EDMO/) EDMONDS M.
 PA (HUI/) HUI L.
 PA (PERR/) PERRONE M.
 PA (POWE/) POWELL J R.
 PA (RAMA/) RAMANATHAN C S.
 PA (SWAN/) SWANSON B.
 PA (TSUC/) TSUCHIHASHI Z.
 PA (ZERR/) ZERBA K.
 XX
 PI Edmonds M, Hui L, Perrone M, Powell JR, Ramanathan CS, Swanson B;
 PI Tsuchihashi Z, Zerba K;
 XX
 DR WPI; 2004-180052/17.
 XX
 PT New nucleic acid comprising a single nucleotide polymorphism at a
 PT specific location, useful in paternity testing, genetic analysis or
 PT diagnosing, preventing or treating cardiovascular diseases e.g.
 PT angioedema or angina pectoris.
 XX
 PS Claim 3; SEQ ID NO 59; 376bp; English.

CC present sequence represents a human single nucleotide polymorphism (SNP)
 CC of the invention.
 XX
 SQ Sequence 41 BP; 9 A; 13 C; 11 G; 8 T; 0 U; 0 Other;
 XX
 OY Query Match 3.4%; Score 33.6; DB 1; Length 41;
 DB Best Local Similarity 90.0%; Pred No. 4.2e+02;
 Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 644 CCAGGCTGAGTGCAGTGGCCGCAATCTTGCTCACTGCA 683
 DB 41 CCAGGCTGAGTGCAGTGGTGCATCTCACTCACTGCA 2
 RESULT 224
 ABZ45510
 ID ABZ45510 standard; DNA; 41 BP.
 XX
 AC ABZ45510;
 XX
 DT 26-JUN-2003 (first entry)
 XX
 DE Human ATP-binding cassette ABCA7 gene polymorphic site, #2294.
 XX
 KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 19;
 KW polymorphic site; drug evaluation; drug screening; genotyping;
 KW genetic profiling; therapeutic customisation; adverse reaction;
 KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT rebase(21,T)
 FT /tag= a
 FT /standard_name= "Single nucleotide polymorphism (SNP)"
 XX
 PN WO200252044-A2.
 XX
 PD 04-JUL-2002.
 XX
 PP 27-DEC-2001; 2001WO-JP011592.
 XX
 PR 27-DEC-2000; 2000JP-00399443.
 PR 02-MAY-2001; 2001JP-00135256.
 PR 27-AUG-2001; 2001JP-00256862.
 XX
 PA (RIKE) RIKEN KK.
 XX
 PI Nakamura Y, Sekine A, Iida A, Saito S;
 PI WPI; 2002-583571/62.
 XX
 PT Identifying individuals having a polymorphism, useful for determining the
 PT effectiveness or side effect of a drug or treatment protocol, comprises
 PT detecting at least one polymorphism in the drug metabolizing enzyme
 PT nucleic acid.
 XX
 PS Claim 23; Page 102; 2785bp; English.

CC in the above respects as they are stable in populations, occur
CC frequently, and have lower mutation rates than other genome variations
CC such as repeating sequences. The detection and analysis of polymorphisms
CC in genes encoding drug metabolizing enzymes allows the customization of
CC drug therapies based upon the genetic profile of individual patients.
CC This would not only take the guesswork out of selecting the drug with the
CC greatest therapeutic effect for a particular patient, but would also
CC reduce the likelihood of adverse reactions, thereby increasing safety.
CC Methods of the invention are also useful in the drug discovery and
CC approval processes. For example, individuals could be selected for
CC clinical trials only if their genetic profiles indicate that they are
CC capable of responding to a particular drug or drug class, and previously
CC failed drug candidates could be revived if they were matched with more
CC appropriate patient populations. The methods, data and compositions of
CC the invention may therefore lead to an increase in the range of
CC possible drug targets and decreases in the number of adverse drug
CC reactions, failed drug trials, the time taken for a drug to be approved,
CC the length of time patients are on medication and the number of different
CC medications a patient needs to take before finding an effective therapy
CC
SQ Sequence 41 BP; 8 A; 14 C; 9 G; 10 T; 0 U; 0 Other;
Query Match 3.4%; Score 33.2; DB 1; Length 41;
Best Local Similarity 92.1%; Pred. No. 4.3e+02;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Gy 667 ATCTTGCTCACTGCACCTCTGCTCCCGGATTCAAG 704
Db 4 ATCTTGCTCACTGCACCTCTGCTCCCGGATTCAAG 41
RESULT 225
ABZ46916
ID ABZ46916 standard; DNA; 41 BP.
XX
AC ABZ46916;
XX
DT 26-JUN-2003 (first entry)
XX
DE Human ATP-binding cassette ABCA7 gene polymorphic site, #3700.
XX
KW Human; drug metabolizing enzyme; gene; drug metabolism; chromosome 19;
XX polymorphic site; drug evaluation; drug screening; genotyping;
XX genetic profiling; therapeutic customisation; adverse reaction;
XX clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(21,T)
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN WO200252044-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-JP011592.
XX
PR 27-DEC-2000; 2000JP-00399443.
XX 02-MAY-2001; 2001JP-00135256.
XX 27-AUG-2001; 2001JP-00256862.
XX
PA (RIKE) RIKEN KK.
XX
PI Nakamura Y, Sekine A, Iida A, Saito S;
XX
DR WPI, 2002-583571/62.
XX
PT Identifying individuals having a polymorphism, useful for determining the
PT effectiveness or side effect of a drug or treatment protocol, comprises
PT detecting at least one polymorphism in the drug metabolizing enzyme
PT nucleic acid.

XX
PS Claim 23; Page 129; 2785pp; English.
XX
CC Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes
CC encoding enzymes associated with drug metabolism. The invention relates
CC to methods and compositions for identifying individuals who have at least
CC one polymorphism in such drug metabolizing enzyme-encoding genes. The
CC polymorphisms may be identified in a nucleic acid sample using probes or
CC primers specific for a sequence selected from ABZ43217-ABZ50887 using a
CC variety of detection assays, including hybridisation assays, nucleic acid
CC arrays and PCR-based methods. The invention also encompasses methods of
CC evaluating and screening drugs using genetic polymorphism data. Genetic
CC polymorphism data, particularly that relating to single nucleotide
CC polymorphisms (SNPs), may be used in studying the relationship between
CC DNA sequence variations and human diseases, conditions, and responses to
CC drugs. SNPs are also useful as polymorphism markers for discovering genes
CC that cause or exacerbate certain diseases. SNPs are particularly useful
CC in the above respects as they are stable in populations, occur
CC frequently, and have lower mutation rates than other genome variations
CC such as repeating sequences. The detection and analysis of polymorphisms
CC in genes encoding drug metabolizing enzymes allows the customization of
CC drug therapies based upon the genetic profile of individual patients.
CC This would not only take the guesswork out of selecting the drug with the
CC greatest therapeutic effect for a particular patient, but would also
CC reduce the likelihood of adverse reactions, thereby increasing safety.
CC Methods of the invention are also useful in the drug discovery and
CC approval processes. For example, individuals could be selected for
CC clinical trials only if their genetic profiles indicate that they are
CC capable of responding to a particular drug or drug class, and previously
CC failed drug candidates could be revived if they were matched with more
CC appropriate patient populations. The methods, data and compositions of
CC the invention may therefore lead to an increase in the range of
CC possible drug targets and decreases in the number of adverse drug
CC reactions, failed drug trials, the time taken for a drug to be approved,
CC the length of time patients are on medication and the number of different
CC medications a patient needs to take before finding an effective therapy
CC
SQ Sequence 41 BP; 8 A; 14 C; 9 G; 10 T; 0 U; 0 Other;
Query Match 3.4%; Score 33.2; DB 1; Length 41;
Best Local Similarity 92.1%; Pred. No. 4.3e+02;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Gy 667 ATCTTGCTCACTGCACCTCTGCTCCCGGATTCAAG 704
Db 4 ATCTTGCTCACTGCACCTCTGCTCCCGGATTCAAG 41
RESULT 226
ACC84461
ID ACC84461 standard; DNA; 33 BP.
XX
AC ACC84461;
XX
DT 28-AUG-2003 (first entry)
XX
DE NTP peptide encoding sequence #8.
XX
KW Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
XX neural thread protein; NTP; tumour; ds.
XX
OS Unidentified.
XX
PN WO2003008443-A2.
XX
PD 30-JAN-2003.
XX
PF 19-JUL-2002; 2002WO-CA001105.
XX
PR 19-JUL-2001; 2001US-0306150P.
XX 19-JUL-2001; 2001US-0306151P.
XX 16-NOV-2001; 2001US-0331477P.
XX

PA (NTMO-) NTMOX CORP.
 XX
 PS Averbach PA;
 XX
 DR WPI; 2003-247999/24.
 DR P-PSDB; ABR63256.
 XX
 XX Novel neural thread protein peptide, referred as cell death peptide,
 PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
 PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.
 PS Disclosure; Page 17, 77pp; English.
 XX
 XX The present invention relates to a neural thread protein (NTP) peptide
 CC referred to as cell death peptide. Thought to be cytostatic,
 CC antibacterial, immunosuppressive and antiinflammatory. It is useful for
 CC treating a condition in a patient requiring removal or destruction of
 CC cells, for treating a condition such as benign or malignant tumor,
 CC inflammatory disease, autoimmune disease and infectious disease. The
 CC peptide useful for treatment is derived from the amino acid sequence for
 CC a pancreatic thread protein. The peptide is conjugated, linked or bound
 CC to a molecule chosen from antibody or its fragment, antibody-like binding
 CC molecule, where the molecule has a higher affinity for binding to a tumor
 CC or other target than binding to other cells. Treatment using NTP peptides
 CC can remove benign tumors with less risk and fewer of the undesirable side
 CC effects of surgery. The present sequence is an NTP encoding sequence
 XX
 SQ Sequence 33 BP; 7 A; 10 C; 9 G; 7 T; 0 U; 0 Other;
 Query Match 3.3%; Score 33; DB 1; Length 33;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 378 CTCAGCCTCCCAAGTCGTGGAATTACAGGCGT 410
 Db 1 CTCAGCCTCCCAAGTCGTGGAATTACAGGCGT 33
 RESULT 227
 AA199796
 ID AA199796 standard; DNA; 41 BP.
 XX
 AC AA199796;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human eukaryotic acetyl transferase 10 probe SEQ ID NO 8.
 XX
 XX Human; eukaryotic acetyl transferase 10; cytosolic; virucidal;
 KW immunomodulatory; antiinflammatory; haemostatic; malignant tumour;
 KW human immunodeficiency virus; HIV; infection; immunological disease;
 KW gene therapy; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175026-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 19-MAR-2001; 2001MO-CN000378.
 XX
 PR 22-MAR-2000; 2000CN-00115031.
 XX
 PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-025848/03.
 XX
 PT Human eucaryotic acetyl transferase 10 and encoded polynucleotide, used
 PT in diagnosis and treatment of malignant tumors, hemopathy, human
 PT immunodeficiency virus infection, immunological diseases and
 PT inflammation.

XX
 PS Example 6; Page 15; 33pp; Chinese.
 XX
 XX The invention relates to human eukaryotic acetyl transferase 10 with
 CC cytosolic, virucidal, immunomodulatory, antiinflammatory and haemostatic
 CC activity. The protein and encoding polynucleotide are used in diagnosis
 CC and treatment of malignant tumour, haemopathy, human immunodeficiency
 CC virus (HIV) infection, immunological diseases and various inflammations.
 CC The polynucleotide is useful in gene therapy. The present sequence is
 CC that of a probe, useful to the invention
 XX
 SQ Sequence 41 BP; 9 A; 10 C; 8 G; 14 T; 0 U; 0 Other;
 Query Match 3.3%; Score 33; DB 1; Length 41;
 Best Local Similarity 87.8%; Pred. No. 4.4e+02;
 Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1051 TGGCACACACCGCGCTAATTTGTGATTTTCATTAGAGCG 1091
 Db 1 TGGCACACACCGCGCTAATTTGTGATTTTCATTAGAGAGC 41
 RESULT 228
 AB152956/C
 ID AB152956 standard; DNA; 41 BP.
 XX
 AC AB152956;
 XX
 DT 24-MAY-2002 (first entry)
 XX
 DE Serine proteinase 10 probe #2.
 XX
 DE Serine proteinase 10; enzyme; cancer; HIV infection; anti-HIV;
 KW cytosolic; probe; ss.
 KW
 XX
 OS Unidentified.
 XX
 PN CN1325996-A.
 XX
 PD 12-DEC-2001.
 XX
 PF 31-MAY-2000; 2000CN-00116278.
 XX
 PR 31-MAY-2000; 2000CN-00116278.
 XX
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-196715/26.
 XX
 PT Polypeptide-serine proteinase 10 and polynucleotide encoding it.
 PS Example 6; Page 19 (disclosure); 32pp; Chinese.
 XX
 CC The present invention relates to serine proteinase 10 (AAM48453). Serine
 CC proteinase 10 and its coding sequence can be used for treating diseases
 CC such as cancer and HIV infection. The present sequence is a probe, which
 CC was used in an example from the invention
 XX
 SQ Sequence 41 BP; 9 A; 15 C; 12 G; 5 T; 0 U; 0 Other;
 Query Match 3.3%; Score 33; DB 1; Length 41;
 Best Local Similarity 87.8%; Pred. No. 4.4e+02;
 Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 637 CTGTACCCAGGCTGAGTGCAGTGGCGCATCTGGCTCA 677
 Db 41 CTGTACCCAGGCTGAGTGCAGTGGCGCATCTGGCTCA 1
 RESULT 229
 ABZ4124/C

ID AB244124 standard; DNA; 41 BP.
XX
AC AB244124;
XX
XX 26-JUN-2003 (first entry)
XX
XX Human NDUF51 gene polymorphic site, #908.
XX
DE Human; drug metabolising enzyme; gene; drug metabolism; chromosome 2;
XX polymorphic site; drug evaluation; drug screening; genotyping;
KM genetic profiling; therapeutic customisation; adverse reaction;
KM clinical trial; drug approval; single nucleotide polymorphism; SNP; db.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT variation /tag=a
FT /standard_name="Single nucleotide polymorphism (SNP)"
XX
XX MO200252044-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-JP011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
XX 02-MAY-2001; 2001JP-00135256.
XX 27-AUG-2001; 2001JP-00256862.
XX
XX (RIKEN) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Satto S;
XX
XX WPI; 2002-583571/62.
XX
XX Identifying individuals having a polymorphism, useful for determining the
PT effectiveness or side effect of a drug or treatment protocol, comprises
PT detecting at least one polymorphism in the drug metabolizing enzyme
PT nucleic acid.
XX
XX Claim 23; Page 79; 2785pp; English.
XX
XX Sequences AB243217-AB250887 represent polymorphic sites within genes
CC encoding enzymes associated with drug metabolism. The invention relates
CC to methods and compositions for identifying individuals who have at least
CC one polymorphism in such drug metabolising enzyme-encoding genes. The
CC polymorphisms may be identified in a nucleic acid sample using probes or
CC primers specific for a sequence selected from AB243217-AB250887 using a
CC variety of detection assays, including hybridisation assays, nucleic acid
CC arrays and PCR-based methods. The invention also encompasses methods of
CC evaluating and screening drugs using genetic polymorphism data. Genetic
CC polymorphisms (SNPs), particularly that relating to single nucleotide
CC polymorphisms (SNPs), may be used in studying the relationship between
CC DNA sequence variations and human diseases, conditions, and responses to
CC drugs. SNPs are also useful as polymorphism markers for discovering genes
CC that cause or exacerbate certain diseases. SNPs are particularly useful
CC in the above respects as they are stable in populations, occur
CC frequently, and have lower mutation rates than other genome variations
CC such as repeating sequences. The detection and analysis of polymorphisms
CC in genes encoding drug metabolising enzymes allows the customisation of
CC drug therapies based upon the genetic profile of individual patients.
CC This would not only take the guesswork out of selecting the drug with the
CC greatest therapeutic effect for a particular patient, but would also
CC reduce the likelihood of adverse reactions, thereby increasing safety.
CC Methods of the invention of adverse reactions in the drug discovery and
CC approval processes. For example, individuals could be selected for
CC clinical trials only if their genetic profiles indicate that they are
CC capable of responding to a particular drug or drug class, and previously
CC failed drug candidates could be revived if they were matched with more
CC appropriate patient populations. The methods, data and compositions of
CC the invention may therefore lead to an increase in the range of
CC possible drug targets and decreases in the number of adverse drug

CC reactions, failed drug trials, the time taken for a drug to be approved,
CC the length of time patients are on medication and the number of different
CC medications a patient needs to take before finding an effective therapy
XX
XX Sequence 41 BP; 8 A; 14 C; 12 G; 7 T; 0 U; 0 Other;
SO
Query Match 3.3%; Score 33; DB 1; Length 41;
Best Local Similarity 87.8%; Pred. No. 4.4e+02;
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Gy 643 CCCAGGCTGAGTGCAGTGCAGCAATCTTGGCTCAGTCA 683
Db 41 CCCAGGCTGAGTGCAGTGCAGTGCAGTCACTCACTGTA 1
RESULT 230
AB245508
ID AB245508 standard; DNA; 41 BP.
XX
XX AB245508;
XX
XX 26-JUN-2003 (first entry)
XX
XX Human ATP-binding cassette ABCA7 gene polymorphic site, #2292.
XX
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 19;
XX polymorphic site; drug evaluation; drug screening; genotyping;
XX genetic profiling; therapeutic customisation; adverse reaction;
XX clinical trial; drug approval; single nucleotide polymorphism; SNP; db.
XX
XX Homo sapiens.
XX
XX Key location/Qualifiers
XX variation /tag=a
XX /standard_name="Single nucleotide polymorphism (SNP)"
XX
XX MO200252044-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-JP011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
XX 02-MAY-2001; 2001JP-00135256.
XX 27-AUG-2001; 2001JP-00256862.
XX
XX (RIKEN) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Satto S;
XX
XX WPI; 2002-583571/62.
XX
XX Identifying individuals having a polymorphism, useful for determining the
PT effectiveness or side effect of a drug or treatment protocol, comprises
PT detecting at least one polymorphism in the drug metabolizing enzyme
PT nucleic acid.
XX
XX Claim 23; Page 102; 2785pp; English.
XX
XX Sequences AB243217-AB250887 represent polymorphic sites within genes
CC encoding enzymes associated with drug metabolism. The invention relates
CC to methods and compositions for identifying individuals who have at least
CC one polymorphism in such drug metabolising enzyme-encoding genes. The
CC polymorphisms may be identified in a nucleic acid sample using probes or
CC primers specific for a sequence selected from AB243217-AB250887 using a
CC variety of detection assays, including hybridisation assays, nucleic acid
CC arrays and PCR-based methods. The invention also encompasses methods of
CC evaluating and screening drugs using genetic polymorphism data. Genetic
CC polymorphisms (SNPs), particularly that relating to single nucleotide
CC polymorphisms (SNPs), may be used in studying the relationship between
CC DNA sequence variations and human diseases, conditions, and responses to
CC drugs. SNPs are also useful as polymorphism markers for discovering genes

XX MO200252044-A2.
 PN 04-JUL-2002.
 XX 27-DEC-2001; 2001WO-JP011592.
 XX 27-DEC-2000; 2000JP-00399443.
 XX 02-MAY-2001; 2001JP-00135256.
 PR 27-AUG-2001; 2001JP-00256862.
 XX (RIKE) RIKEN KK.
 PA Nakamura Y, Sekine A, Iida A, Saito S;
 PI WPI; 2002-583571/62.
 DR WPI; 2002-583571/62.
 PT Identifying individuals having a polymorphism, useful for determining the
 PT effectiveness or side effect of a drug or treatment protocol, comprises
 PT detecting at least one polymorphism in the drug metabolizing enzyme
 PT nucleic acid.
 PS Claim 23; Page 196; 2785pp; English.
 XX Sequences AB243217-AB250887 represent polymorphic sites within genes
 CC encoding enzymes associated with drug metabolism. The invention relates
 CC to methods and compositions for identifying individuals who have at least
 CC one polymorphism in such drug metabolizing enzyme-encoding genes. The
 CC polymorphisms may be identified in a nucleic acid sample using probes or
 CC primers specific for a sequence selected from AB243217-AB250887 using a
 CC variety of detection assays, including hybridisation assays, nucleic acid
 CC arrays and PCR-based methods. The invention also encompasses methods of
 CC evaluating and screening drugs using genetic polymorphism data. Genetic
 CC polymorphisms (SNPs), particularly that relating to single nucleotide
 CC polymorphisms (SNPs), may be used in studying the relationship between
 CC DNA sequence variations and human diseases, conditions, and responses to
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes
 CC that cause or exacerbate certain diseases. SNPs are particularly useful
 CC in the above respects as they are stable in populations, occur
 CC frequently, and have lower mutation rates than other genome variations
 CC such as repeating sequences. The detection and analysis of polymorphisms
 CC in genes encoding drug metabolizing enzymes allows the customisation of
 CC drug therapies based upon the genetic profile of individual patients.
 CC This would not only take the guesswork out of selecting the drug with the
 CC greatest therapeutic effect for a particular patient, but would also
 CC reduce the likelihood of adverse reactions, thereby increasing safety.
 CC Methods of the invention are also useful in the drug discovery and
 CC approval processes. For example, individuals could be selected for
 CC clinical trials only if their genetic profiles indicate that they are
 CC capable of responding to a particular drug or drug class, and previously
 CC failed drug candidates could be revived if they were matched with more
 CC appropriate patient populations. The methods, data and compositions of
 CC the invention may therefore lead to an increase in the range of
 CC possible drug targets and decreases in the number of adverse drug
 CC reactions, failed drug trials, the time taken for a drug to be approved,
 CC the length of time patients are on medication and the number of different
 CC medications a patient needs to take before finding an effective therapy
 XX
 SQ Sequence 41 BP; 7 A; 10 C; 14 G; 10 T; 0 U; 0 Other;
 Query Match 3.3%; Score 33; DB 1; Length 41;
 Best Local Similarity 87.8%; Pred. No. 4.4e-02;
 Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 643 CCCAGGCTGAGTGCAGTGGCCGAATCTTGCTCACTGCAG 683
 DB 1 CCCAGGCTGAGTGCAGTGGCTGATCTGCGCTCACTGCAG 41

RESULT 233
 AB250134/C
 ID AB250134 standard; DNA; 41 BP.
 XX

AC AB250134;
 XX 26-JUN-2003 (first entry)
 DT Human NDUF51 gene polymorphic site, #6916.
 DE Human NDUF51 gene polymorphic site, #6916.
 XX Human; drug metabolizing enzyme; gene; drug metabolism; chromosome 2;
 XX polymorphic site; drug evaluation; drug screening; genotyping;
 KW genetic profiling; therapeutic customisation; adverse reaction;
 KM clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH replace(21..T)
 FT variation /tag= a
 FT /standard_name= "Single nucleotide polymorphism (SNP)"
 XX MO200252044-A2.
 XX 04-JUL-2002.
 XX 27-DEC-2001; 2001WO-JP011592.
 XX 27-DEC-2000; 2000JP-00399443.
 PR 02-MAY-2001; 2001JP-00135256.
 PR 27-AUG-2001; 2001JP-00256862.
 XX (RIKE) RIKEN KK.
 PI Nakamura Y, Sekine A, Iida A, Saito S;
 DR WPI; 2002-583571/62.
 PT Identifying individuals having a polymorphism, useful for determining the
 PT effectiveness or side effect of a drug or treatment protocol, comprises
 PT detecting at least one polymorphism in the drug metabolizing enzyme
 PT nucleic acid.
 PS Claim 23; Page 206; 2785pp; English.
 XX Sequences AB243217-AB250887 represent polymorphic sites within genes
 CC encoding enzymes associated with drug metabolism. The invention relates
 CC to methods and compositions for identifying individuals who have at least
 CC one polymorphism in such drug metabolizing enzyme-encoding genes. The
 CC polymorphisms may be identified in a nucleic acid sample using probes or
 CC primers specific for a sequence selected from AB243217-AB250887 using a
 CC variety of detection assays, including hybridisation assays, nucleic acid
 CC arrays and PCR-based methods. The invention also encompasses methods of
 CC evaluating and screening drugs using genetic polymorphism data. Genetic
 CC polymorphisms (SNPs), particularly that relating to single nucleotide
 CC polymorphisms (SNPs), may be used in studying the relationship between
 CC DNA sequence variations and human diseases, conditions, and responses to
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes
 CC that cause or exacerbate certain diseases. SNPs are particularly useful
 CC in the above respects as they are stable in populations, occur
 CC frequently, and have lower mutation rates than other genome variations
 CC such as repeating sequences. The detection and analysis of polymorphisms
 CC in genes encoding drug metabolizing enzymes allows the customisation of
 CC drug therapies based upon the genetic profile of individual patients.
 CC This would not only take the guesswork out of selecting the drug with the
 CC greatest therapeutic effect for a particular patient, but would also
 CC reduce the likelihood of adverse reactions, thereby increasing safety.
 CC Methods of the invention are also useful in the drug discovery and
 CC approval processes. For example, individuals could be selected for
 CC clinical trials only if their genetic profiles indicate that they are
 CC capable of responding to a particular drug or drug class, and previously
 CC failed drug candidates could be revived if they were matched with more
 CC appropriate patient populations. The methods, data and compositions of
 CC the invention may therefore lead to an increase in the range of
 CC possible drug targets and decreases in the number of adverse drug
 CC reactions, failed drug trials, the time taken for a drug to be approved,
 CC the length of time patients are on medication and the number of different

```
CC medications a patient needs to take before finding an effective therapy
XX
XX Sequence 41 BP; 8 A; 14 C; 12 G; 7 T; 0 U; 0 Other;
SQ
Query Match 3.3%; Score 33; DB 1; Length 41;
Best Local Similarity 87.8%; Pred. No. 4.4e+02;
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

643 CCCAGGCTGAGTGCAGTGGCCGCAATCTTGCTCACTGCAA 683
DB 41 CCCAGGCTGAGTGCAGTGGCCGCAATCTTGCTCACTGCAA 1

RESULT 234
AB243560
ID AB243560 standard; DNA; 41 BP.
XX
XX AB243560;
AC
XX
XX 26-JUN-2003 (first entry)
XX
XX Human sulphotransferase TPST2 gene polymorphic site, #344.
XX
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;
XX
XX polymorphic site; drug evaluation; drug screening; genotyping;
XX
XX genetic profiling; therapeutic customisation; adverse reaction;
XX
XX clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT replace(21,C)
XX FT /*tag= a
XX FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX WO200252044-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-JP011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
XX
XX 02-MAY-2001; 2001JP-00135256.
XX
XX 27-AUG-2001; 2001JP-00256862.
XX
XX (RIKE ) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Satto S;
XX
XX WPI; 2002-563571/62.
XX
XX Identifying individuals having a polymorphism, useful for determining the
XX
XX effectiveness or side effect of a drug or treatment protocol, comprises
XX
XX detecting at least one polymorphism in the drug metabolizing enzyme
XX
XX nucleic acid.
XX
XX Claim 23; Page 69; 2785pp; English.
XX
XX Sequences AB243217-AB250887 represent polymorphic sites within genes
XX
XX encoding enzymes associated with drug metabolism. The invention relates
XX
XX to methods and compositions for identifying individuals who have at least
XX
XX one polymorphism in such drug metabolizing enzyme-encoding genes. The
XX
XX polymorphisms may be identified in a nucleic acid sample using probes or
XX
XX primers specific for a sequence selected from AB243217-AB250887 using a
XX
XX variety of detection assays, including hybridisation assays, nucleic acid
XX
XX arrays and PCR-based methods. The invention also encompasses methods of
XX
XX evaluating and screening drugs using genetic polymorphism data. Genetic
XX
XX polymorphism data, particularly that relating to single nucleotide
XX
XX polymorphisms (SNPs), may be used in studying the relationship between
XX
XX DNA sequence variations and human diseases, conditions, and responses to
XX
XX drugs. SNPs are also useful as polymorphism markers for discovering genes
XX
XX that cause or exacerbate certain diseases. SNPs are particularly useful
XX
XX in the above respects as they are stable in populations, occur
```

```
CC frequently, and have lower mutation rates than other genome variations
CC such as repeating sequences. The detection and analysis of polymorphisms
CC in genes encoding drug metabolising enzymes allows the customisation of
CC drug therapies based upon the genetic profile of individual patients.
CC This would not only take the guesswork out of selecting the drug with the
CC greatest therapeutic effect for a particular patient, but would also
CC reduce the likelihood of adverse reactions, thereby increasing safety.
CC Methods of the invention are also useful in the drug discovery and
CC approval processes. For example, individuals could be selected for
CC clinical trials only if their genetic profiles indicate that they are
CC capable of responding to a particular drug or drug class, and previously
CC failed drug candidates could be revived if they were matched with more
CC appropriate patient populations. The methods, data and compositions of
CC the invention may therefore lead to an increase in the range of
CC possible drug targets and decreases in the number of adverse drug
CC reactions, failed drug trials, the time taken for a drug to be approved,
CC the length of time patients are on medication and the number of different
CC medications a patient needs to take before finding an effective therapy
XX
XX Sequence 41 BP; 7 A; 10 C; 14 G; 10 T; 0 U; 0 Other;
SQ
Query Match 3.3%; Score 33; DB 1; Length 41;
Best Local Similarity 87.8%; Pred. No. 4.4e+02;
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

643 CCCAGGCTGAGTGCAGTGGCCGCAATCTTGCTCACTGCAA 683
DB 1 CCCAGGCTGAGTGCAGTGGCCGCAATCTTGCTCACTGCAA 41

RESULT 235
AB243980/c
ID AB243980 standard; DNA; 41 BP.
XX
XX AB243980;
AC
XX
XX 26-JUN-2003 (first entry)
XX
XX Human glutathione-S-transferase MGST3 gene polymorphic site, #764.
XX
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 1;
XX
XX polymorphic site; drug evaluation; drug screening; genotyping;
XX
XX genetic profiling; therapeutic customisation; adverse reaction;
XX
XX clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT replace(21,C)
XX FT /*tag= a
XX FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX WO200252044-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-JP011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
XX
XX 02-MAY-2001; 2001JP-00135256.
XX
XX 27-AUG-2001; 2001JP-00256862.
XX
XX (RIKE ) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Satto S;
XX
XX WPI; 2002-563571/62.
XX
XX Identifying individuals having a polymorphism, useful for determining the
XX
XX effectiveness or side effect of a drug or treatment protocol, comprises
XX
XX detecting at least one polymorphism in the drug metabolizing enzyme
XX
XX nucleic acid.
XX
```


DT 26-JUN-2003 (first entry)
XX Human ATP-binding cassette ABC1 gene polymorphic site, #4080.
DE
XX Human; drug metabolising enzyme; gene; drug metabolism; polymorphic site;
KM drug evaluation; drug screening; genotyping; genetic profiling;
KM therapeutic customisation; adverse reaction; clinical trial;
KW drug approval; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
FH
FH Key Location/Qualifiers
FT variation replace(21, G)
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX WO200252044-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-JP011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
XX 02-MAY-2001; 2001JP-00135256.
XX 27-AUG-2001; 2001JP-00256862.
XX
XX (RIKE) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Saito S;
PI
XX WPI; 2002-583571/62.
XX
XX Identifying individuals having a polymorphism, useful for determining the
PT effectiveness or side effect of a drug or treatment protocol, comprises
PT detecting at least one polymorphism in the drug metabolizing enzyme
PT nucleic acid.
XX
XX Claim 23; Page 138; 2785pp; English.
XX
XX Sequences AB243217-AB250887 represent polymorphic sites within genes
CC encoding enzymes associated with drug metabolism. The invention relates
CC to methods and compositions for identifying individuals who have at least
CC one polymorphism in such drug metabolising enzyme-encoding genes. The
CC polymorphisms may be identified in a nucleic acid sample using probes or
CC primers specific for a sequence selected from AB243217-AB250887 using a
CC variety of detection assays, including hybridisation assays, nucleic acid
CC arrays and PCR-based methods. The invention also encompasses methods of
CC evaluating and screening drugs using genetic polymorphism data. Genetic
CC polymorphism data, particularly that relating to single nucleotide
CC DNA sequence variations and human diseases, conditions, and responses to
CC drugs. SNPs are also useful as polymorphism markers for discovering genes
CC that cause or exacerbate certain diseases. SNPs are particularly useful
CC in the above respects as they are stable in populations, occur
CC frequently, and have lower mutation rates than other genome variations
CC such as repeating sequences. The detection and analysis of polymorphisms
CC in genes encoding drug metabolising enzymes allows the customisation of
CC drug therapies based upon the genetic profile of individual patients.
CC This would not only take the guesswork out of selecting the drug with the
CC greatest therapeutic effect for a particular patient, but would also
CC reduce the likelihood of adverse reactions, thereby increasing safety.
CC Methods of the invention are also useful in the drug discovery and
CC approval processes. For example, individual profiles could be selected for
CC clinical trials only if their genetic profiles indicate that they are
CC capable of responding to a particular drug or drug class, and previously
CC failed drug candidates could be revived if they were matched with more
CC appropriate patient populations. The methods, data and compositions of
CC the invention may therefore lead to an increase in the range of
CC possible drug targets and decreases in the number of adverse drug
CC reactions, failed drug trials, the time taken for a drug to be approved,
CC the length of time patients are on medication and the number of different
CC medications a patient needs to take before finding an effective therapy
XX

SEQ Sequence 41 BP; 11 A; 12 C; 12 G; 6 T; 0 U; 0 Other;
Query Match 3.3%; Score 33; DB 1; Length 41;
Best Local Similarity 87.8%; Pred. No. 4.4e+02;
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 369 TCCACCTGCTGAGCTCCCAAGCTGCTGATTCACAGCG 409
DB 41 TCCACTGCTGCTGAGCTCCCAAGCTGCTGATTCACAGCT 1
RESULT 238
ABA94080
ID ABA94080 standard; DNA; 41 BP.
AC
XX ABA94080;
XX
XX 08-MAY-2002 (first entry)
XX
XX Human multi-copper oxidase 12 probe 1 SEQ ID NO:8.
XX
XX Human; multi-copper oxidase 12; enzyme; cytostatic; haemostatic;
XX virocid; immunomodulatory; antiinflammatory; gene therapy;
XX malignant tumour; haemopathy; human immunodeficiency virus infection;
XX HIV infection; immunological disease; inflammation; probe; ss.
XX
XX Homo sapiens.
XX
XX WO200196572-A1.
XX
XX 20-DEC-2001.
XX
XX 14-MAY-2001; 2001WO-CN000786.
XX
XX 19-MAY-2000; 2000CN-00115756.
XX
XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
XX Mao Y, Xie Y;
PI
XX WPI; 2002-075593/10.
XX
XX Multi-copper oxidase 12 and encoding polynucleotide, used in diagnosis
PT and treatment of malignant tumors, hemopathy, human immunodeficiency
PT virus infection, immunological diseases and inflammation.
XX
XX Example 7; Page 14; 31pp; Chinese.
XX
XX The present invention describes human multi-copper oxidase 12 (I). (I)
CC has cytostatic, haemostatic, virocid, immunomodulatory and
CC antiinflammatory activities. The polynucleotide (II) encoding (I) can be
CC used in gene therapy. (I) and (II) can be used in the diagnosis and
CC treatment of malignant tumour, haemopathy, human immunodeficiency virus
CC (HIV) infection, immunological diseases and various inflammations. The
CC present sequence represents a probe which is used in an example from the
CC present invention
XX
XX Sequence 41 BP; 6 A; 6 C; 14 G; 15 T; 0 U; 0 Other;
QY
Query Match 3.3%; Score 33; DB 1; Length 41;
Best Local Similarity 87.8%; Pred. No. 4.4e+02;
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
DB 172 TTTTATTAGTAGAGATGAGTTTCTCCATGTTGTCAGGCT 212
1 TGTTTTATTAGTAGAGGCGGTTTCCACCATGTTGTCAGGCT 41
RESULT 239
AAS15590
ID AAS15590 standard; DNA; 41 BP.
XX
XX AAS15590;
AC

XX 14-FEB-2002 (first entry)
 XX Human DNA mismatch repair protein 10, probe #1.
 DE Human DNA mismatch repair protein 10, probe #1.
 XX Human; DNA mismatch repair protein 10; cytosolic; viral; cytidal;
 KW immunomodulatory; anti-inflammatory; haemostatic; anti-HIV; inflammation;
 KW human immunodeficiency virus; malignancy; haemopathy; infection;
 KW immunological disease; probe; ss.
 XX Homo sapiens.
 OS WO200175100-A1.
 PN 11-OCT-2001.
 PD 19-MAR-2001; 2001WO-CN000337.
 XX 22-MAR-2000; 2000CN-00115057.
 PR (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
 PA Mao Y, Xie Y;
 P1 WPI; 2002-025860/03.
 DR New human DNA mismatch repair protein 10 for diagnosing and treating
 XX malignancy, hemopathy, human immunodeficiency virus infection,
 PT immunological diseases and inflammation.
 PT Example 6; Page 15; 36pp; Chinese.
 PS The invention relates to an isolated polypeptide of human DNA mismatch
 XX repair protein 10. The polypeptide can be used for screening mimics,
 CC agonists, antagonists or inhibitors, or in peptide fingerprinting
 CC identification. The polynucleotide can be used as primers for nucleic
 CC acid amplification reactions, as probes for hybridisation reactions, or
 CC in producing gene chips or microarrays. Drug compositions, which contain
 CC the polypeptide, polynucleotide, mimics, agonists, antagonists,
 CC inhibitors and their preparations, can be used for treatment and diagnosis of
 CC diseases relating to the polypeptide. In particular, the polypeptide and
 CC encoded polynucleotide are applicable in diagnosis and treatment of
 CC malignancy, haemopathy, human immunodeficiency virus (HIV) infection,
 CC immunological diseases and various inflammations. The present sequence
 CC represents probe #1 used in Northern blot analysis of human DNA mismatch
 CC repair protein 10
 XX Sequence 41 BP; 8 A; 10 C; 11 G; 12 T; 0 U; 0 Other;
 SQ
 Query Match 3.3%; Score 33; DB 1; Length 41;
 Best Local Similarity 87.8%; Pred. No. 4.4e+02;
 Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 200 TGTTCAGAGCTGCTCGAAGCTCCGACCTCAGATGATC 240
 |||||
 Db 1 TGTTCAGAGCTGCTCGAAGCTCCGACCTCAGATGATC 41
 |||||
 RESULT 240
 ADL64285
 ID ADL64285 standard; DNA; 41 BP.
 AC
 XX ADL64285;
 XX 20-MAY-2004 (first entry)
 DE Human single nucleotide polymorphism (SNP) #208.
 XX
 KW ss; human; single nucleotide polymorphism; SNP;
 KW C1 S subcomponent protein; C1S; alanyl aminopeptidase protein; ANPP;
 KW meprin A beta protein; aminopeptidase P-like protein; XPN-PEPL;
 KW tissue kallikrein protein; KTK1; aminopeptidase P protein; MEPIB;
 KW soluble guanylate cyclase 1 alpha-2 subunit protein; GUCY1A2; haplotype;

KW angioedema; angioedema-like disorder; paternity testing;
 KW cardiovascular diseases; angina pectoris; hypertension; heart failure;
 KW myocardial infarction; aneurysm; stroke; embolism; thrombosis;
 KW coronary artery disease; arteriosclerosis; hypersensitivity;
 KW haemodialysis; sepsis; inflammatory disease; inflammatory arthritis;
 KW asthma; chronic obstructive pulmonary disease; cough reflex; allergy;
 KW cancer; ANPP.
 XX
 OS Homo sapiens.
 XX US2004033582-A1.
 PN 19-FEB-2004.
 PD 03-JUN-2003; 2003US-00453827.
 XX 03-JUN-2002; 2002US-0384980P.
 PR (EDMO/) EDMONDS M.
 PA (HUI/) HUI L.
 PA (PERR/) PERRONE M.
 PA (POWE/) POWELL J R.
 PA (RAMA/) RAMANATHAN C S.
 PA (SWAN/) SWANSON B.
 PA (TSUC/) TSUCHIHASHI Z.
 PA (ZERR/) ZERRA K.
 XX Edmonds M, Hui L, Perrone M, Powell JR, Ramanathan CS, Swanson B;
 P1 Tsuchihashi Z, Zerba K;
 P1 WPI; 2004-180052/17.
 DR
 XX New nucleic acid comprising a single nucleotide polymorphism at a
 PT specific location, useful in paternity testing, genetic analysis or
 PT diagnosing, preventing or treating cardiovascular diseases e.g.
 PT angioedema or angina pectoris.
 PS Claim 3; SEQ ID NO 208; 376pp; English.
 XX The invention relates to an isolated nucleic acid (1) derived from a
 CC human gene encoding a protein, such as the C1 S subcomponent protein
 CC (C1S), the alanyl aminopeptidase protein (ANPP), the meprin A, beta
 CC protein (MEPIB), the aminopeptidase P-like protein (XPN-PEPL), the tissue
 CC kallikrein protein (KTK1), the membrane bound aminopeptidase P protein
 CC (XNPP2), or the soluble guanylate cyclase 1, alpha-2 subunit protein
 CC (GUCY1A2). The nucleic acid comprises at least one polymorphic position,
 CC including the alleles, reference alleles and alternate alleles of the
 CC single nucleotide polymorphisms, listed in the specification. The
 CC polymorphic position resides in a (non)coding position within the genomic
 CC sequence of the gene. The polymorphic position residing in the translated
 CC position results in a missense or silent mutation of the translated
 CC product of the gene. The polymorphic position residing in a non-coding
 CC position resides within the untranslated region or an intronic region of
 CC the gene. Constructing haplotypes using the nucleic acids above further
 CC comprises using the haplotypes to identify an individual for the presence
 CC of a disease phenotype, and correlating the presence of the disease
 CC phenotype with the haplotype. The disease phenotype is angioedema or an
 CC angioedema-like disorder. The nucleic acids, primers and probes are
 CC useful in phenotype correlations, paternity testing, medicine and genetic
 CC analysis. The nucleic acids and polypeptides can be used in diagnosing,
 CC preventing or treating cardiovascular diseases, e.g. angioedema, angina
 CC pectoris, hypertension, heart failure, myocardial infarction, aneurysm,
 CC stroke, embolism, thrombosis, coronary artery disease or
 CC arteriosclerosis, hypersensitivity reactions during haemodialysis,
 CC sepsis, inflammatory diseases, inflammatory arthritis, asthma, chronic
 CC obstructive pulmonary disease, cough reflex, allergies, or cancer. The
 CC present sequence represents a human single nucleotide polymorphism (SNP)
 CC of the invention.
 XX Sequence 41 BP; 5 A; 14 C; 11 G; 11 T; 0 U; 0 Other;
 SQ
 Query Match 3.3%; Score 33; DB 1; Length 41;
 Best Local Similarity 87.8%; Pred. No. 4.4e+02;

Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 659 GGGGGCAATCTGGCTCACTGCAACCTCTGCTCCGGAT 699
 DB 1 GTGTGTGATCTCGGCTCACTGCAACCTCTGCTCCAGAT 41

RESULT 241

ADL64286
 ID ADL64286 strand; DNA; 41 BP.

ADL64286;
 AC 20-MAY-2004 (first entry)

DE Human single nucleotide polymorphism (SNP) #209.

XX ss; human; single nucleotide polymorphism; SNP;
 KW C1 S subcomponent protein; C1S; alanyl aminopeptidase protein; ANPEP;
 KW mepirin A beta protein; aminopeptidase P-like protein; XPN-PEP;
 KW tissue kallikrein protein; KLK1; aminopeptidase P protein; MEPIB;
 KW soluble guanylate cyclase 1 alpha-2 subunit protein; GUCY1A2; haploctype;
 KW angioedema; angioedema-like disorder; paternity testing; heart failure;
 KW cardiovascular diseases; angina pectoris; hypertension; heart failure;
 KW myocardial infarction; aneurysm; stroke; embolism; thrombosis;
 KW coronary artery disease; arteriosclerosis; hypersensitivity;
 KW haemodialysis; sepsis; inflammatory disease; inflammatory arthritis;
 KW asthma; chronic obstructive pulmonary disease; cough reflex; allergy;
 KW cancer; ANPEP.

XX Homo sapiens.

XX US2004033582-A1.

XX 19-FEB-2004.

XX 03-JUN-2003; 2003US-00453827.

XX 03-JUN-2002; 2002US-0384980P.

XX (EDMO/) EDMONDS M.

XX (HUI/) HUI L.

XX (PERR/) PERRONE M.

XX (POWE/) POWELL J R.

XX (RAMA/) RAMANATHAN C S.

XX (SWAN/) SWANSON B.

XX (TSUC/) TSUCHIHASHI Z.

XX (ZERR/) ZERRA K.

XX Edmonds M, Hui L, Perrone M, Powell JR, Ramanathan CS, Swanson B;
 PI Tsuchihashi Z, Zerba K;
 DR WPI; 2004-180052/17.

XX New nucleic acid comprising a single nucleotide polymorphism at a
 PT specific location, useful in paternity testing, genetic analysis or
 PT diagnosing, preventing or treating cardiovascular diseases e.g.
 PT angioedema or angina pectoris.

XX Claim 3; SEQ ID NO 209; 376pp; English.

XX The invention relates to an isolated nucleic acid (I) derived from a
 CC human gene encoding a protein, such as the C1 S subcomponent protein
 CC (C1S), the alanyl aminopeptidase protein (ANPEP), the mepirin A, beta
 CC protein (MEPIB), the aminopeptidase P-like protein (XPN-PEP), the tissue
 CC kallikrein protein (KLK1), the membrane bound aminopeptidase P protein
 CC (XPNPEP2), or the soluble guanylate cyclase 1, alpha-2 subunit protein
 CC (GUCY1A2). The nucleic acid comprises at least one polymorphic position,
 CC including the alleles, reference alleles and alternate alleles of the
 CC single nucleotide polymorphisms, listed in the specification. The
 CC polymorphic position resides in a (non)coding position within the genomic
 CC sequence of the gene. The polymorphic position residing in a coding
 CC position results in a missense or silent mutation of the translated

CC product of the gene. The polymorphic position residing in a non-coding
 CC position resides within the untranslated region or an intronic region of
 CC the gene. Constructing haplotypes using the nucleic acids above further
 CC comprises using the haplotypes to identify an individual for the presence
 CC of a disease phenotype, and correlating the presence of the disease
 CC phenotype with the haplotype. The disease phenotype is angioedema or an
 CC angioedema-like disorder. The nucleic acids, primers and probes are
 CC useful in phenotype correlations, paternity testing, medicine and genetic
 CC analysis. The nucleic acids and polypeptides can be used in diagnosing,
 CC preventing or treating cardiovascular diseases, e.g. angioedema, angina
 CC pectoris, hypertension, heart failure, myocardial infarction, aneurysm,
 CC stroke, embolism, thrombosis, coronary artery disease or
 CC arteriosclerosis, hypersensitivity reactions during haemodialysis,
 CC sepsis, inflammatory diseases, inflammatory arthritis, asthma, chronic
 CC obstructive pulmonary disease, cough reflex, allergies, or cancer. The
 CC present sequence represents a human single nucleotide polymorphism (SNP)
 CC of the invention.

XX Sequence 41 BP; 11 A; 13 C; 8 G; 9 T; 0 U; 0 Other;

XX Query Match 3.3%; Score 33; DB 1; Length 41;
 XX Best Local Similarity 87.8%; Pred. No. 4.4e+02;

XX Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 557 AGCTGGACCAAGACATGACACCTACACCTGGCTAATT 597
 DB 1 AGCTGGATTACAGACATGCCCCACACACCTGGCTAATT 41

RESULT 242

ABZ48532
 ID ABZ48532 strand; DNA; 40 BP.

XX ABZ48532;

XX 26-JUN-2003 (first entry)

XX Human oligopeptide transporter PEPT1 gene polymorphic site, #5315.

XX Human; drug metabolizing enzyme; gene; drug metabolism; polymorphic site;
 KW drug evaluation; drug screening; genotyping; genetic profiling;
 KW therapeutic customisation; adverse reaction; clinical trial;

XX drug approval; ds.

XX Homo sapiens.

XX OS

XX Key

XX variation

XX Location/Qualifiers

XX replace(20..21,GGT)

XX /tag= a

XX MO200252044-A2.

XX 04-JUL-2002.

XX 27-DEC-2001; 2001WO-DP011592.

XX 27-DEC-2000; 2000JP-00399443;

XX 02-MAY-2001; 2001JP-00135256.

XX 27-AUG-2001; 2001JP-00256862.

XX (RIKE) RIKEN KK.

XX Nakamura Y, Sekine A, Iida A, Saito S;
 PI WPI; 2002-583571/62.

XX Identifying individuals having a polymorphism, useful for determining the
 PT effectiveness or side effect of a drug or treatment protocol, comprises
 PT detecting at least one polymorphism in the drug metabolizing enzyme
 PT nucleic acid.

XX Claim 23; Page 168; 2785pp; English.

CC Sequences AB243217-AB250887 represent polymorphic sites within genes
CC encoding enzymes associated with drug metabolism. The invention relates
CC to methods and compositions for identifying individuals who have at least
CC one polymorphism in such drug metabolizing enzyme-encoding genes. The
CC polymorphisms may be identified in a nucleic acid sample using probes or
CC primers specific for a sequence selected from AB243217-AB250887 using a
CC variety of detection assays, including hybridisation assays, nucleic acid
CC arrays and PCR-based methods. The invention also encompasses methods of
CC evaluating and screening drugs using genetic polymorphism data. Genetic
CC polymorphism data, particularly that relating to single nucleotide
CC polymorphisms (SNPs), may be used in studying the relationship between
CC DNA sequence variations and human diseases, conditions, and responses to
CC drugs. SNPs are also useful as polymorphism markers for discovering genes
CC that cause or exacerbate certain diseases. SNPs are particularly useful
CC in the above respects as they are stable in populations, occur
CC frequently, and have lower mutation rates than other genome variations
CC such as repeating sequences. The detection and analysis of polymorphisms
CC in genes encoding drug metabolizing enzymes allows the customisation of
CC drug therapies based upon the genetic profile of individual patients.
CC This would not only take the guesswork out of selecting the drug with the
CC greatest therapeutic effect for a particular patient, but would also
CC reduce the likelihood of adverse reactions, thereby increasing safety.
CC Methods of the invention are also useful in the drug discovery and
CC approval processes. For example, individuals could be selected for
CC clinical trials only if their genetic profiles indicate that they are
CC capable of responding to a particular drug or drug class, and previously
CC failed drug candidates could be revived if they were matched with more
CC appropriate patient populations. The methods, data and compositions of
CC the invention may therefore lead to an increase in the range of
CC possible drug targets and decreases in the number of adverse drug
CC reactions, failed drug trials, the time taken for a drug to be approved,
CC the length of time patients are on medication and the number of different
CC medications a patient needs to take before finding an effective therapy

CC SQ Sequence 40 BP; 9 A; 7 C; 11 G; 13 T; 0 U; 0 Other;

Query Match 3.2%; Score 32; DB 1; Length 40;
Best Local Similarity 87.5%; Pred. No. 4.9e+02;
Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1076 TATTTTCATTAGAGCGGGGTTTCACCATTTTGTTCAGGC 1115
DB 1 TATTTTATAGTAGAGCGGGGTTTCACCATTTTGTTCAGGC 40

RESULT 243

AAQ45257/c
ID AAQ45257 standard; DNA; 35 BP.

AC AAQ45257;

DT 25-MAR-2003 (revised)
DT 28-OCT-1994 (first entry)

XX Alu primer PDJ34 to amplify Yeast Artificial Chromosome DNA.

XX Yeast Artificial Chromosome; YAC; polymerase chain reaction; PCR;

KW sequence tagged site; genetic disorder; diagnosis; abnormality;
KW Prader-Willi; Angelman; Beckwith-Wiedemann; syndrome; ss.

XX Synthetic.

XX WO9406936-A1.

XX 31-MAR-1994.

XX 10-SEP-1993; 93WO-US008501.

XX 11-SEP-1992; 92US-00943639.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX Althart SD, Multirangura A, Ledbetter DH;

XX WPI; 1994-118484/14.

XX Diagnosis of genetic disorders associated with chromosomal abnormalities
XX and uniparental disomy, e.g. Prader-Willi/Angelman syndrome - using in
XX situ hybridisation using probes spanning the 1R4-3R or GABRB3 regions.

XX Example 5; Page 32; 91pp; English.

XX The Alu primers PDJ34 and 2484 (AAQ45257 and AAQ45258) were used to
XX amplify DNA from yeast artificial chromosomes as part of a cloning
XX procedure to isolate probes for specific chromosomal abnormalities. In
XX particular, probes to diagnose Prader-Willi/Angelman Syndrome were
XX identified. The majority of PWS/Angelman patients are deleted for a
XX common set of markers including MLJ4, IR4-3R, TD189-1 and TD3- 21.
XX (Updated on 25-MAR-2003 to correct PW field.)

CC SQ Sequence 35 BP; 5 A; 9 C; 8 G; 5 T; 0 U; 8 Other;

Query Match 3.2%; Score 31.8; DB 1; Length 35;
Best Local Similarity 77.1%; Pred. No. 4.5e+02;
Matches 27; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

OY 643 CCCAGGCTGAGTGTGAGTGGCGCAATCTTGCTCA 677
DB 35 CCCAGGCTGAGTGTGAGTGGCGCAATCTTGCTCA 1

RESULT 244

ABA93847/c
ID ABA93847 standard; DNA; 35 BP.

AC ABA93847;

DT 02-MAY-2002 (first entry)

XX Human GASCT PCR primer SEQ ID NO:5.

XX Human; GASCT; gene amplified in squamous cell carcinoma 1; cancer;

KW chromosome 9; chromosome 9p23-24; cell differentiation; gene therapy;
KW cell proliferation; PCR primer; ss.

XX Homo sapiens.

XX WO200196566-A1.

XX 20-DEC-2001.

XX 12-JUN-2001; 2001WO-JP004959.

XX 12-JUN-2000; 2000JP-00174946.

XX (SAKA) OTSUKA PHARM CO LTD.

XX Inazawa J, Imoto I;

XX WPI; 2002-090209/12.

XX Gene GASCT amplified in squamous cell carcinoma and its expression
XX product for diagnosis investigation and treatment of disorders involving
XX cell proliferation such as cancer.

XX Example 1; Page 77; 82pp; Japanese.

XX The present invention describes human GASCT (gene amplified in squamous
XX cell carcinoma 1). GASCT has been located to the p23-24 region of human
XX chromosome 9. GASCT can be used in the diagnosis and investigation of
XX diseases with which cell differentiation and proliferation are
XX associated, such as cancer. It can also be used in gene therapy of these
XX diseases, and screening substances for their ability to modify the
XX expression of GASCT and for use as drugs. The present sequence represents
XX a PCR primer for human GASCT, which is used in an example from the
XX present invention

XX Sequence 35 BP; 5 A; 9 C; 8 G; 5 T; 0 U; 8 Other;
 SQ Query Match 3.2%; Score 31.8; DB 1; Length 35;
 Best Local Similarity 77.1%; Pred. No. 4.5e+02;
 Matches 27; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
 QY 643 CCCAGGCTGAGTGCAGTGGCCCAATCTTGCTCA 677
 DB 35 CCCAGGCTGAGTGCAGTGGCCCAATCTTGCTCA 1
 RESULT 245
 AAQ27392/c
 ID AAQ27392 standard; DNA; 35 BP.
 XX
 AC AAQ27392;
 DT 25-MAR-2003 (revised)
 DT 27-JAN-1993 (first entry)
 XX
 DE Inter-Alu specific primer PDJ34.
 KM Polymerase chain reaction; PCR; repetitive element; ss.
 XX
 OS Synthetic.
 XX
 PN MO9213101-A1.
 XX
 PD 06-AUG-1992.
 XX
 PF 24-JAN-1992; 92MO-NL000018.
 XX
 PR 25-JAN-1991; 91NL-00000132.
 XX
 PA (INGE-) INGENY BV.
 XX
 PI Uiterlinden AG, Vlij J;
 XX
 DR MPI; 1992-284683/34.
 XX
 PT Detection of genetic variation by 2-D electrophoresis of fragments - and
 PT hybridisation with labelled probes, carried out on fragments consisting
 PT of inter-repeat sequences generated by PCR.
 XX
 PS Claim 6; Page 6; 31pp; English.
 XX
 CC Primer PDJ34 is one of several primers which are preferred for use in
 CC amplifying inter-Alu regions of DNA. The amplified fragments are then
 CC subjected to 2-D electrophoresis on the basis of length and differences
 CC in base sequence. The resulting separation pattern is transferred to a
 CC filter for screening with a probe. The method can be used to detect
 CC genetic variation. See AAQ27389-Q27404 and AAQ33141-Q33144. (Updated on
 CC 25-MAR-2003 to correct FN field.)
 CC
 XX
 SQ Sequence 35 BP; 6 A; 12 C; 11 G; 5 T; 0 U; 1 Other;
 QY Query Match 3.2%; Score 31.4; DB 1; Length 35;
 Best Local Similarity 91.4%; Pred. No. 4.7e+02;
 Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 643 CCCAGGCTGAGTGCAGTGGCCCAATCTTGCTCA 677
 DB 35 CCCAGGCTGAGTGCAGTGGCCCAATCTTGCTCA 1
 RESULT 246
 ADE14248/c
 ID ADE14248 standard; DNA; 32 BP.
 XX
 AC ADE14248;
 XX
 DT 29-JAN-2004 (first entry)

XX Optineurin promoter motif, repeat element or regulatory region #357.
 DE Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
 XX SNP; glaucoma; progressive ocular hypertensive disorder;
 KM glaucoma related disorder; motif; repeat element; regulatory region.
 XX
 OS Homo sapiens.
 XX
 PN US2003190617-A1.
 XX
 PD 09-OCT-2003.
 XX
 PF 06-MAR-2002; 2002US-00091281.
 XX
 PR 06-MAR-2002; 2002US-00091281.
 XX
 PA (SIE/) SI E.
 PA (RAYM/) RAYMOND V.
 PA (MORI/) MORISSETTE J.
 XX
 PI Raymond V, Morissette J, Si E;
 XX
 DR MPI; 2003-864168/80.
 XX
 PT New nucleic acid sequences of the optineurin gene are useful to detect
 PT polymorphisms particularly single nucleotide polymorphisms in the
 PT optineurin promoter to diagnose, prognose and treat glaucoma and related
 PT disorders.
 XX
 PS Claim 11; SEQ ID NO 359; 159pp; English.
 XX
 CC The invention relates to an isolated nucleic acid (NI) comprising at
 CC least 20 but not more than 1500 consecutive nucleotides of the optineurin
 CC promoter appearing as ADE13890. Also included are the optineurin promoter
 CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
 CC detecting a single nucleotide polymorphism (SNP) in the optineurin
 CC promoter, a host cell comprising the promoter operably linked to a
 CC heterologous sequence, diagnosing or prognosing glaucoma in a sample
 CC obtained from a cell or bodily fluid (comprising detecting a polymorphism
 CC in a promoter region of the optineurin gene, associated with a glaucoma
 CC phenotype), detecting a SNP sequence variation in a sample containing
 CC DNA, detecting the presence of an optineurin promoter sequence variation
 CC in a sample containing DNA, determining the presence or increased
 CC susceptibility to glaucoma or to a progressive ocular hypertensive
 CC disorder resulting in loss of visual field in a patient (or the severity
 CC or progression of glaucoma in a patient, comprising providing
 CC amplification reaction primers that direct amplification of a selected
 CC nucleic acid region containing the variation within the optineurin
 CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
 CC obtaining a sample containing human genomic DNA, providing a nucleic acid
 CC capable of detecting a SNP located within an optineurin promoter, and
 CC detecting the polymorphism). The invention is used to diagnose and
 CC prognose glaucoma and also to treat glaucoma related disorders. The
 CC present sequence is an optineurin promoter motif, repeat element or
 CC putative regulatory region.
 CC
 XX
 SQ Sequence 32 BP; 5 A; 12 C; 8 G; 7 T; 0 U; 0 Other;
 QY Query Match 3.1%; Score 30.4; DB 1; Length 32;
 Best Local Similarity 96.9%; Pred. No. 5e+02;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 860 AAGTGTGGGATTACAGGCGTGAGCCACGACG 891
 DB 32 AAGTGTGGGATTACAGGCGTGAGCCACGCG 1
 RESULT 247
 AAH91142/c
 ID AAH91142 standard; DNA; 36 BP.
 XX
 AC AAH91142;

XX	09-OCT-2001	(first entry)	
DT			
XX	Human inflammatory bowel disease associated polymorphic site #217.		
XX			
XX	Human inflammatory bowel disease; Crohn's disease; ulcerative colitis;		
KW	single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;		
KW	chromosome 5q31-33; forensic test; gene therapy; db.		
XX			
OS	Homo sapiens.		
XX			
FH			
FT	Key	Location/Qualifiers	
FT	misc_feature	19	
XX		/*tag= a	
XX		/note= "SNP, optionally G or T at this position"	
PN	WO200142511-A2.		
PD	14-JUN-2001.		
XX			
PF	11-DEC-2000; 2000WO-US033632.		
XX			
PR	10-DEC-1999; 99US-0170257P.		
PR	10-APR-2000; 2000US-0196046P.		
XX			
PA	(WHED) WHITEHEAD INST BIOMEDICAL RES.		
XX	(ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.		
PI	Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;		
XX			
DR	WPI; 2001-367874/38.		
XX			
PT	Testing for the presence of polymorphisms associated with inflammatory		
PT	bowel disease, using a hybridization assay.		
XX			
PS	Claim 1; Page 48; 463pp; English.		
XX			
CC	The present invention describes a method for detecting the presence of		
CC	polymorphisms associated with inflammatory bowel diseases such as		
CC	ulcerative colitis and Crohn's disease. The methods can be used to detect		
CC	the presence of genetic polymorphisms associated with inflammatory bowel		
CC	disease and correlating their occurrence with disease states. They may be		
CC	used in this way for phenotypic correlations, forensics, paternity		
CC	testing, medicine and genetic analysis. The present sequence is a		
CC	polymorphic site described in the exemplification of the invention.		
XX			
SO	Sequence 36 BP; 5 A; 10 C; 13 G; 7 T; 0 U; 1 Other;		
	Query Match	3.1%; Score 30.2; DB 1; Length 36;	
	Best Local Similarity	88.9%; Pred. No. 5.5e+02;	
	Matches	32; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
QY	1032 AGCTGGATTACGGGACACTGCACACACCCCGCT	1067	
Db	36 AGCTGGATTACAGGCANCTGCACACACCCCGCT	1	
	RESULT 248		
	ACC84462		
ID	ACC84462 standard; DNA; 30 BP.		
XX			
AC	ACC84462;		
XX			
DT	28-AUG-2003 (first entry)		
XX			
DE	NTP peptide encoding sequence #9.		
XX			
KW	Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;		
KW	neural thread protein; NTP; tumour; db.		
XX			
OS	Unidentified.		
XX			
PN	WO2003008443-A2.		

XX 30-JAN-2003.
PD
XX
PF 19-JUL-2002; 2002W0-CA001105.
XX
PR 19-JUL-2001; 2001US-0306150P.
XX
PR 19-JUL-2001; 2001US-030615P.
XX
PR 16-NOV-2001; 2001US-0331477P.
XX
PA (NTMO-) NTMOX CORP.
XX
PI Averbach PA;
XX
DR MPI: 2003-247999/24.
XX
P-PDB: ABR63257.
XX
PT Novel neural thread protein peptide, referred as cell death peptide,
XX useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
XX atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.
PS Disclosure; Page 17; 77pp; English.
XX
XX The present invention relates to a neural thread protein (NTP) peptide
CC referred to as cell death peptide. Thought to be cytostatic,
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for
CC treating a condition in a patient requiring removal or destruction of
CC cells, for treating a condition such as benign or malignant tumor,
CC inflammatory disease, autoimmune disease and infectious disease. The
CC peptide useful for treatment is derived from the amino acid sequence for
CC a pancreatic thread protein. The peptide is conjugated, linked or bound
CC to a molecule chosen from antibody or its fragment, antibody-like binding
CC molecule, where the molecule has a higher affinity for binding to a tumor
CC or other target than binding to other cells. Treatment using NTP peptides
CC can remove benign tumors with less risk and fewer of the undesirable side
XX effects of surgery. The present sequence is an NTP encoding sequence

Seq Sequence 30 BP; 6 A; 9 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 3.0%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 720 AGCTTCCTGAGTAGCTGGGATACAGCGC 749
|||||
1 AGCTTCCTGAGTAGCTGGGACTACAGCGC 30

RESULT 249
ADEI4029/C
ID ADEI4029 standard; DNA; 32 BP.
XX
AC ADEI4029;
XX
DT 29-JAN-2004 (first entry)
XX
DS Optineurin promoter motif, repeat element or regulatory region #18.
XX
KW Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
XX SNP; glaucoma; progressive ocular hypertensive disorder;
XX glaucoma related disorder; motif; repeat element; regulatory region.
XX
OS Homo sapiens.
XX
PN US2003190617-A1.
XX
PD 09-OCT-2003.
XX
PF 06-MAR-2002; 2002US-00091281.
XX
PR 06-MAR-2002; 2002US-00091281.
XX
PA (SIEE/) SI E.
XX (RAYM/) RAYMOND V.

PA (MORI/) MORISSETTE J.
 XX
 PI Raymond V, Morissette J, Si E;
 XX
 XX WPI; 2003-864168/80.
 DR
 XX New nucleic acid sequences of the optineurin gene are useful to detect
 PT polymorphisms particularly single nucleotide polymorphisms in the
 PT optineurin promoter to diagnose, prognose and treat glaucoma and related
 PT disorders.
 XX
 PS Claim 11; SEQ ID NO 140; 159pp; English.
 XX
 XX The invention relates to an isolated nucleic acid (N1) comprising at
 CC least 20 but not more than 1500 consecutive nucleotides of the optineurin
 CC promoter appearing as ABE13890. Also included are the optineurin promoter
 CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
 CC detecting a single nucleotide polymorphism (SNP) in the optineurin
 CC promoter, a host cell comprising the promoter operably linked to a
 CC heterologous sequence, diagnosing or prognosing glaucoma in a sample
 CC obtained from a cell or bodily fluid (comprising detecting a polymorphism
 CC in a promoter region of the optineurin gene, associated with a glaucoma
 CC phenotype), detecting the presence of an optineurin promoter sequence variation
 CC in a sample containing DNA, determining the presence or increased
 CC susceptibility to glaucoma or to a progressive ocular hypertensive
 CC disorder resulting in loss of visual field in a patient (or the severity
 CC or progression of glaucoma in a patient, comprising providing
 CC amplification reaction primers that direct amplification of a selected
 CC nucleic acid region containing the variation within the optineurin
 CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
 CC obtaining a sample containing human genomic DNA, providing a nucleic acid
 CC capable of detecting a SNP located within an optineurin promoter, and
 CC detecting the polymorphism). The invention is used to diagnose and
 CC prognose glaucoma and also to treat glaucoma related disorders. The
 CC present sequence is an optineurin promoter motif, repeat element or
 CC putative regulatory region.
 XX
 SQ Sequence 32 BP; 5 A; 11 C; 9 G; 7 T; 0 U; 0 Other;
 Query Match 3.0%; Score 29.4; DB 1; Length 32;
 Best Local Similarity 96.8%; Pred. No. 5.5e+02;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 860 AAGTCTGGATTACAGCGGTGAGCCACGAC 890
 DB 32 AAGTCTGGATTACAGCGGTGAGCCACGAC 2
 RESULT 250
 AAQ73572
 ID AAQ73572 standard; DNA; 31 BP.
 XX
 XX AAQ73572;
 AC
 XX 25-MAR-2003 (revised)
 DT 25-JUN-1995 (first entry)
 DT
 XX Enhancer element er-4 conserved basepair sequence.
 DE
 XX Enhancer element; carcinoma; tumor; cancer; SLP1 gene;
 KW secretory leukoprotease-inhibitor gene; cytokeatin gene-8; ss.
 KW
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH misc_difference 14
 FT /*tag= a
 FT /label= purine
 FT misc_difference 24
 FT /*tag= b
 FT /label= pyrimidine
 XX

PN MO9421118-A1.
 XX
 XX 29-SEP-1994.
 PD
 XX 24-MAR-1994; 94WO-US003197.
 XX
 XX 24-MAR-1994;
 PF
 XX 24-MAR-1993; 93US-00035435.
 PR
 XX (UABR-) UAB RES FOUND.
 PA
 XX Garver RI, Sorscher EJ;
 PI
 XX WPI; 1994-316537/39.
 DR
 XX
 XX DNA construct for treating human carcinoma - includes a cancer-
 PT therapeutic gene under the control of a promoter and a gp. of enhancer
 PT sequences.
 PS
 XX Claim 1; Fig 6; 54pp; English.
 XX
 XX This enhancer element is part of a DNA construct used for treating human
 CC carcinoma which contains a cancer therapeutic protein under the control
 CC of a promoter and 3 enhancer sequences in a specific 5'-3' order. This
 CC enhancer element is derived from the flanking region of the human
 CC epithelial cell cytokeratin-8 gene. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 CC
 SQ Sequence 31 BP; 6 A; 10 C; 8 G; 5 T; 0 U; 2 Other;
 Query Match 2.9%; Score 29; DB 1; Length 31;
 Best Local Similarity 93.5%; Pred. No. 5.7e+02;
 Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 378 CTCAGCTCCCAAGTCTGGATTACAGC 408
 DB 1 CTCAGCTCCCAAGTCTGGATTACAGC 31
 RESULT 251
 AAA04659
 ID AAA04659 standard; DNA; 29 BP.
 XX
 XX AAA04659;
 AC
 XX 22-MAY-2000 (first entry)
 DT
 DT Polymorphic fragment of hypertension associated gene TBXA2R.
 DE
 XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
 KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
 KW Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
 KW polycystic kidney disease; von Willebrand disease; forensic; human;
 KW tuberosus sclerosis; hereditary hemorrhagica telangiectasia;
 KW familial colonic polyposis; osteogenesis imperfecta; porphyria;
 KW Ehlers-Danlos syndrome; ss.
 KW
 OS Homo sapiens.
 XX
 XX EP955382-A2.
 PN
 XX 10-NOV-1999.
 PD
 XX 07-MAY-1999; 99EP-00250150.
 XX
 XX 07-MAY-1998; 98US-0084641P.
 PR
 XX 03-MAY-1999; 99US-00304232.
 XX
 XX (AFFY-) AFFYMETRIX INC.
 PA (UYCA-) UNIV CASE WESTERN RESERVE.
 PA
 XX Fan JB, Chakravarti A, Haisuka MK;
 PI
 XX WPI; 2000-107928/10.
 DR

XX Novel nucleic acids containing polymorphisms used in the diagnosis of
PT hypertension.
PS Claim 1; Page 43; 53pp; English.
XX The invention provides polymorphic fragments of genes associated with
CC hypertension. The nucleic acids including the polymorphic sites can be
CC used as probes or primers for expressing variant proteins. Detection of
CC the polymorphisms is useful in designing prophylactic and therapeutic
CC regimes customized to underlying abnormalities. The polymorphisms can be
CC used for association studies for hypertension, and in hypertension
CC diagnostic assays. Where the polymorphisms have strong correlation with
CC hypertension, within a gene, they are likely to have a causative role in
CC hypertension. This information can be used to find the precise role of a
CC polymorphism in the disease, and this can be used to identify potential
CC drugs which combat the disease. The polymorphisms can be tested for
CC association with other diseases e.g. agammaglobulinemia, diabetes
CC insipidus, Leach-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,
CC tuberos sclerosis, hereditary hemorrhagica telangiectasia, familial
CC colonic polyps, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
CC acute intermittent porphyria. The polymorphic forms can also be used in
CC forensics to identify individuals
XX
SQ Sequence 29 BP; 5 A; 8 C; 10 G; 5 T; 0 U; 1 Other;
Query Match 2.8%; Score 27.6; DB 1; Length 29;
Best Local Similarity 96.4%; Pred. No. 6.3e+02;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Gy 643 CCAGGCTGAGTGCAGTGGCCATCT 670
Db 1 CCCAGCTGAGTGTAGTGGCCATCT 28
RESULT 252
AAH37977/C
ID AAH37977 standard; DNA; 29 BP.
AC AAH37977;
DT 14-AUG-2001 (first entry)
DE SNP specific upper PCR primer SEQ ID 773.
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
KW Leach-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX Homo sapiens.
OS
XX MO200129262-A2.
PN 26-APR-2001.
PD 13-OCT-2000; 2000WO-US028436.
PF 15-OCT-1999; 99US-0160096P.
PR (ORCH-) ORCHID BIOSCIENCES INC.
PA Picoult-Newburg L, Fohl M;
PI
XX MPI; 2001-290930/30.
DR New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.

XX Claim 1; Page 53; 83pp; English.
PS Sequences AAH37205 - AAH09944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinemia, diabetes insipidus, Leach-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence
XX
SQ Sequence 29 BP; 12 A; 7 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 2.8%; Score 27.4; DB 1; Length 29;
Best Local Similarity 96.6%; Pred. No. 6.4e+02;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Gy 774 GTATTTAGTAGAGATGGGTTCCACCAT 802
Db 29 GTATTTAGTAGAGATGGGTTCCACCAT 1
RESULT 253
AAH06467
ID AAH06467 standard; DNA; 31 BP.
AC AAH06467;
DT 31-MAR-1999 (first entry)
DE Human biallelic polymorphic DNA fragment SGC34924.
XX Polymorphism; biallelic; paternity testing; forensic; genetic mapping;
KW phenotypic typing; medication; disease; marker; human; ss.
XX Homo sapiens.
OS
XX WO9858529-A2.
PN 30-DEC-1998.
PD 22-JUN-1998; 98WO-US012930.
PF 24-JUN-1997; 97US-0050594P.
PR (AFFY-) AFFYMETRIX INC.
PA Lipschutz RJ, Chee M, Fan J, Berno A;
PI
XX MPI; 1999-080963/07.
DR New nucleic acid segments containing polymorphic sites - used for, e.g.
PT detecting a disease phenotype, in forensics, paternity testing or genetic
PT mapping of phenotypic traits.
PS Claim 1; Page 29; 61pp; English.
XX

CC Sequences AAX06101-X06558 represent human DNA fragments which contain
CC diallelic polymorphic markers. The base occupying the polymorphic site is
CC indicated by the appropriate IUPAC-IUB ambiguity code. These fragments
CC can be used in a method for determining polymorphic forms in an
CC individual. The invention further provides computer-readable storage
CC medium for storing data for access by an application programme being
CC executed on a data processing system. Such a method comprises a data
CC structure stored in the computer-readable storage medium, the data
CC structure including information resident in a database used by the
CC application programme and including records, each record comprising
CC information identifying a polymorphism shown in the above sequences. The
CC products and methods can be used for analysing polymorphic sites in
CC individuals for testing for the presence of a disease phenotype or in
CC forensics, paternity testing or genetic mapping of phenotypic traits.
CC They can also be used for the production of polypeptides expressed by
CC variant genes and for the production of transgenic animals. The nucleic
CC acid segments can also be used in the manufacture of medicaments for the
CC treatment or prophylaxis of diseases

XX
SQ Sequence 31 BP; 8 A; 9 C; 8 G; 5 T; 0 U; 1 Other;

Query Match 2.8%; Score 27.4; DB 1; Length 31;
Best Local Similarity 90.3%; Pred. No. 6.7e+02;
Matches 28; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 863 TGCTGGATTACAGCGGTGAGCCACCCGCC 893
DB 1 TGCTAGATTACAGGTGTGAGCCACCCACCC 31

RESULT 254
AAQ27389
ID AAQ27389 standard; DNA; 32 BP.

XX
AC AAQ27389;
XX
DT 25-MAR-2003 (revised)
DT 27-JAN-1993 (first entry)

XX
DE Inter-Alu specific primer PDJ33A.

XX
KW Polymerase chain reaction; PCR; repetitive element; ss.

XX
OS Synthetic.

XX
PN MO9213101-Al.

XX
PD 06-AUG-1992.

XX
PF 24-JAN-1992; 92MO-NL000018.

XX
PR 25-JAN-1991; 91NL-00000132.

XX
PA (INGENY) INGENY BV.

XX
PI Uiterlinden AG, Vijg J;

XX
DR WPI; 1992-284683/34.

XX
PT Detection of genetic variation by 2-D electrophoresis of fragments - and
PT hybridisation with labelled probes, carried out on fragments consisting
PT of inter-repeat sequences generated by PCR.

XX
PS Claim 6; Page 6; 31pp; English.

XX
CC Primer PDJ33A is one of several primers which are preferred for use in
CC amplifying inter-Alu regions of DNA. The amplified fragments are then
CC subjected to 2-D electrophoresis on the basis of length and differences
CC in base sequence. The resulting separation pattern is transferred to a
CC filter for screening with a probe. The method can be used to detect
CC genetic variation. See also AAQ27390-Q27404 and AAQ3141-Q31144. (Updated
CC on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 32 BP; 7 A; 9 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 2.8%; Score 27.4; DB 1; Length 32;
Best Local Similarity 96.6%; Pred. No. 6.9e+02;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 379 TCAGCTCCCAAGCTGGGATTACAG 407
DB 4 TCAGCTCCCAAGCTGGGATTACAG 32

RESULT 255
ADE14206/c
ID ADE14206 standard; DNA; 32 BP.

XX
AC ADE14206;
XX
DT 29-JAN-2004 (first entry)

XX
DE Optineurin promoter motif, repeat element or regulatory region #315.

XX
KW Human; optineurin; de; ophthalmological; single nucleotide polymorphism;
KW SNP; glaucoma; progressive ocular hypertensive disorder;
KW glaucoma related disorder; motif; repeat element; regulatory region.

XX
OS Homo sapiens.

XX
PN US2003190617-Al.

XX
PD 09-OCT-2003.

XX
PF 06-MAR-2002; 2002US-00091281.

XX
PR 06-MAR-2002; 2002US-00091281.

XX
PA (SITE/) SI E.
PA (RAYM/) RAYMOND V.
PA (MORI/) MORISSETTE J.

XX
PI Raymond V, Morissette J, Si E;

XX
DR WPI; 2003-064168/80.

XX
PT New nucleic acid sequences of the optineurin gene are useful to detect
PT polymorphisms particularly single nucleotide polymorphisms in the
PT optineurin promoter to diagnose, prognose and treat glaucoma and related
PT disorders.

XX
PS Claim 11; SEQ ID NO 317; 159pp; English.

XX
XX
XX The invention relates to an isolated nucleic acid (NI) comprising at
XX least 20 but not more than 1500 consecutive nucleotides of the optineurin
XX promoter appearing as ADE13890. Also included are the optineurin promoter
XX CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
XX detecting a single nucleotide polymorphism (SNP) in the optineurin
XX promoter, a host cell comprising the promoter operably linked to a
XX heterologous sequence, diagnosing or prognosing glaucoma in a sample
XX obtained from a cell or bodily fluid (comprising detecting a polymorphism
XX in a promoter region of the optineurin gene, associated with a glaucoma
XX phenotype), detecting a SNP sequence variation in a sample containing
XX DNA, detecting the presence of an optineurin promoter sequence variation
XX in a sample containing DNA, determining the presence or increased
XX susceptibility to glaucoma or to a progressive ocular hypertensive
XX disorder resulting in loss of visual field in a patient (or the severity
XX or progression of glaucoma in a patient, comprising providing
XX amplification reaction primers that direct amplification of a selected
XX nucleic acid region containing the variation within the optineurin
XX promoter and amplifying the DNA) and detecting a polymorphism (comprising
XX obtaining a sample containing human genomic DNA, providing a nucleic acid
XX capable of detecting a SNP located within an optineurin promoter, and
XX detecting the polymorphism). The invention is used to diagnose and
XX prognose glaucoma and also to treat glaucoma related disorders. The
XX present sequence is an optineurin promoter motif, repeat element or

[illegible]

PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251779P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-488785/53.
XX
XX New isolated nucleic acids and polypeptides, useful for diagnosing,
PT treating and/or preventing human diseases and disorders.
XX
XX Disclosure; SEQ ID NO 338; 520bp + Sequence Listing; English.
XX
XX The present invention provides the protein and coding sequences of a
XX number of ovarian and breast antigens. These are shown in AAI62467-
CC AAI62572 and AAM42240-AAM42345. The sequences can be used in the
CC diagnosis, prevention and treatment of breast and ovarian cancers, and
CC their metastases. The present sequence is a genomic sequence of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from Wipo at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 33 BP; 8 A; 12 C; 9 G; 4 T; 0 U; 0 Other;
SQ
Query Match 2.7%; Score 27.2; DB 1; Length 33;
Best Local Similarity 90.6%; Pred. No. 7.2e+02;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 932 TCACTCTGTTACCCAGGCTGAGTGCATGCG 963
DB 33 TCGCTCTGTTCCCGAGCTGAGTGCATGCGC 2
RESULT 257
AAI6807/c
ID AAI6807 standard; DNA; 33 BP.
XX
XX AAI6807;
XX
XX 21-NOV-2001 (first entry)
DT
XX
XX Human reproductive system related antigen DNA SEQ ID NO: 9495.
DE
XX
XX Human; reproductive system related antigen; reproductive system disorder;
KM cancer; gene therapy; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200155320-A2.
PN
XX

PD 02-AUG-2001;
XX
XX 17-JAN-2001; 2001WO-US001339.
XX
XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
XX 24-FEB-2000; 2000US-0184664P.
XX 02-MAR-2000; 2000US-0186350P.
XX 16-MAR-2000; 2000US-0189874P.
XX 17-MAR-2000; 2000US-0190076P.
XX 18-APR-2000; 2000US-0198123P.
XX 19-MAY-2000; 2000US-0205515P.
XX 07-JUN-2000; 2000US-0209467P.
XX 28-JUN-2000; 2000US-0214886P.
XX 30-JUN-2000; 2000US-0215135P.
XX 07-JUL-2000; 2000US-021647P.
XX 07-JUL-2000; 2000US-0216880P.
XX 11-JUL-2000; 2000US-0217487P.
XX 11-JUL-2000; 2000US-0217496P.
XX 14-JUL-2000; 2000US-0218290P.
XX 26-JUL-2000; 2000US-0220963P.
XX 26-JUL-2000; 2000US-0220964P.
XX 14-AUG-2000; 2000US-0224518P.
XX 14-AUG-2000; 2000US-0224519P.
XX 14-AUG-2000; 2000US-0225213P.
XX 14-AUG-2000; 2000US-0225214P.
XX 14-AUG-2000; 2000US-0225266P.
XX 14-AUG-2000; 2000US-0225267P.
XX 14-AUG-2000; 2000US-0225268P.
XX 14-AUG-2000; 2000US-0225270P.
XX 14-AUG-2000; 2000US-0225447P.
XX 14-AUG-2000; 2000US-0225757P.
XX 14-AUG-2000; 2000US-0225758P.
XX 14-AUG-2000; 2000US-0225759P.
XX 18-AUG-2000; 2000US-0226279P.
XX 22-AUG-2000; 2000US-0226681P.
XX 22-AUG-2000; 2000US-0226686P.
XX 22-AUG-2000; 2000US-0227182P.
XX 23-AUG-2000; 2000US-0227009P.
XX 30-AUG-2000; 2000US-0228924P.
XX 01-SEP-2000; 2000US-0229287P.
XX 01-SEP-2000; 2000US-0229343P.
XX 01-SEP-2000; 2000US-0229344P.
XX 01-SEP-2000; 2000US-0229345P.
XX 05-SEP-2000; 2000US-0229509P.
XX 05-SEP-2000; 2000US-0229513P.
XX 06-SEP-2000; 2000US-0230437P.
XX 06-SEP-2000; 2000US-0230438P.
XX 08-SEP-2000; 2000US-0231242P.
XX 08-SEP-2000; 2000US-0231243P.
XX 08-SEP-2000; 2000US-0231244P.
XX 08-SEP-2000; 2000US-0231413P.
XX 08-SEP-2000; 2000US-0231414P.
XX 08-SEP-2000; 2000US-0232080P.
XX 08-SEP-2000; 2000US-0232081P.
XX 08-SEP-2000; 2000US-0232081P.
XX 12-SEP-2000; 2000US-0231968P.
XX 14-SEP-2000; 2000US-0232397P.
XX 14-SEP-2000; 2000US-0232398P.
XX 14-SEP-2000; 2000US-0232399P.
XX 14-SEP-2000; 2000US-0232400P.
XX 14-SEP-2000; 2000US-0232401P.
XX 14-SEP-2000; 2000US-0233063P.
XX 14-SEP-2000; 2000US-0233064P.
XX 14-SEP-2000; 2000US-0233065P.
XX 21-SEP-2000; 2000US-0234223P.
XX 21-SEP-2000; 2000US-0234274P.
XX 25-SEP-2000; 2000US-0234997P.
XX 25-SEP-2000; 2000US-0234998P.
XX 26-SEP-2000; 2000US-0235484P.
XX 27-SEP-2000; 2000US-0235834P.
XX 27-SEP-2000; 2000US-0235836P.
XX 29-SEP-2000; 2000US-0236337P.
XX 29-SEP-2000; 2000US-0236367P.
XX

PR	29-SEP-2000	2000US-0236368P	
PR	29-SEP-2000	2000US-0236369P	
PR	29-SEP-2000	2000US-0236370P	
PR	02-OCT-2000	2000US-0236380P	
PR	02-OCT-2000	2000US-02370367P	
PR	02-OCT-2000	2000US-02370368P	
PR	02-OCT-2000	2000US-02370369P	
PR	02-OCT-2000	2000US-02370370P	
PR	02-OCT-2000	2000US-02370371P	
PR	13-OCT-2000	2000US-02393357P	
PR	13-OCT-2000	2000US-0239337P	
PR	20-OCT-2000	2000US-0240360P	
PR	20-OCT-2000	2000US-0241821P	
PR	20-OCT-2000	2000US-0241785P	
PR	20-OCT-2000	2000US-0241786P	
PR	20-OCT-2000	2000US-0241787P	
PR	20-OCT-2000	2000US-0241808P	
PR	20-OCT-2000	2000US-0241809P	
PR	20-OCT-2000	2000US-0241810P	
PR	20-OCT-2000	2000US-0241811P	
PR	01-NOV-2000	2000US-0244617P	
PR	08-NOV-2000	2000US-0246474P	
PR	08-NOV-2000	2000US-0246475P	
PR	08-NOV-2000	2000US-0246476P	
PR	08-NOV-2000	2000US-0246477P	
PR	08-NOV-2000	2000US-0246478P	
PR	08-NOV-2000	2000US-0246523P	
PR	08-NOV-2000	2000US-0246524P	
PR	08-NOV-2000	2000US-0246525P	
PR	08-NOV-2000	2000US-0246526P	
PR	08-NOV-2000	2000US-0246527P	
PR	08-NOV-2000	2000US-0246528P	
PR	08-NOV-2000	2000US-0246532P	
PR	08-NOV-2000	2000US-0246603P	
PR	08-NOV-2000	2000US-0246611P	
PR	08-NOV-2000	2000US-0246613P	
PR	08-NOV-2000	2000US-0246613P	
PR	17-NOV-2000	2000US-0249207P	
PR	17-NOV-2000	2000US-0249208P	
PR	17-NOV-2000	2000US-0249209P	
PR	17-NOV-2000	2000US-0249211P	
PR	17-NOV-2000	2000US-0249211P	
PR	17-NOV-2000	2000US-0249212P	
PR	17-NOV-2000	2000US-0249244P	
PR	17-NOV-2000	2000US-0249245P	
PR	17-NOV-2000	2000US-0249264P	
PR	17-NOV-2000	2000US-0249265P	
PR	17-NOV-2000	2000US-0249267P	
PR	17-NOV-2000	2000US-0249291P	
PR	17-NOV-2000	2000US-0249291P	
PR	17-NOV-2000	2000US-0249297P	
PR	17-NOV-2000	2000US-0249299P	
PR	17-NOV-2000	2000US-0249300P	
PR	01-DEC-2000	2000US-0250316P	
PR	01-DEC-2000	2000US-0250391P	
PR	05-DEC-2000	2000US-0251038P	
PR	05-DEC-2000	2000US-0251038P	
PR	05-DEC-2000	2000US-0251671P	
PR	06-DEC-2000	2000US-0251679P	
PR	06-DEC-2000	2000US-0251856P	
PR	08-DEC-2000	2000US-0251868P	
PR	08-DEC-2000	2000US-0251869P	
PR	08-DEC-2000	2000US-0251890P	
PR	11-DEC-2000	2000US-0254097P	
PR	05-JAN-2001	2001US-0259678P	
XX			
PA	(HOMA-) HUMAN GENOME SCI INC.		
XX			
PI	Rosen CA, Barish SC, Ruben SM,		
XX	WPI; 2001-465570/50.		

[illegible]

DB 2 ATGATCCTCATTTGTTACCCAGGCTGAGT 33

RESULT 259
ACC84460
ID ACC84460 standard; DNA; 27 BP.
XX
XX
AC ACC84460;
XX
DT 28-AUG-2003 (first entry)
XX
XX NTP peptide encoding sequence #7.
XX
XX Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
KW neural thread protein; NTP; tumour; ds.
XX
OS Unidentified.
XX
PN WO2003008443-A2.
XX
XX 30-JAN-2003.
XX
PF 19-JUL-2002; 2002WO-CA001105.
XX
PR 19-JUL-2001; 2001US-0306150P.
XX
PR 19-JUL-2001; 2001US-0306161P.
XX
PR 16-NOV-2001; 2001US-0331477P.
XX
PA (NYMO-) NYMOX CORP.
XX
PI Averbach PA;
XX
XX WPI: 2003-247999/24.
XX
XX P-PSDB; ABR63255.
XX
XX Novel neural thread protein peptide, referred as cell death peptide,
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
XX atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.
XX
XX Disclosure; Page 17; 77pp; English.
XX
XX The present invention relates to a neural thread protein (NTP) peptide
CC referred to as cell death peptide. Thought to be cytostatic,
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for
CC treating a condition in a patient requiring removal or destruction of
CC cells, for treating a condition such as benign or malignant tumor.
CC inflammatory disease, autoimmune disease and infectious disease. The
CC peptide useful for treatment is derived from the amino acid sequence for
CC a pancreatic thread protein. The peptide is conjugated, linked or bound
CC to a molecule chosen from antibody or its fragment, antibody-like binding
CC molecule, where the molecule has a higher affinity for binding to a tumor
CC or other target than binding to other cells. Treatment using NTP peptides
CC can remove benign tumors with less risk and fewer of the undesirable side
XX effects of surgery. The present sequence is an NTP encoding sequence
XX
SQ Sequence 27 BP; 6 A; 10 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.7%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1017 CTCAGCCTCCCAAGCAGCTGGATTAC 1043
DB 1 CTCAGCCTCCCAAGCAGCTGGATTAC 27

RESULT 260
AAA04371
ID AAA04371 standard; DNA; 29 BP.
XX
XX
AC AAA04371;
XX
DT 22-MAY-2000 (first entry)

XX
DE Polymorphic fragment of hypertension associated gene HSTSGENE.
XX
XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
KW Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
KW polycystic kidney disease; von Willebrand's disease; forensic; human;
KW tuberculous sclerosis; hereditary hemorrhagica telangiectasia;
KW familial colonic polyposis; osteogenesis imperfecta; porphyria;
KW Ehlers-Danlos syndrome; ss.
XX
XX Homo sapiens.
XX
XX EP955382-A2.
XX
XX 10-NOV-1999.
XX
XX 07-MAY-1999; 99EP-00250150.
XX
XX 07-MAY-1998; 98US-0084641P.
XX
XX 03-MAY-1999; 99US-00304232.
XX
XX (APFY-) AFFYMETRIX INC.
PA (UYCA-) UNIT CASE WESTERN RESERVE.
XX
XX Fan JB, Chakravarti A, Haluska MK;
XX
XX WPI: 2000-107928/10.
XX
XX Novel nucleic acids containing polymorphisms used in the diagnosis of
PT hypertension.
PT
PS Claim 1; Page 34; 53pp; English.
XX
XX The invention provides polymorphic fragments of genes associated with
CC hypertension. The nucleic acids including the polymorphic sites can be
CC used as probes or primers for expressing variant proteins. Detection of
CC the polymorphisms is useful in designing prophylactic and therapeutic
CC regimens customized to underlying abnormalities. The polymorphisms can be
CC used for association studies for hypertension, and in hypertension
CC diagnostic assays. Where the polymorphisms have strong correlation with
CC hypertension, within a gene, they are likely to have a causative role in
CC hypertension. This information can be used to find the precise role of a
CC polymorphism in the disease, and this can be used to identify potential
CC drugs which combat the disease. The polymorphisms can be tested for
CC association with other diseases e.g. agammaglobulinemia, diabetes
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,
CC tuberculous sclerosis, hereditary hemorrhagica telangiectasia, familial
CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
CC acute intermittent porphyria. The polymorphic forms can also be used in
XX forensics to identify individuals
XX
SQ Sequence 29 BP; 6 A; 8 C; 9 G; 5 T; 0 U; 1 Other;

Query Match 2.7%; Score 27; DB 1; Length 29;
Best Local Similarity 93.1%; Pred. No. 6.7e+02;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 856 CCCAAGTGTGGATTACAGCGCTAGC 884
DB 1 CCCAAGTGTGGATTACAGCGCTAGC 29

RESULT 261
AAA04506
ID AAA04506 standard; DNA; 29 BP.
XX
XX
AC AAA04506;
XX
DT 22-MAY-2000 (first entry)

Polymorphic fragment of hypertension associated gene PGIS.

XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
XX Leisch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
XX polycystic kidney disease; von Willebrand's disease; fornicis; human;
XX tuberculous sclerosis; hereditary hemorrhagica telangiectasia;
XX familial colonic polypoid; osteogenesis imperfecta; porphyria;
XX Ehlers-Danlos syndrome; ss.

OS Homo sapiens.
XX EP955382-A2.
XX 10-NOV-1999.
XX 07-MAY-1999; 99EP-00250150.
XX 07-MAY-1998; 98US-0084641P.
XX 03-MAY-1999; 99US-00304232.
XX (AFPMY-) AFFYMETRIX INC.
XX (UYCA-) UNIV CASE WESTERN RESERVE.
XX Fan JB, Chakravarti A, Haluska MK;
XX WPI; 2000-107928/10.
XX Novel nucleic acids containing polymorphisms used in the diagnosis of
XX hypertension.

PT Claim 1; Page 38; 53pp; English.

XX The invention provides polymorphic fragments of genes associated with
XX hypertension. The nucleic acids including the polymorphic sites can be
XX used as probes or primers for expressing variant proteins. Detection of
XX the polymorphisms is useful in designing prophylactic and therapeutic
XX regimens customized to underlying abnormalities. The polymorphisms can be
XX used for association studies for hypertension, and in hypertension
XX diagnostic assays. Where the polymorphisms have strong correlation with
XX hypertension, within a gene, they are likely to have a causative role in
XX hypertension. This information can be used to find the precise role of a
XX polymorphism in the disease, and this can be used to identify potential
XX drugs which combat the disease. The polymorphisms can be tested for
XX association with other diseases e.g. agammaglobulinemia, diabetes
XX insipidus, Leisch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
XX syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
XX kidney disease, hereditary spherocytosis, von Willebrand's disease,
XX tuberculous sclerosis, hereditary hemorrhagica telangiectasia, familial
XX colonic polypoid, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
XX acute intermittent porphyria. The polymorphic forms can also be used in
XX forensics to identify individuals

XX Sequence 29 BP; 5 A; 8 C; 11 G; 4 T; 0 U; 1 Other;
XX

Query Match 2.7%; Score 27; DB 1; Length 29;
Best Local Similarity 93.1%; Pred. No. 6.7e+02;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 864 GCTGGATTACAGCGGTAGCCACCGC 892
DB 1 GCTGGATTACAGCGGTAGCCACCGC 29

RESULT 262
AAA04303
ID AAA04303 standard; DNA; 29 BP.
XX
XX AAA04303;
AC
XX
XX 22-MAY-2000 (first entry)
DT
XX
XX Polymorphic fragment of hypertension associated gene GLUT4.

XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
XX Leisch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
XX polycystic kidney disease; von Willebrand's disease; fornicis; human;
XX tuberculous sclerosis; hereditary hemorrhagica telangiectasia;
XX familial colonic polypoid; osteogenesis imperfecta; porphyria;
XX Ehlers-Danlos syndrome; ss.

OS Homo sapiens.
XX EP955382-A2.
XX 10-NOV-1999.
XX 07-MAY-1999; 99EP-00250150.
XX 07-MAY-1998; 98US-0084641P.
XX 03-MAY-1999; 99US-00304232.
XX (AFPMY-) AFFYMETRIX INC.
XX (UYCA-) UNIV CASE WESTERN RESERVE.
XX Fan JB, Chakravarti A, Haluska MK;
XX WPI; 2000-107928/10.
XX Novel nucleic acids containing polymorphisms used in the diagnosis of
XX hypertension.

PT Claim 1; Page 32; 53pp; English.

XX The invention provides polymorphic fragments of genes associated with
XX hypertension. The nucleic acids including the polymorphic sites can be
XX used as probes or primers for expressing variant proteins. Detection of
XX the polymorphisms is useful in designing prophylactic and therapeutic
XX regimens customized to underlying abnormalities. The polymorphisms can be
XX used for association studies for hypertension, and in hypertension
XX diagnostic assays. Where the polymorphisms have strong correlation with
XX hypertension, within a gene, they are likely to have a causative role in
XX hypertension. This information can be used to find the precise role of a
XX polymorphism in the disease, and this can be used to identify potential
XX drugs which combat the disease. The polymorphisms can be tested for
XX association with other diseases e.g. agammaglobulinemia, diabetes
XX insipidus, Leisch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
XX syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
XX kidney disease, hereditary spherocytosis, von Willebrand's disease,
XX tuberculous sclerosis, hereditary hemorrhagica telangiectasia, familial
XX colonic polypoid, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
XX acute intermittent porphyria. The polymorphic forms can also be used in
XX forensics to identify individuals

XX Sequence 29 BP; 5 A; 8 C; 10 G; 5 T; 0 U; 1 Other;
XX

Query Match 2.7%; Score 27; DB 1; Length 29;
Best Local Similarity 93.1%; Pred. No. 6.7e+02;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 862 GTGCTGGATTACAGCGGTAGCCACAC 890
DB 1 GTGCTGGATTACAGCGGTAGCCACAC 29

RESULT 263
AAA04500
ID AAA04500 standard; DNA; 29 BP.
XX
XX AAA04500;
AC
XX
XX 22-MAY-2000 (first entry)
DT
XX
XX Polymorphic fragment of hypertension associated gene PGIS.

XX	Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
XX	Leesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
XX	Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
XX	polycystic kidney disease; von Willebrand's disease; forensic; human;
XX	tuberos sclerosi; hereditary hemorrhagica telangiectasia;
XX	familial colonic polyposis; osteogenesis imperfecta; porphyria;
XX	Ehlers-Danlos syndrome; ss.
OS	Homo sapiens.
XX	
XX	EP955382-A2.
XX	10-NOV-1999.
XX	
XX	07-MAY-1999; 99EP-00250150.
XX	
XX	07-MAY-1998; 98US-0084641P.
XX	03-MAY-1999; 99US-00304232.
XX	
XX	(AFRY-) AFFYMETRIX INC.
XX	(UYCA-) UNIV CASE WESTERN RESERVE.
XX	
XX	Fan JB, Chakravarti A, Haluska MK;
XX	WPI; 2000-107928/10.
XX	
XX	Novel nucleic acids containing polymorphisms used in the diagnosis of
XX	hypertension.
XX	
XX	Claim 1; Page 38; 53pp; English.
XX	
XX	The invention provides polymorphic fragments of genes associated with
XX	hypertension. The nucleic acids including the polymorphic sites can be
XX	used as probes or primers for expressing variant proteins. Detection of
XX	the polymorphisms is useful in designing prophylactic and therapeutic
XX	regimes customized to underlying abnormalities. The polymorphisms can be
XX	used for association studies for hypertension, and in hypertension
XX	diagnostic assays. Where the polymorphisms have strong correlation with
XX	hypertension, within a gene, they are likely to have a causative role in
XX	hypertension. This information can be used to find the precise role of a
XX	polymorphism in the disease, and this can be used to identify potential
XX	drugs which combat the disease. The polymorphisms can be tested for
XX	association with other diseases e.g. agammaglobulinemia, diabetes
XX	insipidus, Leesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
XX	syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
XX	kidney disease, hereditary spherocytosis, von Willebrand's disease,
XX	tuberos sclerosi, hereditary hemorrhagica telangiectasia, familial
XX	colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
XX	acute intermittent porphyria. The polymorphic forms can also be used in
XX	forensics to identify individuals
XX	
XX	Sequence 29 BP; 4 A; 10 C; 8 G; 6 T; 0 U; 1 Other;
XX	
XX	Query Match 2.7%; Score 27; DB 1; Length 29;
XX	Best Local Similarity 93.1%; Pred. No. 6.7e+02;
XX	Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX	
XX	713 CTGCCACAGCCTTCGTAGTAGCTGGGACT 741
XX	: :
XX	1 CTGCCACAGCCTTCGTAGTAGCTGGGACT 29
XX	
XX	RESULT 264
XX	AAA03996
XX	ID AAA03996 standard; DNA; 29 BP.
XX	AC AAA03996;
XX	
XX	DT 22-MAY-2000 (first entry)
XX	
XX	Polymorphic fragment of hypertension associated gene APOC4.
XX	
XX	Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;

KM Leach-Nyman syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
KM Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
KM polycystic kidney disease; von Willebrand's disease; forensic; human;
KM tuberos sclerosis; hereditary hemorrhagica telangiectasia;
KM familial colonic polyposis; osteogenesis imperfecta; porphyria;
KM Ehlers-Danlos syndrome; ss.
XX
OS Homo sapiens.
XX
PM EP955382-A2.
XX
PD 10-NOV-1999.
XX
PF 07-MAY-1999; 99EP-00250150.
XX
PR 07-MAY-1998; 98US-0084641P.
XX 03-MAY-1999; 99US-00304232.
PR
PA (AFPP-) AFFYMETRIX INC.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
PI Fan JB, Chakravarti A, Haluska MK;
XX
XX wpi; 2000-107928/10.
DR
XX
PT Novel nucleic acids containing polymorphisms used in the diagnosis of
PT hypertension.
PS Claim 1; Page 22; 53pp; English.
PS The invention provides polymorphic fragments of genes associated with
CC hypertension. The nucleic acids including the polymorphic sites can be
CC used as probes or primers for expressing variant proteins. Detection of
CC the polymorphisms is useful in designing prophylactic and therapeutic
CC regimens customized to underlying abnormalities. The polymorphisms can be
CC used for association studies for hypertension, and in hypertension
CC diagnostic assays. Where the polymorphisms have strong correlation with
CC hypertension, within a gene, they are likely to have a causative role in
CC hypertension. This information can be used to find the precise role of a
CC polymorphism in the disease, and this can be used to identify potential
CC drugs which combat the disease. The polymorphisms can be tested for
CC association with other diseases e.g. agammaglobulinemia, diabetes
CC insipidus, Leach-Nyman syndrome, muscular dystrophy, Wiskott-Aldrich
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,
CC tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial
CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
CC acute intermittent porphyria. The polymorphic forms can also be used in
CC forensics to identify individuals

SS Sequence 29 BP; 6 A; 7 C; 9 G; 6 T; 0 U; 1 Other;

Query Match 2.7%; Score 27; DB 1; Length 29;
Best Local Similarity 93.1%; Pred. No. 6.7e+02;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0.

DQ 849 TCGGCCTCCCAAAGTGTGGATTACGAG 877
| | | | | | | | | | | | | | | | | | |
DB 1 TTGGCCTCCCAAAGTGCTGGGATTTACAGG 29

RESULT 265
AAA04505
ID AAA04505 standard; DNA; 29 BP.
XX
XX AAA04505;
XX
XX 22-MAY-2000 (first entry)
DT
XX
DE Polymorphic fragment of hypertension associated gene PGIS.
XX
XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KM Leach-Nyman syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

KM Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
KM polycystic kidney disease; von Willebrand's disease; forensic; human;
KM tuberculous sclerosis; hereditary hemorrhagica telangiectasia;
KM familial colonic polyposis; osteogenesis imperfecta; porphyria;
KM Ehlers-Danlos syndrome; ss.
XX
OS Homo sapiens.
XX
PN EP955382-A2.
XX
PD 10-NOV-1999.
XX
PF 07-MAY-1999; 99EP-00250150.
XX
PR 07-MAY-1998; 98US-0084641P.
PR 03-MAY-1999; 99US-00304232.
XX
PA (AFPY-) APFYMETRIX INC.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
XX
PI Fan JB, Chakravarti A, Haluska MK;
XX
DR WPI; 2000-107928/10.
XX
PT Novel nucleic acids containing polymorphisms used in the diagnosis of
PT hypertension.
XX
PS Claim 1; Page 38; 53pp; English.
XX
CC The invention provides polymorphic fragments of genes associated with
CC hypertension. The nucleic acids including the polymorphic sites can be
CC used as probes or primers for expressing variant proteins. Detection of
CC the polymorphisms is useful in designing prophylactic and therapeutic
CC regimes customized to underlying abnormalities. The polymorphisms can be
CC used for association studies for hypertension, and in hypertension with
CC diagnostic assays. Where the polymorphisms have strong correlation with
CC hypertension, within a gene, they are likely to have a causative role in
CC hypertension. This information can be used to find the precise role of a
CC polymorphism in the disease, and this can be used to identify potential
CC drugs which combat the disease. The polymorphisms can be tested for
CC association with other diseases e.g. agammaglobulinemia, diabetes
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,
CC tuberculous sclerosis, hereditary hemorrhagica telangiectasia, familial
CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
CC acute intermittent porphyria. The polymorphic forms can also be used in
CC forensics to identify individuals
XX
SQ Sequence 29 BP; 4 A; 11 C; 7 G; 6 T; 0 U; 1 Other;
XX
Query Match 2.7%; Score 27; DB 1; Length 29;
Best Local Similarity 93.1%; Pred. No. 6.7e+02;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 836 TGATCTGCTGCTGCTGCTGCCAAGTG 864
DB 1 TGATCTGCCGCTTGCTGCTGCCAAGTG 29

RESULT 266
AAQ73570
ID AAQ73570 standard; DNA; 32 BP.
XX
AC AAQ73570;
XX
DT 25-MAR-2003 (revised)
DT 25-JUN-1995 (first entry)
XX
DE Enhancer element er-3 conserved basepair sequence.
XX
KW Enhancer element; carcinoma; tumor; cancer; SLPI gene;
KW secretory leukoprotease-inhibitor gene; cyokeratin gene-8; ss.

XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_difference 29 /*tag= a
FT /label= pyrimidine
XX
PN MO9421118-A1.
XX
PD 29-SEP-1994.
XX
PF 24-MAR-1994; 94WO-US003197.
XX
PR 24-MAR-1993; 93US-00035435.
XX
PA (UNBR-) UAB RES FOUND.
XX
PI Garver RI, Sorscher EJ;
XX
DR WPI; 1994-316537/39.
XX
PT DNA construct for treating human carcinoma - includes a cancer-
PT therapeutic gene under the control of a promoter and a gp. of enhancer
PT sequences.
XX
PS Claim 1; Fig 6; 54pp; English.
XX
CC This enhancer element is part of a DNA construct used for treating human
CC carcinoma which contains a cancer therapeutic protein under the control
CC of a promoter and 3 enhancer sequences in a specific 5'-3' order. This
CC enhancer element is derived from the flanking region of the human
CC epithelial cell cyokeratin-8 gene. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 32 BP; 7 A; 1 C; 8 G; 15 T; 0 U; 1 Other;
XX
Query Match 2.7%; Score 27; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 769 TTTTGTATTTTGTATGATGAGATGGGT 795
DB 2 TTTTGTATTTTGTATGATGAGATGGGT 28

RESULT 267
AAK91040
ID AAK91040 standard; DNA; 32 BP.
XX
AC AAK91040;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human digestive system antigen genomic sequence SEQ ID NO: 4616.
XX
KW Human digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW digestive system disorder; Meckel's diverticulum; ds.
XX
OS Homo sapiens.
XX
PN MO200155314-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001324.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.

CC diagnosis, treatment and prevention of digestive system disorders,
CC including cancer, Meckel's diverticulum, bacterial or parasitic
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC ulcerative colitis. The present sequence is a genomic DNA fragment
CC encoding a digestive system antigen of the invention
XX
SQ Sequence 32 BP; 7 A; 3 C; 7 G; 15 T; 0 U; 0 Other;
Query Match 2.7%; Score 26.8; DB 1; Length 32;
Best Local Similarity 93.3%; Pred. No. 7.3e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Gy 768 TTTTGTATTGTAAGAGATGGGGTTC 797
Db 1 TTTTGTATTGTAAGAGATGGGGTTC 30
RESULT 268
AAS32075 AAS32075 standard; DNA; 32 BP.
XX AAS32075;
AC
XX
DT 04-DEC-2001 (first entry)
XX
DE Human liver associated genomic DNA #249.
XX
XX Liver associated protein; human; mouse; rabbit; goat; horse; cat; dog;
KW chicken; sheep; immunosuppressive; antiarthritic; vasotropic;
KW antirheumatic; antiproliferative; cytostatic; cardiac; neuroprotective;
KW cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer;
KW ophthalmological; vulnery; gene therapy; autoimmune disease; neoplasm;
KW hyperproliferative disorder; breast; liver; cardiovascular disorder; ds;
KW cerebrovascular disorder; nervous system disorder; bacterial infection;
KW fungal infection; viral infection; ocular disorder; endocrine disorder;
KW gastrointestinal disorder; renal disorder; respiratory disorder;
KW wound healing; skin aging; organ transplantation; tissue regeneration;
anti-fertility.
XX
XX Homo sapiens.
OS
XX
XX WO20015355-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001351.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232400P.
PR 08-SEP-2000; 2000US-0232080P.
PR 12-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241121P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.

PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-457728/49.
XX
PT Isolated nucleic acid molecule encoding a human liver related protein is
PT used in preventing, treating or ameliorating disorders of the liver
PT particularly cancer of the liver.
XX
PS Claim 1; SEQ ID NO 551; 526bp; English.
XX
CC Sequences AAS31827-AAS32182 represent genomic DNA molecules, which encode
CC the liver associated polypeptides of the invention. Liver associated
CC polypeptides and their associated polynucleotides are useful in the
CC diagnosis, treatment and prevention of various types of disorders in e.g.
CC humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A
CC pathological condition can be determined by detecting the presence or
CC absence of a mutation in a liver associated polynucleotide. The treatable
CC disorders include autoimmune diseases such as rheumatoid arthritis,
CC hyperproliferative disorders such as neoplasms of the breast or liver,
CC cardiovascular disorders such as cardiac arrest, cerebrovascular
CC disorders such as cerebral ischaemia, nervous system disorders such as
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi,
CC ocular disorders such as corneal infection, endocrine disorders such as
CC premature labour and infertility, gastrointestinal disorders such as
CC Crohn's disease, renal disorders such as glomerulonephritis and
CC respiratory disorders such as asthma and pleurisy. The polypeptides can
CC also be used to aid wound healing, to prevent skin aging due to sunburn,
CC to maintain organs before transplantation, to regenerate tissues and in
CC chemotaxis. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 32 BP; 7 A; 3 C; 7 G; 15 T; 0 U; 0 Other;

Query Match 2.7%; Score 26.8; DB 1; Length 32;
Best Local Similarity 93.3%; Pred. No. 7.3e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY 768 TTTTGTATTTTGTAGATGGGCTTC 797
1 TTTTGTATTTTGTAGTACAGACGGCTTC 30
Db
RESULT 269
ABN90430
ID ABN90430 standard; DNA; 32 BP.
XX
AC ABN90430;
XX
XX 24-JUL-2002 (first entry)
XX
DE Human liver antigen HLDV38 genomic sequence, SEQ ID NO:551.
XX
XX Human; liver antigen; liver disorder; hepatic disorder; infection;
XX hepatitis; viral; parasitic; bacterial; fungal; inflammatory condition;
XX cirrhosis; granulomatous hepatitis; toxin damage; drug damage;
XX autoimmune disease; Wilson's disease; primary biliary cirrhosis;
XX neoplastic disorder; cancer; tumour; portal hypertension;
XX gastrointestinal disorder; hepatitis; drug screening; gene therapy;
XX chromosome mapping; forensic analysis; antibody preparation;
XX hepatotropic; cytostatic; antiinflammatory; virocid; antibacterial;
XX fungicide; parasiticide; antidote; immunosuppressive; gene; ds.
OS Homo sapiens.
XX
XX US2002042096-A1.
XX
PD 11-APR-2002.
XX
XX 17-JAN-2001; 2001US-00764887.
XX
XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
XX 28-JUN-2000; 2000US-0214886P.
XX 07-JUL-2000; 2000US-0216647P.
XX 07-JUL-2000; 2000US-0216880P.
XX 11-JUL-2000; 2000US-0217487P.
XX 11-JUL-2000; 2000US-0217496P.
XX 14-JUL-2000; 2000US-0218290P.
XX 26-JUL-2000; 2000US-0220963P.
XX 26-JUL-2000; 2000US-0220964P.
XX 14-AUG-2000; 2000US-0224518P.
XX 14-AUG-2000; 2000US-0224519P.
XX 14-AUG-2000; 2000US-0225267P.
XX 14-AUG-2000; 2000US-0225268P.
XX 14-AUG-2000; 2000US-0225270P.
XX 14-AUG-2000; 2000US-0225470P.
XX 14-AUG-2000; 2000US-0225757P.
XX 14-AUG-2000; 2000US-0225758P.
XX 22-AUG-2000; 2000US-0226688P.
XX 30-AUG-2000; 2000US-0228924P.
XX 01-SEP-2000; 2000US-0229287P.
XX 01-SEP-2000; 2000US-0229343P.
XX 01-SEP-2000; 2000US-0229344P.
XX 01-SEP-2000; 2000US-0229345P.
XX 05-SEP-2000; 2000US-0229509P.
XX 05-SEP-2000; 2000US-0229513P.
XX 08-SEP-2000; 2000US-0231413P.
XX 21-SEP-2000; 2000US-0231423P.
XX 21-SEP-2000; 2000US-0234274P.
XX 25-SEP-2000; 2000US-0234997P.
XX 27-SEP-2000; 2000US-0235834P.
XX 29-SEP-2000; 2000US-0236327P.
XX 29-SEP-2000; 2000US-0236367P.
XX 29-SEP-2000; 2000US-0236368P.
XX 29-SEP-2000; 2000US-0236369P.

PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239335P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 XX
 PA (ROSE/) ROSEN C. A.
 PA (RUBEN/) RUBEN S. M.
 PA (BARA/) BARASH S. C.
 XX
 PI Rosen CA, Ruben SM, Barash SC;
 XX
 DR WPI: 2002-381944/41.
 XX
 PT New nucleic acid encoding human liver antigens, useful for diagnosis,
 PT treatment and prevention of e.g. hepatitis and hepatic cancer, also
 PT related polypeptides and antibodies.
 XX
 PS Disclosure; SEQ ID NO 551; 181pp; English.
 XX
 CC The invention relates to 145 novel human liver antigens (ABP40831-
 CC ABP40975) and to cDNAs encoding them (ABN90036-ABN90180), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human liver antigen
 CC polynucleotides, antibodies against human liver antigens, and the use of
 CC liver antigen polynucleotides and polypeptides in diagnosing, treating,
 CC prophylaxis or preventing various disorders of the liver. Such conditions
 CC include viral infections (e.g., cytomegalovirus, Epstein-Barr virus,
 CC hepatitis A virus, hepatitis B virus and hepatitis C virus), parasitic
 CC infections (e.g., Clonorchis sinensis, Echinococcus granulosus and
 CC Entamoeba histolytica), and also bacterial and fungal infections. Other
 CC disorders that may be treated include inflammatory conditions (e.g.,
 CC cirrhosis and granulomatous hepatitis), damage caused by drugs or toxins,
 CC autoimmune diseases (e.g., Wilson's disease, primary biliary cirrhosis),
 CC neoplastic disorders (e.g., adenomas, haemangiomas and hepatocellular
 CC carcinoma), portal hypertension, or gastrointestinal disorders (e.g.,
 CC peptic ulcers, gastritis and peritoneal diseases). Liver antigen
 CC polypeptides and polynucleotides may also be used in screening for
 CC compounds which modulate liver antigen expression or activity. The
 CC polynucleotides may further be used for gene therapy, chromosome mapping,
 CC in the identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as molecular weight markers or to prepare
 CC antibodies useful in disease diagnosis, drug targeting and phenotyping.
 CC Sequences ABN90182-ABN90537 represent human liver antigen genomic
 CC sequences. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from the USPTO at seqdata.uspto.gov/sequence/
 XX
 SQ Sequence 32 BP; 7 A; 3 C; 7 G; 15 T; 0 U; 0 Other;
 XX
 Query Match 2.7%; Score 26.8; DB 1; Length 32;
 Best Local Similarity 93.3%; Pred. No. 7.3e+02;
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 QY 768 TTTTGTGATTTTGTAGTAGAGTGGGCTTC 797
 DB 1 TTTTGTGATTTTGTAGTAGAGACAGGCTTC 30
 XX
 RESULT 270
 ADJ15343
 ID ADJ15343 standard; DNA; 32 BP.

XX
 AC ADJ15343;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human liver-related genomic DNA - SEQ ID 551.
 XX
 KW liver; vitruce; fungicide; antibacterial; antiparasitic; hepatotropic;
 KW antineoplastic; cytotoxic; litholytic; antirheumatic; antidiarrhetic;
 KW neuroprotective; antidiabetic; anticoagulant; thrombolytic;
 KW antihypertensive; cardiac; haemostatic; antiarrhythmic;
 KW ophthalmologic; antidiabetic; vasodilator; osteopathic;
 KW ophthalmic; antiparkinsonian; anticonvulsant; neuroleptic; vasodilator;
 KW cytosolic; gynaecological; viral; fungal; bacterial;
 KW parasitic infection; cirrhosis; Wilson's disease;
 KW gastrointestinal disorder; pancreatic; gallbladder; immune; blood;
 KW hyperproliferative; cardiovascular; respiratory; musculoskeletal system;
 KW neurological; endocrine; reproductive system; developmental; inherited;
 KW human; ds.
 XX
 OS Homo sapiens.
 XX
 XX US2003077602-A1.
 XX
 PD 24-APR-2003.
 XX
 PF 14-FEB-2002; 2002US-00073961.
 XX
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226682P.
 PR 23-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227183P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.

Query	Best Local Similarity	Score	DB 1	Length	Indels	Gaps
Db	28; Conservative	0; Mismatches	2; Indels	0; Gaps	0	
Query Match	2.7%;	Score 26.8;	DB 1;	Length 32;		
Best Local Similarity	93.3%;	Pred. No. 7.3e+02;				
Matches	28; Conservative	0; Mismatches	2; Indels	0; Gaps	0	
768	TTTTTGTATTTTGTAGAGATGGGGTTC	797				
1	TTTTTGTATTTTGTAGTGAACAGCGGTTTC	30				
RESULT 271	AAQ77890/C					
ID	AAQ77890 standard; cDNA; 30 BP.					
XX	AAQ77890;					
AC	25-MAR-2003 (revised)					
XX	DT 06-JUL-1995 (first entry)					
XX	Neural thread protein AD10-7 cDNA 5' antisense oligonucleotide.					

```

XX      Neural thread protein AD10-7; Alzheimer's; neuroectodermal tumours;
KW      malignant astrocytomas; glioblastomas; 5' antisense therapy; ss.
XX
XX      Synthetic.
OS
XX      WO9423756-A1.
XX      27-OCT-1994.
XX      PD
XX      20-APR-1994; 94WO-US004321.
XX      PF
XX      20-APR-1993; 93US-00050559.
XX      PR
XX      (GEMO ) GEN HOSPITAL CORP.
XX      PA
XX      De La Monte SM, Wands JR;
XX      PI
XX      WPI; 1994-341497/42.
XX      DR
XX      Detection of neural thread proteins - to detect sporadic and familial
XX      Alzheimer's disease, neuroectodermal tumours, malignant astrocytomas and
XX      glioblastomas (Eng).
XX      PT
XX      Disclosure; Page 48; 158pp; English.
XX      PS
XX      AA077868-077890 are AD10-7 neural thread protein (NTP) antisense
XX      oligonucleotides, that can be used to down regulate or inhibit the
XX      expression of the NTP gene. These oligonucleotides could be used in the
XX      treatment of the following conditions Alzheimer's disease, neuroectodermal
XX      tumours, malignant astrocytomas and glioblastomas. (Updated on 25-MAR-
XX      CC      2003 to correct PN field.)
XX      CC
XX      Sequence 30 BP; 8 A; 4 C; 14 G; 4 T; 0 U; 0 Other;
SQ
Query Match      2.7%; Score 26.4; DB 1; Length 30;
Best Local Similarity 96.4%; Pred. No. 7.3e+02;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1000 TCAAGCGATTCTCCTGCTCAGCCTCCC 1027
DB      29 TCAAGCGATTCTCCTGCTCAGCCTCCC 2

RESULT 272
AAT27744/C
ID      AAT27744 standard; DNA; 30 BP.
XX
XX      AAT27744;
XX      AC
XX      14-NOV-1996 (first entry)
XX      DT
XX      Neural thread protein antisense sequence.
XX      DE
XX      Neural thread protein; NTP; diagnosis; detection; Alzheimer's disease;
KW      neuroectodermal tumour; malignant astrocytoma; monoclonal antibody;
XX      binding fragment; ds.
XX      KW
XX      Synthetic.
XX      OS
XX      WO9615272-A1.
XX      PN
XX      23-MAY-1996.
XX      PD
XX      14-NOV-1995; 95WO-US017111.
XX      PF
XX      14-NOV-1994; 94US-00340426.
XX      PR
XX      (GEMO ) GEN HOSPITAL CORP.
XX      PA
XX      De La Monte S, Wands JR;
XX      PI
XX      WPI; 1996-259665/26.

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XX      Detection of neural thread protein in diagnosis of Alzheimer's disease -
XX      also NTP DNA and protein sequences used in gene and anti:sense therapy.
XX      PT
XX      Disclosure; Page 48; 238pp; English.
XX      PS
XX      A method for detecting the presence of neural thread protein (NTP) having
XX      CC      a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human subject
XX      CC      comprises (a) contacting a sample from a human subject that is suspected
XX      CC      of containing the NTP with at least one molecule capable of binding to
XX      CC      the protein; and (b) detecting any of the molecule bound to the protein.
XX      CC      The binding molecule is selected from an antibody free of natural
XX      CC      impurities, a monoclonal antibody or a binding fragment of either of
XX      CC      these. The method may be used for diagnosing the presence of Alzheimer's
XX      CC      disease, neuroectodermal tumours and a malignant astrocytoma in a human.
XX      CC      Expression of NTP nucleic acid may be inhibited using antisense
XX      CC      oligonucleotides (See AAT27739-44)
XX      CC
XX      Sequence 30 BP; 8 A; 4 C; 14 G; 4 T; 0 U; 0 Other;
SQ
Query Match      2.7%; Score 26.4; DB 1; Length 30;
Best Local Similarity 96.4%; Pred. No. 7.3e+02;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1000 TCAAGCGATTCTCCTGCTCAGCCTCCC 1027
DB      29 TCAAGCGATTCTCCTGCTCAGCCTCCC 2

RESULT 273
AAH91474/C
ID      AAH91474 standard; DNA; 32 BP.
XX
XX      AAH91474;
XX      AC
XX      09-OCT-2001 (first entry)
XX      DT
XX      Human inflammatory bowel disease associated polymorphic site #549.
XX      DE
XX      Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW      single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
XX      KW      chromosome 5q31-33; forensic test; gene therapy; ds.
XX      KW
XX      Homo sapiens.
XX      OS
XX      Key      Location/Qualifiers
XX      FT      misc_feature      17
XX      FT      /*tag= a
XX      FT      /note= "SNP, optionally C or G at this position"
XX      FT
XX      PN      WC200142511-A2.
XX      PD
XX      14-JUN-2001.
XX      PF
XX      11-DEC-2000; 2000WO-US033632.
XX      PR
XX      10-DEC-1999; 99US-0170257P.
XX      PR      10-APR-2000; 2000US-0196046P.
XX      PA      (WHEE ) WHITEHEAD INST BIOMEDICAL RES.
XX      PA      (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX      PI
XX      Daly M, Hudson TV, Lander ES, Rioux J, Siminovitch K;
XX      DR
XX      WPI; 2001-367874/38.
XX      PT
XX      Testing for the presence of polymorphisms associated with inflammatory
XX      PT      bowel disease, using a hybridization assay.
XX      PS
XX      Claim 1; Page 62; 463pp; English.
XX      CC
XX      The present invention describes a method for detecting the presence of
XX      CC      polymorphisms associated with inflammatory bowel diseases such as

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CC tuberosus sclerosis, hereditary hemorrhagica telangiectasia, familial
 CC colonic polypoidosis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
 CC acute intermittent porphyria. The polymorphic forms can also be used in
 CC forensics to identify individuals

XX Sequence 29 BP; 9 A; 5 C; 11 G; 3 T; 0 U; 1 Other;

Query Match 2.6%; Score 26; DB 1; Length 29;
 Best Local Similarity 92.9%; Pred. No. 7.5e+02;
 Matches 26; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 690 CCTCCGGGTTCAAGTATTCCTGCTCC 717
 DB 29 CCTCCGGGTTCAAGTATTCCTGCTCC 2

RESULT 276

AAA03993
 ID AAA03993 standard; DNA; 29 BP.

XX AAA03993;

DT 22-MAY-2000 (first entry)

XX Polymorphic fragment of hypertension associated gene APOC4.

XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
 KM Leesh-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
 KM Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
 KM polycystic kidney disease; von Willebrand's disease; forensic; human;
 KM tuberosus sclerosis; hereditary hemorrhagica telangiectasia;
 KM familial colonic polypoidosis; osteogenesis imperfecta; porphyria;
 KM Ehlers-Danlos syndrome; ss.

XX Homo sapiens.

XX EP955382-A2.

XX 10-NOV-1999.

XX 07-MAY-1999; 99EP-00250150.

XX 07-MAY-1999; 98US-0084641P.

XX 03-MAY-1999; 99US-00304232.

XX (AFRY-) AFFYMETRIX INC.

XX (UYCA-) UNIV CASE WESTERN RESERVE.

XX Fan JB, Chakravarti A, Haluska MK;

XX MPI; 2000-107928/10.

XX Novel nucleic acids containing polymorphisms used in the diagnosis of
 PT hypertension.

XX Claim 1; Page 22; 53pp; English.

XX The invention provides polymorphic fragments of genes associated with
 CC hypertension. The nucleic acids including the polymorphic sites can be
 CC used as probes or primers for expressing variant proteins. Detection of
 CC the polymorphisms is useful in designing prophylactic and therapeutic
 CC regimens customized to underlying abnormalities. The polymorphisms can be
 CC used for association studies for hypertension, and in hypertension can be
 CC diagnostic assays. Where the polymorphisms have strong correlation with
 CC hypertension, within a gene, they are likely to have a causative role in
 CC hypertension. This information can be used to find the precise role of a
 CC polymorphism in the disease, and this can be used to identify potential
 CC drugs which combat the disease. The polymorphisms can be tested for
 CC association with other diseases e.g. agammaglobulinemia, diabetes
 CC insipidus, Leesh-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
 CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
 CC kidney disease, hereditary spherocytosis, von Willebrand's disease,
 CC tuberosus sclerosis, hereditary hemorrhagica telangiectasia, familial

CC colonic polypoidosis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
 CC acute intermittent porphyria. The polymorphic forms can also be used in
 CC forensics to identify individuals

XX Sequence 29 BP; 8 A; 5 C; 9 G; 6 T; 0 U; 1 Other;

Query Match 2.6%; Score 26; DB 1; Length 29;
 Best Local Similarity 92.9%; Pred. No. 7.5e+02;
 Matches 26; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 860 AAGTCTGGGATTACAGCGCTGAGCCAC 887
 DB 1 AAGTCTGGGATTACAGCGCTGAGCCAC 28

RESULT 277

AA077889/c
 ID AA077889 standard; cDNA; 30 BP.

XX AA077889;

DT 25-MAR-2003 (revised)

DT 06-JUL-1995 (first entry)

XX Neural thread protein AD10-7 cDNA 5' antisense oligonucleotide.

XX Neural thread protein AD10-7; Alzheimer's; neuroectodermal tumours;
 KM malignant astrocytomas; glioblastomas; 5' antisense therapy; ss.

XX Synthetic.

XX WO9423756-A1.

XX 27-OCT-1994.

XX 20-APR-1994; 94WO-US004321.

XX 20-APR-1993; 93US-00050559.

XX (GHEO) GEN HOSPITAL CORP.

XX De La Monte SM, Wands JR;

XX MPI; 1994-341497/42.

XX Detection of neural thread proteins - to detect sporadic and familial
 PT Alzheimer's disease, neuroectodermal tumours, malignant astrocytomas and
 PT glioblastomas (Eng).

XX Disclosure; Page 48; 158pp; English.

XX AA077888-Q77890 are AD10-7 neural thread protein (NTP) antisense
 CC oligonucleotides, that can be used to down regulate or inhibit the
 CC expression of the NTP gene. These oligonucleotides could be used in the
 CC treatment of the following conditions Alzheimer's disease, neuroectodermal
 CC tumours, malignant astrocytomas and glioblastomas. (Updated on 25-MAR-
 CC 2003 to correct PN field.)

XX Sequence 30 BP; 5 A; 7 C; 13 G; 5 T; 0 U; 0 Other;

Query Match 2.6%; Score 25.8; DB 1; Length 30;
 Best Local Similarity 93.1%; Pred. No. 7.8e+02;
 Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 980 GCAACCTTGGCTCCCGGCTCAAGCGAT 1008
 DB 29 GCAACCTTGGCTCCCGGCTCAAGCGAT 1

RESULT 278

AA077743/c
 ID AA077743 standard; DNA; 30 BP.

```
AC AAT27743;
XX
DT 14-NOV-1996 (first entry)
XX
DE Neural thread protein antisense sequence.
XX
KW Neural thread protein; NTP; diagnosis; detection; Alzheimer's disease;
KW neuroectodermal tumour; malignant astrocytoma; monoclonal antibody;
KW binding fragment; ds.
XX
OS Synthetic.
XX
PN WO9615272-A1.
XX
PD 23-MAY-1996.
XX
PF 14-NOV-1995; 95WO-US017111.
XX
PR 14-NOV-1994; 94US-00340426.
XX
PA (GEHO ) GEN HOSPITAL CORP.
XX
PI De La Monte S, Mands JR;
XX
DR WPI; 1996-259865/26.
XX
PT Detection of neural thread protein in diagnosis of Alzheimer's disease -
PT also NTP DNA and protein sequences used in gene and anti:sense therapy.
XX
PS Disclosure; Page 48; 238pp; English.
XX
CC A method for detecting the presence of neural thread protein (NTP) having
CC a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human subject
CC comprises (a) contacting a sample from a human subject that is suspected
CC of containing the NTP with at least one molecule capable of binding to
CC the protein; and (b) detecting any of the molecule bound to the protein.
CC The binding molecule is selected from an antibody free of natural
CC impurities, a monoclonal antibody or a binding fragment of either of
CC these. The method may be used for diagnosing the presence of Alzheimer's
CC disease, neuroectodermal tumours and a malignant astrocytoma in a human.
CC Expression of NTP nucleic acid may be inhibited using antisense
CC oligonucleotides (See AAT27739-44)
XX
SQ Sequence 30 BP; 5 A; 7 C; 13 G; 5 T; 0 U; 0 Other;
Query Match 2.6%; Score 25.8; DB 1; Length 30;
Best Local Similarity 93.1%; Pred. No. 7.8e+02;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 980 GCAACCTCTGCTCCCGGCTCAAGCGAT 1008
Db 29 GCAACCTCGGCTCCCGGTTCAAGCGAT 1
AAQ73573
ID AAQ73573 standard; DNA; 31 BP.
XX
AC AAQ73573;
XX
DT 25-MAR-2003 (revised)
DT 25-JUN-1995 (first entry)
XX
DE Enhancer element er-3 conserved basepair sequence.
XX
KW Enhancer element; carcinoma; tumor; cancer; SLP1 gene;
KW secretory leukoprotease-inhibitor gene; cyokeratin gene-8; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH misc_difference 14
FT /*tag= a
```

```
FT /*label= purine
FT misc_difference 24
FT /*tag= b
FT /*label= pyrimidine
XX
PN WO9421118-A1.
XX
PD 29-SEP-1994.
XX
PF 24-MAR-1994; 94WO-US003197.
XX
PR 24-MAR-1993; 93US-00035435.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Garver RI, Sorscher EJ;
XX
DR WPI; 1994-316537/39.
XX
PT DNA construct for treating human carcinoma - includes a cancer-
PT therapeutic gene under the control of a promoter and a gp. of enhancer
PT sequences.
XX
PS Claim 1; Fig 6; 54pp; English.
XX
CC This enhancer element is part of a DNA construct used for treating human
CC carcinoma which contains a cancer therapeutic protein under the control
CC of a promoter and 3 enhancer sequences in a specific 5'-3' order. This
CC enhancer element is derived from the flanking region of the human
CC epithelial cell secretory leukoprotease-inhibitor gene. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
SQ Sequence 31 BP; 7 A; 10 C; 7 G; 5 T; 0 U; 2 Other;
Query Match 2.6%; Score 25.8; DB 1; Length 31;
Best Local Similarity 87.1%; Pred. No. 8e+02;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 378 CTCAGCCTCCCAAGTCTGGATTACAGGC 408
Db 1 CTCAGCCTCCCAANTAGCTGGANTACAGGC 31
AA78748/c
ID AA78748 standard; DNA; 31 BP.
XX
AC AA78748;
XX
DT 20-NOV-2000 (first entry)
XX
DE Human genomic DNA polymorphic site sequence tag SEQ ID NO:118.
XX
KW Human; genomic DNA; polymorphism; genome; allele-specific; primer; probe;
KW hybridisation; polymorphic site; forensic; paternity testing; medicine;
KW phenotypic trait; genetic analysis; genetic mapping; ds.
XX
OS Homo sapiens.
XX
PN EPI024200-A2.
XX
PD 02-AUG-2000.
XX
PF 26-JAN-2000; 2000EP-00250023.
XX
PR 27-JUN-1999; 99US-00238402.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Patil N, Shah N, Warrington JA;
XX
DR WPI; 2000-500198/45.
XX
```

PT Human genomic polymorphic nucleic acid segments, allele specific primers
PT and probes, and methods of analysis, useful for e.g. forensics, paternity
PT testing, genetic mapping,.
PS Claim 1; Page 8; 141pp; English.
XX
XX The present invention describes a nucleic acid segment of 10-100
CC contiguous bases chosen from one of 632 fragments (AAA78631 to AAA79262),
CC where the segment comprises a polymorphic site or an immediately adjacent
CC base, or the complement of the segment. Also described are: (1) an allele
CC -specific oligonucleotide that hybridizes to a segment of the novelty;
CC (2) an isolated nucleic acid comprising a sequence of the novelty where
CC the polymorphic site within the sequence is occupied by a base other than
CC the reference base indicated in the specification; and (3) analysing a
CC nucleic acid, comprising obtaining a nucleic acid from an individual, and
CC determining a base occupying any one of the polymorphic sites of the
CC novelty. The nucleic acid segments and method can be used to analyse an
CC individual's nucleic acid sequences for the presence of polymorphisms. The
CC method can also be used to test for a disease phenotype and correlate the
CC presence of the phenotype with a particular polymorphism. The presence of
CC polymorphic sites are useful for, e.g. forensics, paternity testing,
CC correlation of polymorphisms with phenotypic traits and for genetic
CC mapping of phenotypic traits. AAA78631 to AAA79262 represent sequence
CC tags of human genomic DNA fragments containing polymorphic sites. The
CC base occupying the polymorphic site is indicated using IUPAC-IUB
CC nomenclature
SQ Sequence 31 BP; 10 A; 11 C; 6 G; 3 T; 0 U; 1 Other;
Query Match 2.6%; Score 25.8; DB 1; Length 31;
Best Local Similarity 87.1%; Pred. No. 8e+02;
Matches 27; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 191 GTTCTCATGTTGGTCAGCGCTGCTCGAA 221
DB 31 GTTTCGCATGTTGGTGTGGCTGCTCGAA 1
RESULT 281
AAD63091/C
ID AAD63091 standard; DNA; 32 BP.
XX
XX AAD63091;
AC
XX 12-FEB-2004 (first entry)
DT
XX
XX Human tandem tag DNA #25.
DE
XX
XX Tandem tag; concatenated tag; human; ds.
OS
XX Homo sapiens.
OS
XX
PN US2003190618-A1.
XX
XX 09-OCT-2003.
PD
XX
XX 06-MAR-2002; 2002US-00092885.
PF
XX
XX 06-MAR-2002; 2002US-00092885.
PR
XX
XX (SAMA/) SAMAL B.
PA
XX (LIY/) LI Y.
PA (HERM/) HERMIDA L C.
PA (HOBP/) HOBPA N L.
PA (JOHE/) JOHE K K.
PI Samal B, Li Y, Hermida LC, Hoppa NL, Johe KK;
XX
XX WPI: 2003-831617/77.
DR
XX
XX Generating five prime biased tandem tag libraries of cDNAs by isolating a
PT sample of mRNAs, amplifying the released tags, concatenating the
PT amplified tags to form concatenated tags, amplifying and isolating the

PT concatenated tags.
XX
XX Disclosure; Page 6; 0pp; English.
PS
XX
XX The present invention discloses a method for generating five prime biased
CC tandem tag libraries of cDNAs. The step involves isolating a sample of
CC mRNAs, amplifying the released tags, concatenating the amplified tags to
CC form concatenated tags, amplifying and isolating the concatenated tags.
CC The present sequence is human tandem tag DNA
SQ Sequence 32 BP; 11 A; 10 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 2.6%; Score 25.6; DB 1; Length 32;
Best Local Similarity 87.5%; Pred. No. 8.3e+02;
Matches 28; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 778 TTTTAGTGAAGATGGCGTTCCACCATGTTCCGC 809
DB 32 TTTTAGTAGAGACGCGTTTCGCATGTTGCC 1
RESULT 282
AAA04017
ID AAA04017 standard; DNA; 29 BP.
XX
XX AAA04017;
AC
XX
XX 22-MAY-2000 (first entry)
DT
XX
XX Polymorphic fragment of hypertension associated gene APOC4.
DE
XX
XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KM Lesch-Nyhan syndrome; muscular dystrophy; Miskott-Aldrich syndrome;
KM Fabrys disease; familial hypercholesterolemia; hereditary spherocytosis;
KM polycystic kidney disease; von Willebrands disease; forensic; human;
KM tuberosus sclerosis; hereditary hemorrhagica telangiectasia;
KM familial colonic polyposis; osteogenesis imperfecta; porphyria;
KM Ehlers-Danlos syndrome; ss.
XX
XX
OS Homo sapiens.
OS
XX
PN EP955382-A2.
XX
XX 10-NOV-1999.
PD
XX
XX 07-MAY-1999; 99EP-00250150.
PF
XX
XX 07-MAY-1998; 98US-0084641P.
PR
XX 03-MAY-1999; 99US-00304232.
XX
XX (AFFY-) AFFYMETRIX INC.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
PA
XX Pan JB, Chakravarti A, Haines WK;
XX
XX WPI: 2000-107928/10.
DR
XX
XX Novel nucleic acids containing polymorphisms used in the diagnosis of
PT hypertension.
PT
XX
XX Claim 1; Page 23; 53pp; English.
PS
XX
XX The invention provides polymorphic fragments of genes associated with
CC hypertension. The nucleic acids including the polymorphic sites can be
CC used as probes or primers for expressing variant proteins. Detection of
CC the polymorphisms is useful in designing prophylactic and therapeutic
CC regimes customized to underlying abnormalities. The polymorphisms can be
CC used for association studies for hypertension, and in hypertension
CC diagnostic assays. Where the polymorphisms have strong correlation with
CC hypertension, within a gene, they are likely to have a causative role in
CC hypertension. This information can be used to find the precise role of a
CC polymorphism in the disease, and this can be used to identify potential
CC drugs which combat the disease. The polymorphisms can be tested for

CC association with other diseases e.g. agammaglobulinemia, diabetes
 CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
 CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
 CC kidney disease, hereditary spherocytosis, von Willebrand disease,
 CC tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial
 CC colonic polypoidosis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
 CC acute intermittent porphyria. The polymorphic forms can also be used in
 CC forensics to identify individuals

XX Sequence 29 BP; 3 A; 6 C; 12 G; 7 T; 0 U; 1 Other;

Query Match 2.6%; Score 25.4; DB 1; Length 29;

Best Local Similarity 89.7%; Pred. No. 8e+02;

Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 644 CCAAGCTGAGTGCAGTGGCGCAATCTTG 672

DB 1 CCAAGCTGAGTGCAGTGGCGCAATCTTG 29

RESULT 283

AAA04065/c

ID AAA04065 standard; DNA; 29 BP.

XX AAA04065;

DT 22-MAY-2000 (first entry)

DE Polymorphic fragment of hypertension associated gene BIR.

XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
 XX Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
 XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
 XX polycystic kidney disease; von Willebrand disease; forensic; human;
 XX tuberous sclerosis; hereditary hemorrhagica telangiectasia;
 XX familial colonic polypoidosis; osteogenesis imperfecta; porphyria;
 XX Ehlers-Danlos syndrome; ss.

OS Homo sapiens.

PN EP955382-A2.

PD 10-NOV-1999.

PF 07-MAY-1999; 99BP-00250150.

PR 07-MAY-1998; 98US-0084641P.

PR 03-MAY-1999; 99US-00304232.

XX (AFPM-) AFFYMETRIX INC.

PA (UYCA-) UNIV CASE WESTERN RESERVE.

PI Fan JB, Chakravarti A, Haluska MK;

DR WPI; 2000-107928/10.

PT Novel nucleic acids containing polymorphisms used in the diagnosis of

XX hypertension.

PS Claim 1; Page 24; 53pp; English.

XX The invention provides polymorphic fragments of genes associated with
 CC hypertension. The nucleic acids including the polymorphic sites can be
 CC used as probes or primers for expressing variant proteins. Detection of
 CC the polymorphisms is useful in designing prophylactic and therapeutic
 CC regimens customized to underlying abnormalities. The polymorphisms can be
 CC used for association studies for hypertension, and in hypertension
 CC diagnostic assays. Where the polymorphisms have strong correlation with
 CC hypertension, within a gene, they are likely to have a causative role in
 CC hypertension. This information can be used to find the precise role of a
 CC polymorphism in the disease, and this can be used to identify potential
 CC drugs which combat the disease. The polymorphisms can be tested for
 CC association with other diseases e.g. agammaglobulinemia, diabetes

CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
 CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
 CC kidney disease, hereditary spherocytosis, von Willebrand disease,
 CC tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial
 CC colonic polypoidosis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
 CC acute intermittent porphyria. The polymorphic forms can also be used in
 CC forensics to identify individuals

XX Sequence 29 BP; 7 A; 7 C; 11 G; 3 T; 0 U; 1 Other;

Query Match 2.6%; Score 25.4; DB 1; Length 29;

Best Local Similarity 89.7%; Pred. No. 8e+02;

Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 670 TTGGCTCACTGCAACCTCTGCTCCCGG 698

DB 29 TTGGCTCACTGCAACCTCTGCTCCCGG 1

RESULT 284

AAA03995

ID AAA03995 standard; DNA; 29 BP.

XX AAA03995;

DT 22-MAY-2000 (first entry)

DE Polymorphic fragment of hypertension associated gene APOC4.

XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
 XX Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
 XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
 XX polycystic kidney disease; von Willebrand disease; forensic; human;
 XX tuberous sclerosis; hereditary hemorrhagica telangiectasia;
 XX familial colonic polypoidosis; osteogenesis imperfecta; porphyria;
 XX Ehlers-Danlos syndrome; ss.

OS Homo sapiens.

PN EP955382-A2.

PD 10-NOV-1999.

PF 07-MAY-1999; 99BP-00250150.

PR 07-MAY-1998; 98US-0084641P.

PR 03-MAY-1999; 99US-00304232.

XX (AFPM-) AFFYMETRIX INC.

PA (UYCA-) UNIV CASE WESTERN RESERVE.

PI Fan JB, Chakravarti A, Haluska MK;

DR WPI; 2000-107928/10.

PT Novel nucleic acids containing polymorphisms used in the diagnosis of

XX hypertension.

PS Claim 1; Page 22; 53pp; English.

XX The invention provides polymorphic fragments of genes associated with
 CC hypertension. The nucleic acids including the polymorphic sites can be
 CC used as probes or primers for expressing variant proteins. Detection of
 CC the polymorphisms is useful in designing prophylactic and therapeutic
 CC regimens customized to underlying abnormalities. The polymorphisms can be
 CC used for association studies for hypertension, and in hypertension
 CC diagnostic assays. Where the polymorphisms have strong correlation with
 CC hypertension, within a gene, they are likely to have a causative role in
 CC hypertension. This information can be used to find the precise role of a
 CC polymorphism in the disease, and this can be used to identify potential
 CC drugs which combat the disease. The polymorphisms can be tested for
 CC association with other diseases e.g. agammaglobulinemia, diabetes
 CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich

CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,
CC tuberos scleriosis, hereditary hemorrhagica telangiectasia, familial
CC colonic polypsis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
CC acute intermittent porphyria. The polymorphic forms can also be used in
CC forensics to identify individuals

SQ Sequence 29 BP; 4 A; 10 C; 8 G; 6 T; 0 U; 1 Other;

Query Match 2.6%; Score 25.4; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 8e+02; Indels 0; Gaps 0;
Matches 26; Conservative 1; Mismatches 2;

QY 843 CCTGCCTGCGCTCCCAAGTCTGGAT 871
DB 1 CCCGCTTGCTCTCAAGTCTGGAT 29

RESULT 285
AAA04512
ID AAA04512 standard; DNA; 29 BP.
AC AAA04512;
DT 22-MAY-2000 (first entry)
DE Polymorphic fragment of hypertension associated gene PGIS.
XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
XX Leesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
XX polycystic kidney disease; von Willebrand's disease; forensic; human;
XX tuberos scleriosis; hereditary hemorrhagica telangiectasia;
XX familial colonic polypsis; osteogenesis imperfecta; porphyria;
XX Ehlers-Danlos syndrome; ss.
XX Homo sapiens.
XX EP955382-A2.
XX 10-NOV-1999.
XX 07-MAY-1999; 99EP-00250150.
XX PF 07-MAY-1998; 98US-0084641P.
XX PR 03-MAY-1999; 99US-00304232.
XX PA (AFVY-) AFFYMETRIX INC.
XX PA (UYCA-) UNIV CASE WESTERN RESERVE.
XX PI Fan JB, Chakravarti A, Haluska MK;
XX WPI; 2000-107928/10.
XX Novel nucleic acids containing polymorphisms used in the diagnosis of
XX hypertension.
XX Claim 1; Page 39; 53bp; English.

CC The invention provides polymorphic fragments of genes associated with
CC hypertension. The nucleic acids including the polymorphic sites can be
CC used as probes or primers for expressing variant proteins. Detection of
CC the polymorphisms is useful in designing prophylactic and therapeutic
CC regimes customized to underlying abnormalities. The polymorphisms can be
CC used for association studies for hypertension, and in hypertension
CC diagnostic assays. Where the polymorphisms have strong correlation with
CC hypertension, within a gene, they are likely to have a causative role in
CC hypertension. This information can be used to find the precise role of a
CC polymorphism in the disease, and this can be used to identify potential
CC drugs which combat the disease. The polymorphisms can be tested for
CC association with other diseases e.g. agammaglobulinemia, diabetes
CC insipidus, Leesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic

CC kidney disease, hereditary spherocytosis, von Willebrand's disease,
CC tuberos scleriosis, hereditary hemorrhagica telangiectasia, familial
CC colonic polypsis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
CC acute intermittent porphyria. The polymorphic forms can also be used in
CC forensics to identify individuals

SQ Sequence 29 BP; 7 A; 10 C; 7 G; 4 T; 0 U; 1 Other;

Query Match 2.6%; Score 25.4; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 8e+02; Indels 0; Gaps 0;
Matches 26; Conservative 1; Mismatches 2;

QY 869 GATTACAGCGCTGAGCCACGAGCCCGGC 897
DB 1 GATTACAGCGATGARCACGAGCCCGGC 29

RESULT 286
AAA04499
ID AAA04499 standard; DNA; 29 BP.
AC AAA04499;
DT 22-MAY-2000 (first entry)
DE Polymorphic fragment of hypertension associated gene PGIS.
XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
XX Leesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
XX polycystic kidney disease; von Willebrand's disease; forensic; human;
XX tuberos scleriosis; hereditary hemorrhagica telangiectasia;
XX familial colonic polypsis; osteogenesis imperfecta; porphyria;
XX Ehlers-Danlos syndrome; ss.
XX Homo sapiens.
XX EP955382-A2.
XX 10-NOV-1999.
XX 07-MAY-1999; 99EP-00250150.
XX PF 07-MAY-1998; 98US-0084641P.
XX PR 03-MAY-1999; 99US-00304232.
XX PA (AFVY-) AFFYMETRIX INC.
XX PA (UYCA-) UNIV CASE WESTERN RESERVE.
XX PI Fan JB, Chakravarti A, Haluska MK;
XX WPI; 2000-107928/10.
XX Novel nucleic acids containing polymorphisms used in the diagnosis of
XX hypertension.
XX Claim 1; Page 38; 53bp; English.

CC The invention provides polymorphic fragments of genes associated with
CC hypertension. The nucleic acids including the polymorphic sites can be
CC used as probes or primers for expressing variant proteins. Detection of
CC the polymorphisms is useful in designing prophylactic and therapeutic
CC regimes customized to underlying abnormalities. The polymorphisms can be
CC used for association studies for hypertension, and in hypertension
CC diagnostic assays. Where the polymorphisms have strong correlation with
CC hypertension, within a gene, they are likely to have a causative role in
CC hypertension. This information can be used to find the precise role of a
CC polymorphism in the disease, and this can be used to identify potential
CC drugs which combat the disease. The polymorphisms can be tested for
CC association with other diseases e.g. agammaglobulinemia, diabetes
CC insipidus, Leesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,

CC tuberosus sclerosis, hereditary hemorrhagica telangiectasia, familial
CC colonic polypsis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
CC acute intermittent porphyria. The polymorphic forms can also be used in
CC forensics to identify individuals

XX Sequence 29 BP; 4 A; 12 C; 5 G; 7 T; 0 U; 1 Other;

Query Match 2.6%; Score 25.4; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 8e+02;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 674 CTCACCTGCAACCTCTGCTCCCGGTTCA 702

Db 1 CTCACCTGCAACCTCTGCTCCCGGTTCA 29

RESULT 287
AAA03984/c
ID AAA03984 standard; DNA; 29 BP.

XX AAA03984;

DT 22-MAY-2000 (first entry)

XX Polymorphic fragment of hypertension associated gene APOC3.

KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
KW Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
KW polycystic kidney disease; von Willebrand's disease; forensic; human;
KW tuberosus sclerosis; hereditary hemorrhagica telangiectasia;
KW familial colonic polypsis; osteogenesis imperfecta; porphyria;
KW Ehlers-Danlos syndrome; ss.

XX Homo sapiens.

XX EP955382-A2.

XX 10-NOV-1999.

XX 07-MAY-1999; 99EP-00250150.

XX 07-MAY-1998; 98US-0084641P.

XX 03-MAY-1999; 99US-00304232.

PA (AFPM-) AFFMETRIX INC.

PA (UYCA-) UNIV CASE WESTERN RESERVE.

PI Fan JB, Chakravarti A, Haluska MK;

XX WPI; 2000-107928/10.

PT Novel nucleic acids containing polymorphisms used in the diagnosis of

XX hypertension.

PS Claim 1; Page 22; 53pp; English.

CC The invention provides polymorphic fragments of genes associated with
CC hypertension. The nucleic acids including the polymorphic sites can be
CC used as probes or primers for expressing variant proteins. Detection of
CC the polymorphisms is useful in designing prophylactic and therapeutic
CC regimens customized to underlying abnormalities. The polymorphisms can be
CC used for association studies for hypertension, and in hypertension
CC diagnostic assays. Where the polymorphisms have strong correlation with
CC hypertension, within a gene, they are likely to have a causative role in
CC hypertension. This information can be used to find the precise role of a
CC polymorphism in the disease, and this can be used to identify potential
CC drugs which combat the disease. The polymorphisms can be tested for
CC association with other diseases e.g. agammaglobulinemia, diabetes
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,
CC tuberosus sclerosis, hereditary hemorrhagica telangiectasia, familial

CC colonic polypsis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
CC acute intermittent porphyria. The polymorphic forms can also be used in
CC forensics to identify individuals

XX Sequence 29 BP; 7 A; 4 C; 12 G; 5 T; 0 U; 1 Other;

Query Match 2.6%; Score 25.4; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 8e+02;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 675 TCACCTGCAACCTCTGCTCCCGGTTCAA 703

Db 29 TCACCTGCAACCTCTGCTCCCGGTTCAA 1

RESULT 288
AAA04645
ID AAA04645 standard; DNA; 29 BP.

XX AAA04645;

DT 22-MAY-2000 (first entry)

XX Polymorphic fragment of hypertension associated gene TBXA2R.

KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
KW Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
KW polycystic kidney disease; von Willebrand's disease; forensic; human;
KW tuberosus sclerosis; hereditary hemorrhagica telangiectasia;
KW familial colonic polypsis; osteogenesis imperfecta; porphyria;
KW Ehlers-Danlos syndrome; ss.

XX Homo sapiens.

XX EP955382-A2.

XX 10-NOV-1999.

XX 07-MAY-1999; 99EP-00250150.

XX 07-MAY-1998; 98US-0084641P.

XX 03-MAY-1999; 99US-00304232.

PA (AFPM-) AFFMETRIX INC.

PA (UYCA-) UNIV CASE WESTERN RESERVE.

PI Fan JB, Chakravarti A, Haluska MK;

XX WPI; 2000-107928/10.

PT Novel nucleic acids containing polymorphisms used in the diagnosis of

XX hypertension.

PS Claim 1; Page 43; 53pp; English.

CC The invention provides polymorphic fragments of genes associated with
CC hypertension. The nucleic acids including the polymorphic sites can be
CC used as probes or primers for expressing variant proteins. Detection of
CC the polymorphisms is useful in designing prophylactic and therapeutic
CC regimens customized to underlying abnormalities. The polymorphisms can be
CC used for association studies for hypertension, and in hypertension
CC diagnostic assays. Where the polymorphisms have strong correlation with
CC hypertension, within a gene, they are likely to have a causative role in
CC hypertension. This information can be used to find the precise role of a
CC polymorphism in the disease, and this can be used to identify potential
CC drugs which combat the disease. The polymorphisms can be tested for
CC association with other diseases e.g. agammaglobulinemia, diabetes
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,
CC tuberosus sclerosis, hereditary hemorrhagica telangiectasia, familial
CC colonic polypsis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and

CC acute intermittent porphyria. The polymorphic forms can also be used in
CC forensics to identify individuals
XX
SQ Sequence 29 BP; 6 A; 9 C; 8 G; 5 T; 0 U; 1 Other;

Query Match 2.6%; Score 25.4; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 8e+02;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1017 CTCAGCCTCCAGACGCTGGATTACGG 1045
DB 1 CTCAGCCTCCAGAGAGCTGGATTACAG 29

RESULT 289

AAH38989
ID AAH38989 standard; DNA; 30 BP.

AC AAH38989;

DT 14-AUG-2001 (first entry)

DE SNP specific upper PCR primer SEQ ID 1785.

XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; PCR primer; ss.
OS Homo sapiens.

PN WO200129262-A2.

PD 26-APR-2001.

PF 13-OCT-2000; 2000WO-US028436.

PR 15-OCT-1999; 99US-0160096P.

PA (ORCH-) ORCHID BIOSCIENCES INC.

PI Picoult-Newburg L, Pohl M;

DR WPI; 2001-290930/30.

PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.

PS Claim 1; Page 59; 83pp; English.

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
XX primer extension (SNPE) primers, and the sequences of regions flanking
XX sites of single nucleotide polymorphisms SNPs. The present invention
XX includes kits for determining the presence or absence of a SNP, using the
XX oligonucleotides of the invention. The PCR primers are used to amplify a
XX SNP flanking sequence, the SNPs primer is used as a genotyping primer.
XX The oligonucleotides are useful for genotyping a nucleic acid sample by
XX performing a single-nucleotide primer extension reaction. The
XX oligonucleotides are useful for determining the presence, absence or
XX identity of a SNP and for genotyping nucleic acid samples, for e.g. to
XX assess by association analysis the genotype of an individual or group of
XX individuals, having a pathological phenotypic trait suspected of being
XX caused by one or more SNPs. Phenotypic traits include diseases e.g.
XX agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
XX dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
XX osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
XX traits also include symptoms of or susceptibility to multifactorial
XX disease of which a component is or may be genetic such as autoimmune
XX diseases, including, rheumatoid arthritis, multiple sclerosis,
XX inflammation, cancer, nervous system diseases and infection by pathogenic

CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence
XX

SQ Sequence 30 BP; 6 A; 1 C; 7 G; 16 T; 0 U; 0 Other;

Query Match 2.6%; Score 25.4; DB 1; Length 30;
Best Local Similarity 96.3%; Pred. No. 8.2e+02;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 767 TTTTGTGATTTTGTAGAGATGG 793
DB 4 TTTTGTGATTTTGTAGAGACGG 30

RESULT 290

AAH40734
ID AAH40734 standard; DNA; 30 BP.

AC AAH40734;

DT 14-AUG-2001 (first entry)

DE SNP specific lower PCR primer SEQ ID 3530.

XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; PCR primer; ss.
OS Homo sapiens.

PN WO200129262-A2.

PD 26-APR-2001.

PF 13-OCT-2000; 2000WO-US028436.

PR 15-OCT-1999; 99US-0160096P.

PA (ORCH-) ORCHID BIOSCIENCES INC.

PI Picoult-Newburg L, Pohl M;

DR WPI; 2001-290930/30.

PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.

PS Claim 1; Page 68; 83pp; English.

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
XX primer extension (SNPE) primers, and the sequences of regions flanking
XX sites of single nucleotide polymorphisms SNPs. The present invention
XX includes kits for determining the presence or absence of a SNP, using the
XX oligonucleotides of the invention. The PCR primers are used to amplify a
XX SNP flanking sequence, the SNPE primer is used as a genotyping primer.
XX The oligonucleotides are useful for genotyping a nucleic acid sample by
XX performing a single-nucleotide primer extension reaction. The
XX oligonucleotides are useful for determining the presence, absence or
XX identity of a SNP and for genotyping nucleic acid samples, for e.g. to
XX assess by association analysis the genotype of an individual or group of
XX individuals, having a pathological phenotypic trait suspected of being
XX caused by one or more SNPs. Phenotypic traits include diseases e.g.
XX agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
XX dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
XX osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
XX traits also include symptoms of or susceptibility to multifactorial
XX disease of which a component is or may be genetic such as autoimmune
XX diseases, including, rheumatoid arthritis, multiple sclerosis,

CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence

XX Sequence 30 BP; 7 A; 2 C; 8 G; 13 T; 0 U; 0 Other;

Query Match 2.5%; Score 25.2; DB 1; Length 30;
Best Local Similarity 90.0%; Pred. No. 8.3e+02;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1066 CTAATTTTGTATTTTCATTAGAGCGCGG 1095

Db 1 CTAATTTTGTATTTTGTAGAGCGCGG 30

RESULT 291
AAQ25353/c
ID AAQ25353 standard; DNA; 25 BP.

XX AAQ25353;

XX 21-NOV-1992 (first entry)

XX Sequence of probe Alu 1.

XX Hybridisation rate; chondroitin sulphate; probe; probe cocktail; Alu 1;

XX 88.

XX Synthetic.

XX US5116727-A.

XX 26-MAY-1992.

XX 31-AUG-1989; 89US-00404990.

XX 31-AUG-1989; 89US-00404990.

XX (INIT-) INITIATIVE MARITIME 1991 SRL.

XX Brigati DJ;

XX WPI; 1992-199514/24.

XX Increasing hybridisation rate between complementary polynucleotide cpds.

XX - using water-soluble hetero-polysaccharide with sulphated N-

XX acetyl:galactosamine units.

XX Example; Col 7; 6pp; English.

XX Alu 1 and Alu 2 probes were used in hybridisations carried out in an aq.

XX medium comprising a cocktail of: 10% chondroitin sulphate A; 45%

XX furmide; 5% saline citrate; 25mm phosphate; & 250 micro-g/ml sheared

XX herring sperm DNA. The probes were chemically labelled with 3-4 biotin

XX molecules per probe at the 3' termin. Excellent staining of the DNA of

XX human cell nuclei resulted when either of the Alu 1 or Alu 2 probes were

XX present at 60 ng/ml (or each was present at 30 ng/ml) of the probe

XX cocktail

SQ Sequence 25 BP; 5 A; 6 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 2.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 381 AGCCTCCCAAGTCTGGATTACA 405

Db 25 AGCCTCCCAAGTCTGGATTACA 1

RESULT 292

AAH40799

ID AAH40799 standard; DNA; 25 BP.

XX AAH40799;

XX 14-AUG-2001 (first entry)

XX SNP specific SNPE primer SEQ ID 3595.

XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;

XX SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;

XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;

XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;

XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;

XX inflammation; forensic investigation; paternity analysis; primer; 88.

XX Homo sapiens.

XX MO200129262-A2.

XX 26-APR-2001.

XX 13-OCT-2000; 2000MO-US028436.

XX 15-OCT-1999; 99US-0160096P.

XX (ORCH-) ORCHID BIOSCIENCES INC.

XX Picoult-Newburg L, Pohl M;

XX WPI; 2001-290930/30.

XX New genotyping oligonucleotide, useful for detecting the presence,

XX absence or identity of single polynucleotide polymorphism in a nucleic

XX acid sample.

XX Claim 1; Page 68; 83pp; English.

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide

XX primer extension (SNPE) primers, and the sequences of regions flanking

XX sites of single nucleotide polymorphisms SNPs. The present invention

XX includes kits for determining the presence or absence of a SNP, using the

XX oligonucleotides of the invention. The PCR primers are used to amplify a

XX SNP flanking sequence, the SNPs primer is used as a genotyping primer.

XX The oligonucleotides are useful for genotyping a nucleic acid sample by

XX performing a single-nucleotide primer extension reaction. The

XX oligonucleotides are useful for determining the presence, absence or

XX identity of a SNP and for genotyping nucleic acid samples, for e.g. to

XX assess by association analysis the genotype of an individual or group of

XX individuals, having a pathological phenotypic trait suspected of being

XX caused by one or more SNPs. Phenotypic traits include diseases e.g.

XX agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular

XX dystrophy, familial hypercholesterolaemia, polycystic kidney disease,

XX osteogenesis imperfecta and acute intermittent porphyria. Phenotypic

XX traits also include symptoms of or susceptibility to multifactorial

Qy 860 AAGTCTGGATTACAGCGCTGAGC 884

Db 1 AAGTCTGGATTACAGCGCTGAGC 25

Query Match 2.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ABT03658	standard; DNA, 25 BP.
ID	ABT03658 standard; DNA, 25 BP.
AC	ABT03658;
DT	13-SEP-2002 (first entry)
DE	Human Med-6 gene PCR primer SEQ ID NO: 179.
XX	Human; cancer; neoplastic disease; tumour specific marker; cytostatic;
XX	transcription factor; PCR; primer; ss.
OS	Homo sapiens.
XX	WO200240716-A2.
XX	23-MAY-2002.
XX	13-NOV-2001; 2001WO-US043461.
XX	16-NOV-2000; 2000US-0249508P.
XX	(CEMI-) CEMINES LLC.
XX	Palm K;
XX	WPI; 2002-537346/57.
XX	Determining the presence of neoplastic molecular markers, by identifying
XX	the presence of markers in host test sample using array of neoplastic
XX	molecular marker specific reagents and analyzing the array of the
XX	reagents.
XX	Example 1; Page 16; 41pp; English.
XX	The present invention relates to a method for determining the presence of
XX	neoplastic molecular markers in a host, involving the use of neoplastic
XX	molecular marker specific reagents to detect such markers and analyzing
XX	the array of reagents, allowing the identification of the neoplastic
XX	disease present. This can be used to determine the best treatment for
XX	cancer, in particular neural cell, lung and prostate tumours. The
XX	present sequence is a PCR primer useful for detecting the coding
XX	sequences of markers of the invention.
XX	Sequence 25 BP; 7 A; 4 C; 9 G; 5 T; 0 U; 0 Other;
XX	Query Match
XX	Best Local Similarity 2.5%; Score 25; DB 1; Length 25;
XX	Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	858 CAAAGTGTGGATTACAGCGCTGA 882
XX	
XX	1 CAAAGTGTGGATTACAGCGCTGA 25
XX	RESULT 295
XX	AAH91598
XX	ID AAH91598 standard; DNA; 29 BP.
XX	AAH91598;
XX	09-OCT-2001 (first entry)
XX	Human inflammatory bowel disease associated polymorphic site #673.
XX	Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
XX	single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
XX	chromosome 5q31-33; forensic test; gene therapy; ds.
XX	Homo sapiens.
XX	Key
XX	misc feature 15
XX	Location/Qualifiers

```

FT      /tag= a
XX      /note= "SNP, optionally A or C at this position"
XX      W0200142511-A2.
XX      14-JUN-2001.
XX      11-DEC-2000; 2000WO-US033632.
XX      10-DEC-1999; 99US-0170257P.
XX      10-APR-2000; 2000US-0196046P.
XX      (WHEB-) WHITEHEAD INST BIOMEDICAL RES.
XX      (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX      Daly M, Hudson TJ, Lander ES, Rieux J, Simionovitch K;
XX      WPI; 2001-367874/38.
XX      Testing for the presence of polymorphisms associated with inflammatory
XX      bowel disease, using a hybridization assay.
XX      Claim 1, Page 67; 463pp; English.
XX      The present invention describes a method for detecting the presence of
XX      polymorphisms associated with inflammatory bowel diseases such as
XX      ulcerative colitis and Crohn's disease. The methods can be used to detect
XX      the presence of genetic polymorphisms associated with inflammatory bowel
XX      disease and correlating their occurrence with disease states. They may be
XX      used in this way for phenotypic correlations, forensics, paternity
XX      testing, medicine and genetic analysis. The present sequence is a
XX      polymorphic site described in the exemplification of the invention
XX      SO      Sequence 29 BP; 4 A; 12 C; 6 G; 6 T; 0 U; 1 Other;

Query Match      2.5%; Score 24.8; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 8.5e+02;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      670 TTGGCTCAGTCGCACTGCTGCCGCGG 698
DB      1 TTGGCTCAGTCGCACTGCTGCCGCGG 29

RESULT 296
AAA03985/C
ID      AAA03985 standard; DNA; 29 BP.
XX      AAA03985;
XX      22-MAY-2000 (first entry)
XX      Polymorphic fragment of hypertension associated gene APOC3.
XX      Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
XX      Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
XX      Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
XX      polycystic kidney disease; von Willebrand's disease; forensic; human;
XX      tuberous sclerosis; hereditary hemorrhagic telangiectasia;
XX      familial colonic polyposis; osteogenesis imperfecta; porphyria;
XX      Ehlers-Danlos syndrome; ss.
XX      Homo sapiens.
XX      OS
XX      PN      EP95382-A2.
XX      10-NOV-1999.
XX      07-MAY-1999; 99EP-00250150.
XX      07-MAY-1998; 98US-0084641P.
XX      03-MAY-1999; 99US-00304232.
XX

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PA      (AFRY-) AFRYMETRIX INC.
XX      PA      (UYCA-) UNIV CASE WESTERN RESERVE.
XX      PI      Pan JB, Chakravarti A, Haluska MK;
XX      WPI; 2000-107928/10.
XX      Novel nucleic acids containing polymorphisms used in the diagnosis of
XX      hypertension.
XX      Claim 1, Page 22; 53pp; English.
XX      The invention provides polymorphic fragments of genes associated with
XX      hypertension. The nucleic acids including the polymorphic sites can be
XX      used as probes or primers for expressing variant proteins. Detection of
XX      the polymorphisms is useful in designing prophylactic and therapeutic
XX      regimes customized to underlying abnormalities. The polymorphisms can be
XX      used for association studies for hypertension, and in hypertension
XX      diagnostic assays. Where the polymorphisms have strong correlation with
XX      hypertension, within a gene, they are likely to have a causative role in
XX      hypertension. This information can be used to find the precise role of a
XX      polymorphism in the disease, and this can be used to identify potential
XX      drugs which combat the disease. The polymorphisms can be tested for
XX      association with other diseases e.g. agammaglobulinemia, diabetes
XX      insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
XX      syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
XX      kidney disease, hereditary spherocytosis, von Willebrand's disease,
XX      tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial
XX      colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
XX      acute intermittent porphyria. The polymorphic forms can also be used in
XX      forensics to identify individuals
XX      SO      Sequence 29 BP; 6 A; 8 C; 10 G; 4 T; 0 U; 1 Other;

Query Match      2.5%; Score 24.6; DB 1; Length 29;
Best Local Similarity 96.0%; Pred. No. 8.7e+02;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      635 CTCTGTACCCAGCTGTGAGTGCG 659
DB      25 CTCTGTACCCAGCTGTGAGTGCG 1

RESULT 297
ABK65978
ID      ABK65978 standard; DNA; 26 BP.
XX      ABK65978;
XX      02-JUL-2002 (first entry)
XX      Human gene specific PCR primer #66.
XX      Primer; ss; DNA microarray; differential expression analysis; human.
XX      OS
XX      PN      US6352829-B1.
XX      05-MAR-2002.
XX      05-JAN-1999; 99US-00225928.
XX      21-MAY-1997; 97US-00859998.
XX      (CLON-) CLONTECH LAB INC.
XX      Chenchik A, Jekhadze G, Bibilashvili R;
XX      WPI; 2002-314699/35.
XX      Producing sub-population of labeled nucleic acids, useful for analyzing
XX      differences in RNA profiles between several different physiological
XX

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PT sources, using set of distinct gene specific primers.
XX
XX Example 3; SEQ ID NO 66; 11pp; English.
XX
XX The invention relates to producing a sub-population of labeled nucleic acids (NAs) comprising contacting a NA sample from a physiological source, with a pool of 50 distinct gene specific primers under suitable conditions to enzymatically generate sub-population of NAs, where each CC gene specific primer has a sequence complementary to a distinct mRNA, and CC each labeled NA is generated using a single gene specific primer. The CC method is useful for producing a sub-population of labeled NAs which is CC useful for analyzing the differences in the RNA profiles between several CC different physiological sources, where the method comprises producing CC subpopulation of labeled NAs for the different physiological sources, CC comprising the populations for each physiological source to identify CC differences in the population, where the comparison is preferably CC performed by hybridizing the labeled NAs for each of the distinct CC physiological sources to an array of probe NAs stably associated with the CC surface of a substrate to produce a hybridisation pattern for each of the CC sources, and comparing the patterns for each of the sources, where CC differential gene expression assays are utilised in differential CC tissue, or different tissue or sub-tissue types. The present sequence is a CC human gene specific PCR primer used in the method of the invention. Note: CC The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from USPTO CC at <http://wipo.segdata.uspto.gov/sequence.html?docID=6352829B1>
XX
SQ Sequence 26 BP; 8 A; 4 C; 9 G; 5 T; 0 U; 0 Other;
XX
Query Match 2.5%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 8.3e+02;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 859 AAGGCTGGGATTACAGCGCTGAGC 884
DB 1 AAGGCTAGGATTACAGCGCTGAGC 26
RESULT 298
ABK66984
ID ABK66984 standard; DNA; 26 BP.
XX
XX ABK66984;
XX
XX 02-JUL-2002 (first entry)
XX
XX Human gene specific PCR primer #1072.
XX
XX
XX Primer; ss; DNA microarray; differential expression analysis; human.
XX
XX Homo sapiens.
XX
XX US6352829-B1.
XX
XX 05-MAR-2002.
XX
XX 05-JAN-1999; 99US-00225928.
XX
XX 21-MAY-1997; 97US-00859998.
XX
XX (CLON-) CLONTECH LAB INC.
XX
XX Chenchik A, Johadze G, Bibilashvili R;
XX
XX WPI; 2002-314699/35.
XX
XX
XX Producing sub-population of labeled nucleic acids, useful for analyzing PT differences in RNA profiles between several different physiological PT sources, using set of distinct gene specific primers.
XX
XX Example 3; SEQ ID NO 1072; 11pp; English.
XX
XX

CC The invention relates to producing a sub-population of labeled nucleic acids (NAs) comprising contacting a NA sample from a physiological source, with a pool of 50 distinct gene specific primers under suitable conditions to enzymatically generate sub-population of NAs, where each CC gene specific primer has a sequence complementary to a distinct mRNA, and CC each labeled NA is generated using a single gene specific primer. The CC method is useful for producing a sub-population of labeled NAs which is CC useful for analyzing the differences in the RNA profiles between several CC different physiological sources, where the method comprises producing CC subpopulation of labeled NAs for the different physiological sources, CC comprising the populations for each physiological source to identify CC differences in the population, where the comparison is preferably CC performed by hybridizing the labeled NAs for each of the distinct CC physiological sources to an array of probe NAs stably associated with the CC surface of a substrate to produce a hybridisation pattern for each of the CC sources, and comparing the patterns for each of the sources, where CC differential gene expression assays are utilised in differential CC tissue, or different tissue or sub-tissue types. The present sequence is a CC human gene specific PCR primer used in the method of the invention. Note: CC The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from USPTO CC at <http://wipo.segdata.uspto.gov/sequence.html?docID=6352829B1>
XX
SQ Sequence 26 BP; 5 A; 5 C; 9 G; 7 T; 0 U; 0 Other;
XX
Query Match 2.5%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 8.3e+02;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 650 TGGAGTGGGATGGGCAATCTTGCT 675
DB 1 TGGAGTGGGATGGGCAATCTTGCT 26
RESULT 299
AAH91530
ID AAH91530 standard; DNA; 28 BP.
XX
XX AAH91530;
XX
XX 09-OCT-2001 (first entry)
XX
XX Human inflammatory bowel disease associated polymorphic site #605.
XX
XX Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis; single nucleotide polymorphism; SNP; chromosome 19p13; paternity test; KW chromosome 5q31-33; forensic test; gene therapy; ds.
XX
XX Homo sapiens.
XX
XX
XX Key location/Qualifiers
FT misc_feature 14
FT /*tag= a
FT /note= "SNP, optionally C or G at this position"
XX
XX WO200142511-A2.
XX
XX 14-JUN-2001.
XX
XX 11-DEC-2000; 2000WO-US033632.
XX
XX 10-DEC-1999; 99US-0170257P.
XX
XX 10-APR-2000; 2000US-0196046P.
XX
XX (WHEED) WHITEHEAD INST BIOMEDICAL RES.
XX
XX (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX
XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
XX
XX WPI; 2001-367874/38.
XX
XX Testing for the presence of polymorphisms associated with inflammatory PT

PT bowel disease, using a hybridization assay.

XX Claim 1; Page 64; 463pp; English.

XX The present invention describes a method for detecting the presence of
CC polymorphisms associated with inflammatory bowel diseases such as
CC ulcerative colitis and Crohn's disease. The methods can be used to detect
CC the presence of genetic polymorphisms associated with inflammatory bowel
CC disease and correlating their occurrence with disease states. They may be
CC used in this way for phenotypic correlations, forensics, paternity
CC testing, medicine and genetic analysis. The present sequence is a
CC polymorphic site described in the exemplification of the invention

XX Sequence 28 BP; 4 A; 9 C; 4 G; 10 T; 0 U; 1 Other;

Query Match 2.5%; Score 24.4; DB 1; Length 28;
Best Local Similarity 92.6%; Pred. No. 8.7e+02;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1000 TCAAGGATTCTCTGCTCAGCCTCC 1026

Db 2 TCAAGGATTCTCTGCTCAGCCTCC 28

RESULT 300

AAA04000/c

ID AAA04000 standard; DNA; 29 BP.

XX AAA04000;

DT 22-MAY-2000 (first entry)

DE Polymorphic fragment of hypertension associated gene APOC4.

XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
XX Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
XX polycystic kidney disease; von Willebrand disease; forensic; human;
XX tubercous sclerosis; hereditary hemorrhagica telangiectasia;
XX familial colonic polyposis; osteogenesis imperfecta; porphyria;
XX Ehlers-Danlos syndrome; ss.

XX Homo sapiens.

XX EP955382-A2.

XX 10-NOV-1999.

XX 07-MAY-1999; 99EP-00250150.

XX 07-MAY-1998; 98US-0084641P.

XX 03-MAY-1999; 99US-00304232.

XX (AFFY-) AFFYMETRIX INC.

XX (UYCA-) UNIV CASE WESTERN RESERVE.

XX Fan JB, Chakravarti A, Haluska MK;

XX WPI; 2000-107928/10.

XX Novel nucleic acids containing polymorphisms used in the diagnosis of

XX hypertension.

XX Claim 1; Page 22; 53pp; English.

XX The invention provides polymorphic fragments of genes associated with
CC hypertension. The nucleic acids including the polymorphic sites can be
CC used as probes or primers for expressing variant proteins. Detection of
CC the polymorphisms is useful in designing prophylactic and therapeutic
CC regimens customized to underlying abnormalities. The polymorphisms can be
CC used for association studies for hypertension, and in hypertension
CC diagnostic assays. Where the polymorphisms have strong correlation with
CC hypertension, within a gene, they are likely to have a causative role in

CC hypertension. This information can be used to find the precise role of a

CC polymorphism in the disease, and this can be used to identify potential
CC drugs which combat the disease. The polymorphisms can be tested for
CC association with other diseases e.g. agammaglobulinemia, diabetes
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
CC kidney disease, hereditary spherocytosis, von Willebrand disease,
CC tubercous sclerosis, hereditary hemorrhagica telangiectasia, familial
CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
CC acute intermittent porphyria. The polymorphic forms can also be used in
CC forensics to identify individuals

XX Sequence 29 BP; 7 A; 5 C; 12 G; 4 T; 0 U; 1 Other;

Query Match 2.5%; Score 24.4; DB 1; Length 29;
Best Local Similarity 89.3%; Pred. No. 8.9e+02;
Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1000 TCAAGGATTCTCTGCTCAGCCTCCC 1027

Db 29 TCAAGGATTCTCTGCTCAGCCTCCC 2

RESULT 301

AAA04507

ID AAA04507 standard; DNA; 29 BP.

XX AAA04507;

DT 22-MAY-2000 (first entry)

DE Polymorphic fragment of hypertension associated gene PGLS.

XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
XX Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
XX polycystic kidney disease; von Willebrand disease; forensic; human;
XX tubercous sclerosis; hereditary hemorrhagica telangiectasia;
XX familial colonic polyposis; osteogenesis imperfecta; porphyria;
XX Ehlers-Danlos syndrome; ss.

XX Homo sapiens.

XX EP955382-A2.

XX 10-NOV-1999.

XX 07-MAY-1999; 99EP-00250150.

XX 07-MAY-1998; 98US-0084641P.

XX 03-MAY-1999; 99US-00304232.

XX (AFFY-) AFFYMETRIX INC.

XX (UYCA-) UNIV CASE WESTERN RESERVE.

XX Fan JB, Chakravarti A, Haluska MK;

XX WPI; 2000-107928/10.

XX Novel nucleic acids containing polymorphisms used in the diagnosis of

XX hypertension.

XX Claim 1; Page 38; 53pp; English.

XX The invention provides polymorphic fragments of genes associated with
CC hypertension. The nucleic acids including the polymorphic sites can be
CC used as probes or primers for expressing variant proteins. Detection of
CC the polymorphisms is useful in designing prophylactic and therapeutic
CC regimens customized to underlying abnormalities. The polymorphisms can be
CC used for association studies for hypertension, and in hypertension
CC diagnostic assays. Where the polymorphisms have strong correlation with
CC hypertension, within a gene, they are likely to have a causative role in
CC hypertension. This information can be used to find the precise role of a

CC polymorphism in the disease, and this can be used to identify potential
CC drugs which combat the disease. The polymorphisms can be tested for
CC association with other diseases e.g. agammaglobulinemia, diabetes
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,
CC tuberos sclerosis, hereditary hemorrhagica telangiectasia, familial
CC colonic polypsis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
CC acute intermittent porphyria. The polymorphic forms can also be used in
CC forensics to identify individuals

XX Sequence 29 BP; 6 A; 9 C; 9 G; 4 T; 0 U; 1 Other;

Query Match 2.5%; Score 24.4; DB 1; Length 29;

Best Local Similarity 89.3%; Pred. No. 8.9e+02;

Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 867 GGGATTACAGCGCTGAGCCACACGCC 894

DB 1 GGGATTACAGCTGTTRAGCCACCGCGCC 28

RESULT 302

AAA04369 standard; DNA; 29 BP.

AC AAA04369;

DT 22-MAY-2000 (first entry)

DE Polymorphic fragment of hypertension associated gene HSTSCGENE.

XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
XX Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
XX polycystic kidney disease; von Willebrand's disease; forensic; human;
XX tuberos sclerosis; hereditary hemorrhagica telangiectasia;
XX familial colonic polypsis; osteogenesis imperfecta; porphyria;
XX Ehlers-Danlos syndrome; ss.

OS Homo sapiens.

PN EP955382-A2.

PD 10-NOV-1999.

PF 07-MAY-1999; 99EP-00250150.

PR 07-MAY-1998; 98US-0084641P.

PR 03-MAY-1999; 99US-00304232.

PA (AFPY-) AFFYMETRIX INC.

PA (UYCA-) UNIV CASE WESTERN RESERVE.

PI Pan JB, Chakravarti A, Haluska MK;

DR WPI; 2000-107928/10.

PT Novel nucleic acids containing polymorphisms used in the diagnosis of
PT hypertension.

PS Claim 1; Page 34; 53pp; English.

CC The invention provides polymorphic fragments of genes associated with
CC hypertension. The nucleic acids including the polymorphic sites can be
CC used as probes or primers for expressing variant proteins. Detection of
CC the polymorphisms is useful in designing prophylactic and therapeutic
CC regimens customized to underlying abnormalities. The polymorphisms can be
CC used for association studies for hypertension, and in hypertension
CC diagnostic assays. Where the polymorphisms have strong correlation with
CC hypertension, within a gene, they are likely to have a causative role in
CC hypertension. This information can be used to find the precise role of a
CC polymorphism in the disease, and this can be used to identify potential

CC drugs which combat the disease. The polymorphisms can be tested for
CC association with other diseases e.g. agammaglobulinemia, diabetes
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,
CC tuberos sclerosis, hereditary hemorrhagica telangiectasia, familial
CC colonic polypsis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
CC acute intermittent porphyria. The polymorphic forms can also be used in
CC forensics to identify individuals

XX Sequence 29 BP; 7 A; 9 C; 6 G; 6 T; 0 U; 1 Other;

Query Match 2.5%; Score 24.4; DB 1; Length 29;

Best Local Similarity 89.3%; Pred. No. 8.9e+02;

Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1032 AGCTGGATTACGGGACCTCCACCC 1059

DB 2 AGCTGGATTACAGCCACTCCATCCAC 29

RESULT 303

AAA03994 standard; DNA; 29 BP.

AC AAA03994;

DT 22-MAY-2000 (first entry)

DE Polymorphic fragment of hypertension associated gene APOC4.

XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
XX Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
XX polycystic kidney disease; von Willebrand's disease; forensic; human;
XX tuberos sclerosis; hereditary hemorrhagica telangiectasia;
XX familial colonic polypsis; osteogenesis imperfecta; porphyria;
XX Ehlers-Danlos syndrome; ss.

OS Homo sapiens.

PN EP955382-A2.

PD 10-NOV-1999.

PF 07-MAY-1999; 99EP-00250150.

PR 07-MAY-1998; 98US-0084641P.

PR 03-MAY-1999; 99US-00304232.

PA (AFPY-) AFFYMETRIX INC.

PA (UYCA-) UNIV CASE WESTERN RESERVE.

PI Pan JB, Chakravarti A, Haluska MK;

DR WPI; 2000-107928/10.

PT Novel nucleic acids containing polymorphisms used in the diagnosis of
PT hypertension.

PS Claim 1; Page 22; 53pp; English.

CC The invention provides polymorphic fragments of genes associated with
CC hypertension. The nucleic acids including the polymorphic sites can be
CC used as probes or primers for expressing variant proteins. Detection of
CC the polymorphisms is useful in designing prophylactic and therapeutic
CC regimens customized to underlying abnormalities. The polymorphisms can be
CC used for association studies for hypertension, and in hypertension
CC diagnostic assays. Where the polymorphisms have strong correlation with
CC hypertension, within a gene, they are likely to have a causative role in
CC hypertension. This information can be used to find the precise role of a
CC polymorphism in the disease, and this can be used to identify potential
CC drugs which combat the disease. The polymorphisms can be tested for

CC association with other diseases e.g. agammaglobulinemia, diabetes
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,
CC tubercous sclerosis, hereditary hemorrhagica telangiectasia, familial
CC colonic polyps, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
CC acute intermittent porphyria. The polymorphic forms can also be used in
CC forensics to identify individuals

XX Sequence 29 BP; 5 A; 7 C; 8 G; 8 T; 0 U; 1 Other;

Query Match 2.5%; Score 24.4; DB 1; Length 29;

Best Local Similarity 89.3%; Pred. No. 8.9e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1112 AGGCTGCTCTCAACCTCGACTCAGG 1139
DB 1 AGGCTGCTCTTGAAATCTGACTCAGG 28

RESULT 304

AAA04389/C
ID AAA04389 standard; DNA; 29 BP.

AC AAA04389;

XX 22-MAY-2000 (first entry)

DE Polymorphic fragment of hypertension associated gene IAPP.

XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
XX Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
XX polycystic kidney disease; von Willebrand's disease; forensic; human;
XX tubercous sclerosis; hereditary hemorrhagica telangiectasia;
XX familial colonic polyps; osteogenesis imperfecta; porphyria;
XX Ehlers-Danlos syndrome; ss.

OS Homo sapiens.

PN EP955382-A2.

PD 10-NOV-1999.

PF 07-MAY-1999; 99BP-00250150.

PR 07-MAY-1998; 98US-0084641P.

PR 03-MAY-1999; 99US-00304232.

XX (AFY-) AFFMETRIX INC.

PA (UYCA-) UNIV CASE WESTERN RESERVE.

PI Fan JB, Chakravarti A, Haluska MK;

XX WPI; 2000-107928/10.

PT Novel nucleic acids containing polymorphisms used in the diagnosis of

XX hypertension.

PS Claim 1; Page 35; 53pp; English.

XX The invention provides polymorphic fragments of genes associated with
CC hypertension. The nucleic acids including the polymorphic sites can be
CC used as probes or primers for expressing variant proteins. Detection of
CC the polymorphisms is useful in designing prophylactic and therapeutic
CC regimens customized to underlying abnormalities. The polymorphisms can be
CC used for association studies for hypertension, and in hypertension
CC diagnostic assays. Where the polymorphisms have strong correlation with
CC hypertension, within a gene, they are likely to have a causative role in
CC hypertension. This information can be used to find the precise role of a
CC polymorphism in the disease, and this can be used to identify potential
CC drugs which combat the disease. The polymorphisms can be tested for
CC association with other diseases e.g. agammaglobulinemia, diabetes

CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,
CC tubercous sclerosis, hereditary hemorrhagica telangiectasia, familial
CC colonic polyps, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
CC acute intermittent porphyria. The polymorphic forms can also be used in
CC forensics to identify individuals

XX Sequence 29 BP; 5 A; 8 C; 10 G; 5 T; 0 U; 1 Other;

Query Match 2.5%; Score 24.4; DB 1; Length 29;

Best Local Similarity 89.3%; Pred. No. 8.9e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 927 GAATCTACTCTGTATCCAGGCTGAG 954
DB 28 GAGTCTCACTCTGYCACCCAGCTGAG 1

RESULT 305

AAA04314
ID AAA04314 standard; DNA; 29 BP.

AC AAA04314;

XX 22-MAY-2000 (first entry)

DE Polymorphic fragment of hypertension associated gene GLUT4.

XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
XX Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
XX polycystic kidney disease; von Willebrand's disease; forensic; human;
XX tubercous sclerosis; hereditary hemorrhagica telangiectasia;
XX familial colonic polyps; osteogenesis imperfecta; porphyria;
XX Ehlers-Danlos syndrome; ss.

OS Homo sapiens.

PN EP955382-A2.

PD 10-NOV-1999.

PF 07-MAY-1999; 99BP-00250150.

PR 07-MAY-1998; 98US-0084641P.

PR 03-MAY-1999; 99US-00304232.

XX (AFY-) AFFMETRIX INC.

PA (UYCA-) UNIV CASE WESTERN RESERVE.

PI Fan JB, Chakravarti A, Haluska MK;

XX WPI; 2000-107928/10.

PT Novel nucleic acids containing polymorphisms used in the diagnosis of

XX hypertension.

PS Claim 1; Page 32; 53pp; English.

XX The invention provides polymorphic fragments of genes associated with
CC hypertension. The nucleic acids including the polymorphic sites can be
CC used as probes or primers for expressing variant proteins. Detection of
CC the polymorphisms is useful in designing prophylactic and therapeutic
CC regimens customized to underlying abnormalities. The polymorphisms can be
CC used for association studies for hypertension, and in hypertension
CC diagnostic assays. Where the polymorphisms have strong correlation with
CC hypertension, within a gene, they are likely to have a causative role in
CC hypertension. This information can be used to find the precise role of a
CC polymorphism in the disease, and this can be used to identify potential
CC drugs which combat the disease. The polymorphisms can be tested for
CC association with other diseases e.g. agammaglobulinemia, diabetes
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich

CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
 CC kidney disease, hereditary spherocytosis, von Willebrand's disease,
 CC tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial
 CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
 CC acute intermittent porphyria. The polymorphic forms can also be used in
 CC forensics to identify individuals

XX Sequence 29 BP; 3 A; 11 C; 6 G; 8 T; 0 U; 1 Other;

Query Match 2.5%; Score 24.4; DB 1; Length 29;
 Best Local Similarity 89.3%; Pred. No. 8.9e+02;
 Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 821 GATCTGTGACCTGTGATCTGCTGCC 848
 DB 2 GATCTGTGACCTGTGATCTGCTGCC 29

RESULT 306
 AD182609/C
 ID AD182609 standard; DNA; 30 BP.

XX AD182609;

DT 22-APR-2004 (first entry)

DE Prostate-specific membrane antigen enhancer PCR primer #2.

XX chimeric; prostate-specific-enhancing sequence promoter; PSES promoter;
 XX androgen receptor core region promoter; AREC3 promoter;
 KW prostate-specific-antigen; PSA;
 KW prostate-specific membrane antigen enhancer; PSMA enhancer; PSMEdel2;
 KW angio genesis reduction; prostate carcinoma cell; ss; PCR; primer.

XX Unidentified.

XX US2003235874-A1.

XX 25-DEC-2003.

XX 08-MAY-2003; 2003US-00431791.

XX 08-MAY-2002; 2002US-0378920P.

XX (KAO/C) KAO C.

XX (LEES/) LEES S.

XX (KIMH/) KIM H.

XX (LEEK/) LEE K.

XX (YURR/) YU R.

XX Kao C, Lee S, Kim H, Lee K, Yu R;

XX WPI; 2004-061500/06.

XX Novel chimeric PSES promoter construct comprising androgen receptor
 PT enhancer core region promoter of prostate-specific-antigen gene and
 PT PSME(del2) promoter of PSMA gene, useful for treating prostate cancer.

XX Example 1; SEQ ID NO 5; 29bp; English.

XX The invention comprises a chimeric prostate-specific-enhancing sequence
 CC (PSES) promoter construct, which contains the androgen receptor core
 CC region (AREC3) promoter of the prostate-specific-antigen (PSA) gene and
 CC the prostate-specific membrane antigen (PSMA) enhancer (PSMEdel2)
 CC promoter of the PSMA gene. The PSES promoter construct of the invention
 CC is useful for reducing angiogenesis in prostate carcinoma cells and in
 CC targeting prostate carcinoma cells for destruction. The PSES promoter
 CC construct is also useful for identifying an agent that modulates PSES
 CC promoter activity. The present DNA sequence represents a PCR primer that
 CC was used in an example of the invention.

XX Sequence 30 BP; 5 A; 8 C; 13 G; 4 T; 0 U; 0 Other;

Query Match 2.5%; Score 24.4; DB 1; Length 30;
 Best Local Similarity 96.2%; Pred. No. 9.1e+02;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 673 GCTCAGTCAACCTCTGCTCCCGG 698
 DB 30 GCTCAGTCAACCTCTGCTCCCGG 5

RESULT 307
 AAQ29012/C
 ID AAQ29012 standard; DNA; 25 BP.

XX AAQ29012;

DT 25-MAR-2003 (revised)

DT 23-FEB-1993 (first entry)

XX Alu family consensus sequence-derived probe #1.

XX Low frequency repeat; Alu restriction digest; genetic mapping; ss.

XX Synthetic.

XX EP505605-A2.

XX 30-SEP-1992.

XX 11-APR-1991; 91EP-00105802.

XX 28-MAR-1991; 91US-00676292.

XX (UYWA-) UNIV WAYNE STATE.

XX Duncan CH, Solus JF, Kaplan DJ;

XX WPI; 1992-324992/40.

XX New nucleic acid probes - have a labelled low frequency repetitive
 PT sequence for detecting overlaps among cloned DNA.

XX Disclosure; Page 8; 41pp; English.

XX 500-1000bp fragments from an AluI-digest of human genomic DNA were
 CC ligated to M13mp19 RF DNA. E.coli JM109 were transformed by the ligation
 CC mixture. Filter replicates of the transformant colonies were screened
 CC with probe #1 and a second probe. The probes were derived from the Alu
 CC family consensus sequence. Phage which hybridised to both probes were
 CC plated at lower density and rescreened with the same probes. Single-
 CC stranded template DNA was extd. from cultures of these phage to isolate
 CC low-frequency repeat sequence probes Lf1, Lf2, Lf3, Lf19, Lf20 and Lf21.
 CC See also AAQ29013-Q29017 and AAQ29021-Q29038. (Updated on 25-MAR-2003 to
 CC correct PN field.)

XX Sequence 25 BP; 5 A; 8 C; 5 G; 5 T; 0 U; 2 Other;

Query Match 2.4%; Score 24.2; DB 1; Length 25;
 Best Local Similarity 92.0%; Pred. No. 8.2e+02;
 Matches 23; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 863 TGCTGGATTACAGCGGTGAGCCAC 887
 DB 25 TGCTGGATTACAGCGGTGAGCCAC 1

XX RESULT 308

XX AAH91549
 ID AAH91549 standard; DNA; 30 BP.

XX AAH91549;

XX 09-OCT-2001 (first entry)

```

DE Human inflammatory bowel disease associated polymorphic site #624.
XX
XX Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KM single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
KM chromosome 5q31-33; forensic test; gene therapy; ds.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH misc_feature 14
FT /tag= a
FT /note="SNP, optionally T or C at this position"
FT
FT WO200142511-A2.
XX
XX PD 14-JUN-2001.
XX
XX PF 11-DEC-2000; 2000WO-US033632.
XX
XX PR 10-DEC-1999; 99US-0170257P.
XX PR 10-APR-2000; 2000US-0196046P.
XX
XX PA (WHEB) WHITEHEAD INST BIOMEDICAL RES.
XX PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX
XX PI Daily M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
XX WPI; 2001-367874/38.
XX
XX PT Testing for the presence of polymorphisms associated with inflammatory
XX bowel disease, using a hybridization assay.
XX
XX PS Claim 1, Page 65; 463pp; English.
XX
XX CC The present invention describes a method for detecting the presence of
XX polymorphisms associated with inflammatory bowel diseases such as
XX ulcerative colitis and Crohn's disease. The methods can be used to detect
XX the presence of genetic polymorphisms associated with inflammatory bowel
XX disease and correlating their occurrence with disease states. They may be
XX used in this way for phenotypic correlations, forensics, paternity
XX testing, medicine and genetic analysis. The present sequence is a
XX polymorphic site described in the exemplification of the invention
XX
XX SQ Sequence 30 BP; 6 A; 11 C; 5 G; 7 T; 0 U; 1 Other;
XX
XX Query Match 2.4%; Score 24.2; DB 1; Length 30;
XX Best Local Similarity 86.7%; Pred. No. 9.3e+02;
XX Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 832 CTTGTGATCTGCTGCTCGGCTCCCAAA 861
XX 1 CATGTGATCTGCGGCTCGGCTCCCAAA 30
XX
XX DB
XX
XX RESULT 309
XX AAF29776
XX ID AAF29776 standard; DNA; 30 BP.
XX
XX AC AAF29776;
XX
XX DT 09-APR-2001 (first entry)
XX
XX DE Presentline-1 gene promoter PCR primer Prom6F.
XX
XX KM Human; PSEN1; Alzheimer's disease; polymorphism; diagnosis;
XX Presentline-1; chromosome 14; PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200079000-A1.
XX
XX PD 28-DEC-2000.
XX

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PF 22-JUN-2000; 2000WO-EP005942.
XX
XX PR 22-JUN-1999; 99EP-00201991.
XX
XX PR (VLA-A-) VLAAWS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
XX PA Theuns J, Cruts M, Van Broeckhoven C;
XX
XX PI WPI; 2001-071402/08.
XX
XX DR
XX
XX PT Determining whether a human subject has or is at risk of developing (early
XX onset) Alzheimer's disease comprises detecting the presence/absence of a
XX genetic lesion in the presentline-1 gene.
XX
XX PS Example 1; Page 45; 56pp; English.
XX
XX CC The present invention describes a method for determining the presence of
XX or susceptibility to Alzheimer's disease in humans, involving detecting a
XX genetic lesion in the presentline-1 (PSEN1) gene, found on chromosome 14.
XX The genetic lesion is a polymorphism in the promoter or upstream
XX regulatory region of the gene. The invention also describes transgenic
XX animals which can be used to identify compounds useful in treating
XX Alzheimer's disease
XX
XX SQ Sequence 30 BP; 7 A; 9 C; 6 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 2.4%; Score 24.2; DB 1; Length 30;
XX Best Local Similarity 89.7%; Pred. No. 9.3e+02;
XX Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 205 GTTCAGGCTGTGCTCGAATCTCCGACCTCA 233
XX 1 GTTAGGCTGTGCTAGAACTCCCAACTCA 29
XX
XX DB
XX
XX RESULT 310
XX AAH45830/C
XX ID AAH45830 standard; DNA; 24 BP.
XX
XX AC AAH45830;
XX
XX DT 11-SEP-2001 (first entry)
XX
XX DE Telomere size determination method related oligonucleotide #3.
XX
XX KM Telomere size determination; chromosomal DNA; probe; primer;
XX repetitive sequence; tissue aging; cancer progression; ds.
XX
XX OS Synthetic.
XX
XX PN JP2001095586-A.
XX
XX PD 10-APR-2001.
XX
XX PF 30-SEP-1999; 99JP-00279948.
XX
XX PR 30-SEP-1999; 99JP-00279948.
XX
XX PA (IDET/) IDE T.
XX
XX DR WPI; 2001-360495/38.
XX
XX PT Determining telomere size useful for investigating aging in tissue and
XX progression of cancer.
XX
XX PS Example 2; Page 6; 8pp; Japanese.
XX
XX CC The present invention describes a method for determining the length of
XX telomeres, involving hybridizing a chromosomal DNA extracted from a
XX sample and a labeled DNA probe with a sequence complementary to a
XX repetitive telomeric sequence, and measuring the labeled signal of the
XX hybridised probe to give the size of telomere. This can be used to
XX investigate tissue aging and the progression of cancer and in monitoring
XX

```

CC the prognosis of patients. The present sequence is an oligonucleotide
XX described in the exemplification of the invention
SQ Sequence 24 BP; 5 A; 6 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 2.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 382 GCTCCCAAGTCTGGATTACA 405
DB 24 GCTCCCAAGTCTGGATTACA 1

RESULT 311
AAH45828
ID AAH45828 standard; DNA; 24 BP.

AAH45828;

11-SEP-2001 (first entry)

DE Telomere size determination method related oligonucleotide #1.

KW Telomere size determination; chromosomal DNA; probe; primer;
KW repetitive sequence; tissue aging; cancer progression; ds.

OS Synthetic.

PN JP2001095586-A.

PD 10-APR-2001.

PF 30-SEP-1999; 99JP-00279948.

PR 30-SEP-1999; 99JP-00279948.

PA (IDET/) IDE T.

DR WPI, 2001-360495/38.

PT Determining telomere size useful for investigating aging in tissue and
PT progression of cancer.

PS Disclosure; Page 5; 8pp; Japanese.

CC The present invention describes a method for determining the length of
CC telomeres, involving hybridizing a chromosomal DNA extracted from a
CC sample and a labeled DNA probe with a sequence complementary to a
CC repetitive telomeric sequence, and measuring the labeled signal of the
CC hybridised probe to give the size of telomere. This can be used to
CC investigate tissue aging and the progression of cancer and in monitoring
CC the prognosis of patients. The present sequence is an oligonucleotide
CC described in the exemplification of the invention
XX

SQ Sequence 24 BP; 6 A; 7 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 382 GCTCCCAAGTCTGGATTACA 405
DB 1 GCTCCCAAGTCTGGATTACA 24

RESULT 312
ADL07545/C
ID ADL07545 standard; DNA; 24 BP.

ADL07545;

DT 06-MAY-2004 (first entry)

XX DE Sec24 protein-31.35 RT-PCR primer #1.

XX ss; primer: Sec24 protein-31.35; cancer; HIV infection; PCR; RT-PCR;
KW reverse transcriptase PCR.

XX Unidentified.

OS CN1393472-A.

PN 29-JAN-2003.

PF 29-JUN-2001; 2001CN-00113189.

PR 29-JUN-2001; 2001CN-00113189.

PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

PI Mao Y, Xie Y;

DR WPI, 2003-422176/40.

PT Polypeptide-Sec24 protein-31.35.

PS Example 3; SEQ ID NO 3; 31pp; Chinese.

CC The invention relates to a polypeptide-Sec24 protein-31.35 and the
CC polynucleotide encoding it. Also included are the process for preparing
CC the polypeptide by recombinant DNA technology, the application of the
CC polypeptide in treating diseases such as cancer and HIV infection, the
CC antagonist against the polypeptide (and its therapeutic action) and the
CC application of the polynucleotide encoding this polypeptide. The present
CC sequence is an RT-(reverse transcriptase) PCR primer used to isolate cDNA
CC encoding the Sec24 protein-31.35.
XX

SQ Sequence 24 BP; 4 A; 9 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 864 GCTGGATTACAGCGTGAGCCAC 887
DB 24 GCTGGATTACAGCGTGAGCCAC 1

RESULT 313
AAH91303/C
ID AAH91303 standard; DNA; 28 BP.

AAH91303;

09-OCT-2001 (first entry)

DE Human inflammatory bowel disease associated polymorphic site #378.

KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;

KW chromosome 5q31-33; forensic test; gene therapy; ds.

OS Homo sapiens.

FT Key Location/Qualifiers

FT misc_feature 15

FT /tag= a /note= "SNP, optionally A or G at this position"

PN WO200142511-A2.

PD 14-JUN-2001.

PF 11-DEC-2000; 2000WO-US033632.

PR 10-DEC-1999; 99US-0170257P.
PR 10-APR-2000; 2000US-0196046P.
XX (MHED) WHITEHEAD INST BIOMEDICAL RES.
PA (ELI-) ELIIPSIS BIOTHEAPERTICS CORP.
XX
XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitsh K;
DR WPI; 2001-367874/38.
XX
XX Testing for the presence of polymorphisms associated with inflammatory
PT bowel disease, using a hybridization assay.
XX
PS Claim 1; Page 54; 463BP; English.
XX
CC The present invention describes a method for detecting the presence of
CC polymorphisms associated with inflammatory bowel diseases such as
CC ulcerative colitis and Crohn's disease. The methods can be used to detect
CC the presence of genetic polymorphisms associated with inflammatory bowel
CC disease and correlating their occurrence with disease states. They may be
CC used in this way for phenotypic correlations, forensics, paternity
CC testing, medicine and genetic analysis. The present sequence is a
CC polymorphic site described in the exemplification of the invention
XX
SQ Sequence 28 BP; 7 A; 5 C; 9 G; 6 T; 0 U; 1 Other;
XX
Query Match 2.4%; Score 23.8; DB 1; Length 28;
Best Local Similarity 89.3%; Pred. No. 9.3e+02;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 682 AACCTGCTGCTCCCGGTTCAAGTTATT 709
DB |||||
28 AACCTGCTGCTCCCGGTTCAAGTTATT 1
XX
RESULT 314
AAA03956
ID AAA03956 standard; DNA; 29 BP.
XX
AC AAA03956;
XX
DT 22-MAY-2000 (first entry)
XX
DE Polymorphic fragment of hypertension associated gene APOC1.
XX
XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
XX Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
XX polycystic kidney disease; von Willebrand's disease; forensic; human;
XX tuberculous sclerostis; hereditary hemorrhagica telangiectasia;
XX familial colonic polyposis; osteogenesis imperfecta; porphyria;
XX Ehlers-Danlos syndrome; ss.
XX
OS Homo sapiens.
XX
PN EP955382-A2.
XX
PD 10-NOV-1999.
XX
PP 07-MAY-1999; 99EP-00250150.
XX
PR 07-MAY-1998; 98US-0084641P.
PR 03-MAY-1999; 99US-00304232.
XX
PA (AFPY-) AFFYMETRIX INC.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
XX
PI Fan JB, Chakravarti A, Haluska MK;
XX
DR WPI; 2000-107928/10.
XX
PT Novel nucleic acids containing polymorphisms used in the diagnosis of
XX hypertension.

XX
PS Claim 1; Page 21; 53BP; English.
XX
CC The invention provides polymorphic fragments of genes associated with
CC hypertension. The nucleic acid including the polymorphic sites can be
CC used as probes or primers for expressing variant proteins. Detection of
CC the polymorphisms is useful in designing prophylactic and therapeutic
CC regimes customized to underlying abnormalities. The polymorphisms can be
CC used for association studies for hypertension, and in hypertension with
CC diagnostic assays. Where the polymorphisms have strong correlative role in
CC hypertension, within a gene, they are likely to have a causative role of a
CC polymorphism in the disease, and this can be used to identify potential
CC drugs which combat the disease. The polymorphisms can be tested for
CC association with other diseases e.g. agammaglobulinemia, diabetes
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,
CC tuberculous sclerostis, hereditary hemorrhagica telangiectasia, familial
CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
CC acute intermittent porphyria. The polymorphic forms can also be used in
CC forensics to identify individuals
XX
SQ Sequence 29 BP; 7 A; 4 C; 6 G; 11 T; 0 U; 1 Other;
XX
Query Match 2.4%; Score 23.8; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 9.5e+02;
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1073 TTGTAATTTTCATTAGAGCGGGGTTTCC 1101
DB |||||
1 TTGTAATTTTCATTAGAGCGGGGTTTCC 29
XX
RESULT 315
AAA04662
ID AAA04662 standard; DNA; 29 BP.
XX
AC AAA04662;
XX
DT 22-MAY-2000 (first entry)
XX
DE Polymorphic fragment of hypertension associated gene TBXA2R.
XX
XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
XX Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
XX polycystic kidney disease; von Willebrand's disease; forensic; human;
XX tuberculous sclerostis; hereditary hemorrhagica telangiectasia;
XX familial colonic polyposis; osteogenesis imperfecta; porphyria;
XX Ehlers-Danlos syndrome; ss.
XX
OS Homo sapiens.
XX
PN EP955382-A2.
XX
PD 10-NOV-1999.
XX
PP 07-MAY-1999; 99EP-00250150.
XX
PR 07-MAY-1998; 98US-0084641P.
PR 03-MAY-1999; 99US-00304232.
XX
PA (AFPY-) AFFYMETRIX INC.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
XX
PI Fan JB, Chakravarti A, Haluska MK;
XX
DR WPI; 2000-107928/10.
XX
PT Novel nucleic acids containing polymorphisms used in the diagnosis of
XX hypertension.

PS Claim 1; Page 43; 53pp; English.

XX
CC The invention provides polymorphic fragments of genes associated with
CC hypertension. The nucleic acids including the polymorphic sites can be
CC used as probes or primers for expressing variant proteins. Detection of
CC the polymorphisms is useful in designing prophylactic and therapeutic
CC regimens customized to underlying abnormalities. The polymorphisms can be
CC used for association studies for hypertension, and in hypertension
CC diagnostic assays. Where the polymorphisms have strong correlation with
CC hypertension, within a gene, they are likely to have a causative role in
CC hypertension. This information can be used to find the precise role of a
CC polymorphism in the disease, and this can be used to identify potential
CC drugs which combat the disease. The polymorphisms can be tested for
CC association with other diseases e.g. agammaglobulinemia, diabetes
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
CC syndrome, Fabry disease, familial hypercholesterolemia, polycystic
CC kidney disease, hereditary spherocytosis, von Willebrand disease,
CC tuberculous sclerosis, hereditary hemorrhagic telangiectasia, familial
CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
CC acute intermittent porphyria. The polymorphic forms can also be used in
CC forensics to identify individuals

SO Sequence 29 BP; 6 A; 8 C; 8 G; 6 T; 0 U; 1 Other;

Query Match 2.4%; Score 23.8; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 9.5e+02;
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 652 GAGTCGAGTGGCGCATCTTGGCTCACTG 680
DB 1 GAGTCAGTGGCAGCATCTCGGCTCACTG 29

RESULT 316
AAA04486/c
ID AAA04486 standard; DNA; 29 BP.
AC AAA04486;
XX
XX
XX 22-MAY-2000 (first entry)
DE Polymorphic fragment of hypertension associated gene PGIS.
XX
XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
XX Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
XX Fabry disease; familial hypercholesterolemia; hereditary spherocytosis;
XX polycystic kidney disease; von Willebrand disease; forensic; human;
XX tuberculous sclerosis; hereditary hemorrhagic telangiectasia;
XX familial colonic polyposis; osteogenesis imperfecta; porphyria;
XX Ehlers-Danlos syndrome; ss.
XX
XX Homo sapiens.
XX
XX EP955382-A2.
XX
XX 10-NOV-1999.
XX
XX 07-MAY-1999; 99EP-00250150.
XX
XX 07-MAY-1998; 98US-0084641P.
XX 03-MAY-1999; 99US-00304232.
XX
XX (AFY-) AFFYMETRIX INC.
XX (UYCA-) UNIV CASE WESTERN RESERVE.
XX
XX Fan JB, Chakravarti A, Haluska MK;
XX
XX WPI; 2000-107928/10.
XX
XX Novel nucleic acids containing polymorphisms used in the diagnosis of
XX hypertension.
XX
XX Claim 1; Page 38; 53pp; English.

XX
CC The invention provides polymorphic fragments of genes associated with
CC hypertension. The nucleic acids including the polymorphic sites can be
CC used as probes or primers for expressing variant proteins. Detection of
CC the polymorphisms is useful in designing prophylactic and therapeutic
CC regimens customized to underlying abnormalities. The polymorphisms can be
CC used for association studies for hypertension, and in hypertension
CC diagnostic assays. Where the polymorphisms have strong correlation with
CC hypertension, within a gene, they are likely to have a causative role in
CC hypertension. This information can be used to find the precise role of a
CC polymorphism in the disease, and this can be used to identify potential
CC drugs which combat the disease. The polymorphisms can be tested for
CC association with other diseases e.g. agammaglobulinemia, diabetes
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
CC syndrome, Fabry disease, familial hypercholesterolemia, polycystic
CC kidney disease, hereditary spherocytosis, von Willebrand disease,
CC tuberculous sclerosis, hereditary hemorrhagic telangiectasia, familial
CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
CC acute intermittent porphyria. The polymorphic forms can also be used in
CC forensics to identify individuals

SO Sequence 29 BP; 9 A; 10 C; 4 G; 5 T; 0 U; 1 Other;

Query Match 2.4%; Score 23.8; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 9.5e+02;
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 177 TTAGTAGAGATGAGTTCTCCATGTTGG 205
DB 29 TTAGTAGAGACGCGGRTTCCCATGTTGG 1

RESULT 317
AAA03878/c
ID AAA03878 standard; DNA; 29 BP.
AC AAA03878;
XX
XX
XX 22-MAY-2000 (first entry)
DE Polymorphic fragment of hypertension associated gene AEL.
XX
XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
XX Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
XX Fabry disease; familial hypercholesterolemia; hereditary spherocytosis;
XX polycystic kidney disease; von Willebrand disease; forensic; human;
XX tuberculous sclerosis; hereditary hemorrhagic telangiectasia;
XX familial colonic polyposis; osteogenesis imperfecta; porphyria;
XX Ehlers-Danlos syndrome; ss.
XX
XX Homo sapiens.
XX
XX EP955382-A2.
XX
XX 10-NOV-1999.
XX
XX 07-MAY-1999; 99EP-00250150.
XX
XX 07-MAY-1998; 98US-0084641P.
XX 03-MAY-1999; 99US-00304232.
XX
XX (AFY-) AFFYMETRIX INC.
XX (UYCA-) UNIV CASE WESTERN RESERVE.
XX
XX Fan JB, Chakravarti A, Haluska MK;
XX
XX WPI; 2000-107928/10.
XX
XX Novel nucleic acids containing polymorphisms used in the diagnosis of
XX hypertension.
XX
XX Claim 1; Page 18; 53pp; English.

used as probes or primers for expressing variant proteins. Detection of the polymorphisms is useful in designing prophylactic and therapeutic regimens customized to underlying abnormalities. The polymorphisms can be used for association studies for hypertension, and in hypertension diagnostic assays. Where the polymorphisms have strong correlation with hypertension, within a gene, they are likely to have a causative role in hypertension. This information can be used to find the precise role of a polymorphism in the disease, and this can be used to identify potential drugs which combat the disease. The polymorphisms can be tested for association with other diseases e.g. agammaglobulinemia, diabetes insipidus, Leach-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria. The polymorphic forms can also be used in forensics to identify individuals

Sequence 29 BP; 6 A; 14 C; 6 G; 2 T; 0 U; 1 Other;

Query Match 2.4%; Score 23.8; DB 1; Length 29;

Best Local Similarity 86.2%; Pred. No. 9.5e+02;

Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

1034 CTGGGATTACGGGACCTGCCACACACC 1062

1 CTGGGACTACAGGCGCCGCCACACACC 29

RESULT 320

AAA04661

ID AAA04661 standard; DNA; 29 BP.

AAA04661;

22-MAY-2000 (first entry)

Polymorphic fragment of hypertension associated gene TBXA2R.

Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus; Leach-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome; Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis; polycystic kidney disease; von Willebrand's disease; forensic; human; tuberous sclerosis; hereditary hemorrhagic telangiectasia; familial colonic polyposis; osteogenesis imperfecta; porphyria; Ehlers-Danlos syndrome; ss.

Homo sapiens.

EP955382-A2.

10-NOV-1999.

07-MAY-1999; 99EP-00250150.

07-MAY-1998; 98US-0084641P.

03-MAY-1999; 99US-00304232.

(AFV-) AFFYMETRIX INC.

(UYCA-) UNIV CASE WESTERN RESERVE.

Fan JB, Chakravarti A, Haluska MK;

WPI; 2000-107928/10.

Novel nucleic acids containing polymorphisms used in the diagnosis of hypertension.

Claim 1; Page 43; 53pp; English.

The invention provides polymorphic fragments of genes associated with hypertension. The nucleic acids including the polymorphic sites can be used as probes or primers for expressing variant proteins. Detection of

the polymorphisms is useful in designing prophylactic and therapeutic regimens customized to underlying abnormalities. The polymorphisms can be used for association studies for hypertension, and in hypertension diagnostic assays. Where the polymorphisms have strong correlation with hypertension, within a gene, they are likely to have a causative role in hypertension. This information can be used to find the precise role of a polymorphism in the disease, and this can be used to identify potential drugs which combat the disease. The polymorphisms can be tested for association with other diseases e.g. agammaglobulinemia, diabetes insipidus, Leach-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria. The polymorphic forms can also be used in forensics to identify individuals

Sequence 29 BP; 5 A; 8 C; 9 G; 6 T; 0 U; 1 Other;

Query Match 2.4%; Score 23.8; DB 1; Length 29;

Best Local Similarity 86.2%; Pred. No. 9.5e+02;

Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

650 TGGAGTGCAGTGGCGCATCTTGCTCAC 678

1 TGGAGTACAGTGGCGCATCTTGCTCAC 29

RESULT 321

AAA04307

ID AAA04307 standard; DNA; 29 BP.

AAA04307;

22-MAY-2000 (first entry)

Polymorphic fragment of hypertension associated gene GLUT4.

Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus; Leach-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome; Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis; polycystic kidney disease; von Willebrand's disease; forensic; human; tuberous sclerosis; hereditary hemorrhagic telangiectasia; familial colonic polyposis; osteogenesis imperfecta; porphyria; Ehlers-Danlos syndrome; ss.

Homo sapiens.

EP955382-A2.

10-NOV-1999.

07-MAY-1999; 99EP-00250150.

07-MAY-1998; 98US-0084641P.

03-MAY-1999; 99US-00304232.

(AFV-) AFFYMETRIX INC.

(UYCA-) UNIV CASE WESTERN RESERVE.

Fan JB, Chakravarti A, Haluska MK;

WPI; 2000-107928/10.

Novel nucleic acids containing polymorphisms used in the diagnosis of hypertension.

Claim 1; Page 32; 53pp; English.

The invention provides polymorphic fragments of genes associated with hypertension. The nucleic acids including the polymorphic sites can be used as probes or primers for expressing variant proteins. Detection of the polymorphisms is useful in designing prophylactic and therapeutic

regimes customized to underlying abnormalities. The polymorphisms can be used for association studies for hypertension, and in hypertension diagnostic assays. Where the polymorphisms have strong correlation with hypertension, within a gene, they are likely to have a causative role in hypertension. This information can be used to find the precise role of a polymorphism in the disease, and this can be used to identify potential drugs which combat the disease. The polymorphisms can be tested for association with other diseases e.g. agammaglobulinemia, diabetes insipidus, Leech-Myhan syndrome, muscular dystrophy, Miskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polygenic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberosus sclerosis, hereditary hemorrhagica telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria. The polymorphic forms can also be used in forensics to identify individuals

Sequence 29 BP; 7 A; 12 C; 6 G; 3 T; 0 U; 1 Other;

Query Match 2.4%; Score 23.8; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 9.5e+02;
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

1034 CTGGGATTACGGGACCTGCGACACACC 1062
|||||
1 CTGGGACTACAGGCGCATGCGACACACC 29

RESULT 322

AA209548/C
ID AA209548 standard; DNA; 25 BP.

AA209548;

08-NOV-1999 (first entry)

Human Apo E oligonucleotide primer 4.

Apo E; Apo B; hyperlipidemia; human; treatment; hepatocyte; apoprotein;

Apo A1; low density lipoprotein; LDL; blood; therapy; atherosclerosis;

high density lipoprotein; HDL; cholesterol; coronary heart disease;

Alzheimer's disease; hypobetalipoproteinemia; dysbetalipoproteinemia;

primer; ss.

Synthetic.

Homo sapiens.

MO940789-A1.

19-AUG-1999.

28-AUG-1998; 98MO-US017908.

12-FEB-1998; 98US-0074497P.

30-JUN-1998; 98US-00108006.

(MINU) UNIV MINNESOTA.

(YESH) UNIV YESHIVA EINSTEIN COLLEGE.

Steer CJ, Kren BT, Bandyopadhyay PT, Roy-Chowdhury J;

WPI; 1999-527333/44.

Mutating apolipoprotein genes in hepatocytes to control cholesterol

levels, e.g. for treating or preventing hyperlipidemia, particularly

atherosclerosis.

an apo E gene in hepatocytes by introducing the mutations Arg112Cys, Arg158Cys or Cys158Arg and a method for ameliorating atherosclerosis by altering the apo A1 gene in a hepatocyte so that the altered protein can diesterize. Altering expression of apo genes regulates levels of high and low density lipoprotein cholesterol. Altering expression of apo B, E and A1 genes is used to treat or prevent atherosclerosis, coronary heart disease, Alzheimer's disease, hypobetalipoproteinemia, and dysbetalipoproteinemia. AA209545-209548 represented primers used in the manipulation of the human Apo E protein described in the method of the invention

Sequence 25 BP; 7 A; 5 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 2.4%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 9e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1113 GGCTGCTCAACACTGCTGACCTCA 1137
|||||
25 GGCTGCTCAACACTGCTGACCTTA 1

RESULT 323

AA216609
ID AA216609 standard; DNA; 25 BP.

AA216609;

29-APR-1999 (first entry)

Interleukin 1 (44112332) haplotype PCR primer #3.

Interleukin 1; IL-1; haplotype; inflammatory disorder; alopecia areata;

coronary artery disease; osteoporosis; nephropathy; diabetes mellitus;

Graves disease; systemic lupus erythematosus; lichen sclerosis;

ulcerative colitis; PCR primer; ss.

Synthetic.

Homo sapiens.

MO9854359-A1.

03-DEC-1998.

21-MAY-1998; 98MO-GB001481.

29-MAY-1997; 97GB-00011040.

(DUFF/) DUFF G.

(COXA/) COX A.

(CAMP/) CAMP N J.

(DGIO/) DE GIOVINE F S.

Duff G, Cox A, Camp NJ, De Giovine FS;

WPI; 1999-080814/07.

New method of determining a patient's susceptibility to inflammatory

disorder - by detecting the presence of an IL-1 (44112332) haplotype,

useful in designing treatment strategies that modulate the activity of

proteins produced by the IL-1 gene cluster.

Claim 3; Page 33; 49pp; English.

A method has been developed for determining a patient's susceptibility to

an inflammatory disorder. The method comprises the detection of an

CC diseases. The present sequence represents a PCR primer used to amplify a
CC region containing an SNP (single-nucleotide polymorphism) from human
CC SNAP23
XX
SQ Sequence 25 BP; 7 A; 7 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.4%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 9e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 383 CCTCCCAAGTGTGGATTACAG 407
DB 1 CCTCCCAAGTGTGGATTACAG 25

RESULT 326
ABK70489/c
ID ABK70489 standard; DNA; 25 BP.

AC ABK70489;

DT 15-JUL-2002 (first entry)

DE In-situ analysis synthetic probe #57.

XX Human; oligonucleotide label-domain; CMV; cytomegalovirus; EBV;

XX Epstein-Barr virus; lambda-immunoglobulin light chain; hapten;

XX kappa-immunoglobulin light chain; repetitive Alu sequence; EBER;

XX Epstein-Barr early RNA; probe; ss.

XX Synthetic.

XX MO20022874-A2.

XX 21-MAR-2002.

XX 06-SEP-2001; 2001WO-US028014.

XX 15-SEP-2000; 2000US-0233177P.

XX (VENT-) VENTANA MEDICAL SYSTEMS INC.

XX Utermohlen JG, Connaughton J;

XX WPI; 2002-371972/40.

XX Novel oligonucleotide label-domain for incorporation into oligonucleotide

XX probes useful for detecting or localizing nucleic acid target genes

XX within a cell or tissue sample.

XX PS Disclosure; Page 69; 71pp; English.

XX The present invention relates to a new oligonucleotide label-domain

XX comprising the sequence (CTATT) n and its complement (AAATAG) n, where

XX n is 1. The probe sets of the invention are useful for detecting kappa or

XX lambda-immunoglobulin light chain mRNA or corresponding heteronuclear

XX RNA, CMV (cytomegalovirus) immediate early RNA, EBV (Epstein-Barr virus)

XX early RNA 1 and RNA 2, and human Alu repetitive satellite genomic

XX sequences. The invention is a useful generic sequence for incorporation

XX into oligonucleotide probes for detecting gene-specific sequences within

XX cells or tissue samples in in situ hybridisation analysis and for

XX attaching a label to immunoglobulin or other proteins for detecting

XX CC haplens and antigens in immunohistochemical analyses. The present nucleic

XX acid sequence represents one of a collection (ABK70376-ABK70501) of

XX oligonucleotide probes that were used in the invention for detecting or

XX localising a plurality nucleic acid target gene or antigen within a cell

XX or tissue sample

XX Sequence 25 BP; 4 A; 5 C; 13 G; 3 T; 0 U; 0 Other;

XX Query Match 2.4%; Score 23.4; DB 1; Length 25;

XX Best Local Similarity 96.0%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;

XX Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 672 GGCTCAGCAGACCTGCTCCCG 696
DB 25 GGCTCAGCAGACCTGCTCCCG 1

RESULT 327
AAD27391
ID AAD27391 standard; DNA; 25 BP.

AC AAD27391;

DT 18-APR-2002 (first entry)

DE PCR primer #1, used for genotyping human IL-1A (gz5/gz6) marker.

XX Human; interleukin-1; inflammatory disorder; coronary artery disease;

XX periodontal disease; Alzheimer's disease; atherosclerosis; osteoporosis;

XX immune response; insulin-dependent diabetes; diabetic retinopathy;

XX renal disease; diabetic nephropathy; hepatic fibrosis; alopecia areata;

XX Graves disease; Graves ophthalmopathy; systemic lupus erythematosus;

XX extrathyroid disease; lichen sclerosis; juvenile chronic arthritis;

XX rheumatoid arthritis; gastric cancer; ulcerative colitis; asthma;

XX interstitial lung disease; idiopathic pulmonary fibrosis; sepsis;

XX multiple sclerosis; acne; cardiac; dermatological; neuroprotective;

XX nootropic; osteopathic; ophthalmological; IL-1A; PCR primer; ss.

XX Homo sapiens.

XX MO200200933-A2.

XX 03-JAN-2002.

XX 22-JUN-2001; 2001WO-US020079.

XX 23-JUN-2000; 2000US-0213853P.

XX (INTE-) INTERLEUKIN GENETICS INC.

XX Duff GW, Korman KS;

XX WPI; 2002-139934/18.

XX Screening a substance in a subject for modulating an immune response.

XX comprises genotyping to identify the test subject, and observing a

XX biomarker before and after contacting the subject with the test

XX substance.

XX PS Example; Page 42; 54pp; English.

XX The present invention relates to methods for identifying a test substance

XX that modulate the immune response in a genotype specific manner. Methods

XX of the invention involve genotyping subjects to identify those having a

XX genotype (e.g. interleukin-1; IL-1) associated with one or more

XX inflammatory disorder. The method comprises genotyping a subject having

XX an inflammatory disease-associated genotype and observing a biomarker in

XX the subject before and after the subject is contacted with the test

XX substance. The method or cells associated with inflammatory diseases are

XX useful for identifying a substance that is likely to prevent or diminish

XX a specific biological response in subjects having inflammatory disease-

XX associated genotype, where the genotype is associated a pre-disposition

XX to one or more of periodontal disease, coronary artery disease,

XX Alzheimer's disease, atherosclerosis, osteoporosis, insulin- dependent

XX diabetes, diabetic retinopathy, end-stage renal disease, diabetic

XX nephropathy, hepatic fibrosis, alopecia areata, Graves disease, Graves

XX ophthalmopathy, extrathyroid disease, systemic lupus erythematosus,

XX lichen sclerosis, rheumatoid arthritis, juvenile chronic arthritis,

XX gastric cancer, ulcerative colitis, asthma, interstitial lung disease,

XX multiple sclerosis, idiopathic pulmonary fibrosis, sepsis and acne. The

XX invention also relates to a kit comprising primers for the identification

XX of one or more IL-1 polymorphism. The present sequence is a PCR primer

XX which is used for amplifying IL-1A (gz5/gz6) gene. This primer is used in

XX the exemplification of the invention for genotyping IL-1A (gz5/gz6)

CC marker
XX
SQ Sequence 25 BP; 5 A; 7 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 2.4%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 9e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 867 GGGATTACAGCGGTGAGCCACG 891
DB 1 GGGATTACAGCGGTGAGCCACG 25

RESULT 328
ADB04743
ID ADB04743 standard; DNA; 25 BP.

AC ADB04743;
DT 20-NOV-2003 (first entry)

XX Human MDZ7 scanning oligonucleotide SEQ ID 5729.

XX Cyclostatic; immunostimulant; gene therapy; vaccine; human;
KM zinc finger protein; MD23; MD24; MD27; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.

XX Homo sapiens.

XX EP1281758-A2.

XX 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.

XX 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AECOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23.
PT MD24, MD27 or MD212, e.g. cancer.

PS Example 8; SEQ ID NO 5729; 103pp; English.

XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23.
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic loci. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.

SQ Sequence 25 BP; 5 A; 1 C; 8 G; 11 T; 0 U; 0 Other;

Query Match 2.4%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 770 TTTTGATTTTATTAGTAGAGTGGG 794
DB 1 TTTTGATTTTATTAGTAGAGTGGG 25

RESULT 329
ADN48862
ID ADN48862 standard; DNA; 25 BP.

XX ADN48862;

DT 15-JUL-2004 (first entry)

XX Human interleukin-1A (gz5/gz6) amplifying PCR primer #1.

XX Early-onset menopause; EOM; diagnosis; therapy; human; interleukin-1A;
KM IL-1A; PCR; primer; ss.

XX Homo sapiens.

XX US6730476-B1.

XX 04-MAY-2004.

XX 04-AUG-2000; 2000US-00632657.

XX 30-JUN-1999; 99US-00345217.

XX (INTE-) INTERLEUKIN GENETICS INC.

XX Duff G, Kornman K, Van Dijk S;

XX WPI; 2004-354679/33.

PT Determining the predisposition to early-onset menopause comprises
PT detecting in the subject interleukin (IL)-1RN (+2018) allele 2.

PS Example; SEQ ID NO 25; 57pp; English.

XX The present invention provides a method for determining the
CC predisposition of a subject to early-onset menopause (EOM). The invention
CC is useful in diagnosing, treating and preventing early-onset menopause.
CC The present sequence is human secreted interleukin-1A (IL-1A) amplifying
CC PCR primer. The sequence is used in exemplification of the invention.

SQ Sequence 25 BP; 5 A; 7 C; 10 G; 3 T; 0 U; 0 Other;
Query Match 2.4%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 9e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 867 GGGATTACAGCGGTGAGCCACG 891
DB 1 GGGATTACAGCGGTGAGCCACG 25

RESULT 330
AAZ37279/C
ID AAZ37279 standard; DNA; 27 BP.

XX AAZ37279;

DT 01-FEB-2000 (first entry)

XX PCR primer for SGRF coding sequence.

XX SGRF; human; Interleukin-6 G-CSF related factor; cell proliferation;
KM immune system; haematopoietic system; therapy; PCR primer; ss.

XX Synthetic.

XX Homo sapiens.

XX WO954357-A1.

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XX 28-OCT-1999.
PD 14-APR-1999; 99WO-JP001997.
XX 14-APR-1998; 98BP-00121805.
XX 14-APR-1998; 98BP-00121805.
XX (CHUS ) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX Hirata Y;
XX WPI; 2000-013230/01.
XX Novel cytokine-like protein, with activity of supporting proliferation of
PT myeloid cells, useful in treating abnormality of cell proliferation in
PT immune and hematopoiesis systems.
XX Example 5; Page 23; 69pp; Japanese.
XX This sequence represents a PCR primer used to isolate DNA encoding the
CC Interleukin-6-G-CSF related factor (SGRF) protein of the invention. The
CC protein is a member of the IL-6/G-CSF/MSF family. The protein can be used
CC in drugs for treating diseases due to abnormality of cell proliferation
CC in the immune system and haematopoietic system
XX Sequence 27 BP; 4 A; 5 C; 12 G; 6 T; 0 U; 0 Other;
SQ
Query Match 2.4%; Score 23.4; DB 1; Length 27;
Best Local Similarity 96.0%; Pred. No. 9.4e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 537 CCGGCTCAAGCTTCCCAAGTAGCTG 561
DB 27 CCGGCTCAAGCTTCCCAAGTAGCTG 3
RESULT 331
ID AAH38611/c
ID AAH38611 standard; DNA; 27 BP.
AC AAH38611;
XX 14-AUG-2001 (first entry)
XX SNP specific SNPE primer SEQ ID 1407.
DE Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; primer; ss.
XX Homo sapiens.
OS
XX WO200129262-A2.
PN 26-APR-2001.
PD 13-OCT-2000; 2000WO-US028436.
XX 15-OCT-1999; 99US-0160096P.
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX Picoult-Newburg L, Pohl M;
XX WPI; 2001-290930/30.
XX New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polymorphic polymorphism in a nucleic
PT acid sample.
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```
PS Claim 1; Page 57; 83pp; English.
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC diseases of which a component is or may be genetic such as autoimmune
CC disease, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a single nucleotide
CC primer extension (SNPE) primer specific for a human SNP containing DNA
CC sequence
XX Sequence 27 BP; 6 A; 6 C; 10 G; 3 T; 0 U; 2 Other;
SQ
Query Match 2.4%; Score 23.4; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 673 GCTCACTGCAACCTGCTCCCGGCT 699
DB 27 GCTCACTGCAACCTGCTCCCGGCT 1
RESULT 332
ID AAA27185
ID AAA27185 standard; DNA; 28 BP.
AC AAA27185;
XX 11-SEP-2000 (first entry)
XX Reverse primer IL10 for target sequence human interleukin 10.
DE P2; CX5C chemokine; Chromosome 5q31; gene therapy; asthma; PCR primer;
XX allergic rhinitis; urticaria; anaphylactic shock; hives; hay fever; human;
XX ss.
XX Homo sapiens.
OS
XX WO200029621-A2.
PN 25-MAY-2000.
PD 12-NOV-1999; 99WO-US026931.
XX 16-NOV-1998; 98US-00193320.
XX (GENE-) GENELABS TECHNOLOGIES INC.
XX Dolganov G, Novikov A;
XX WPI; 2000-387825/33.
XX Measuring target polymorphic sequences in biological samples by
PT contacting sequence-selective primer pairs, forming conjugates with
PT adaptor molecules, polymerizing target-identifier dimers and quantifying
PT them.
```

PS Disclosure; Page 100; 103pp; English.

CC A novel method for simultaneously determining the level of a number of
CC target polynucleotides in a sample has been disclosed. The method
CC involves forming double stranded copies of the target sequence in direct
CC proportion to the target levels in the original sample. The target
CC sequence is copied using primer pairs designed to flank a defined region
CC in the target sequence. The double stranded copies are then cleaved and
CC reacted with either first or second adaptor sequences. The first and
CC second conjugate mixtures are then allowed to form dimers with each other
CC through the target sequences. The adaptor sequences are then removed to
CC leave target sequence dimers. These dimers are then polymerised to form
CC dimer multimers. The relative abundances of target identifiers in the
CC multimer allow expression levels to be determined. This method is useful
CC for developing polynucleotide abundance level profiles for cells and
CC tissues under various conditions, stages of development and disease
CC states, particularly where the target polynucleotide is present at low
CC levels. The method may also be used in the discovery and evaluation of
CC candidate therapeutic agents and their effective dosage levels. In
CC addition to the method described above, the invention also includes the
CC polynucleotide and polypeptide of P2. P2 is thought to be a member of a
CC novel chemokine family, denoted CX5C and may be associated with immune
CC function. Compositions of the P2 polypeptide may be useful in the
CC treatment of asthma, allergic rhinitis (hay fever), urticaria (hives),
CC anaphylactic shock and conditions involving immune system
CC hypersensitivity. The P2 polynucleotide to treat conditions using gene
CC therapy. The human P2 gene has been localised to chromosome 5, within the
CC cytokine gene cluster at 5q31. The present sequence is the reverse primer
CC IL10 for target sequence human interleukin 10

XX SQ Sequence 28 BP; 5 A; 8 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 2.4%; Score 23.4; DB 1; Length 28;
Best Local Similarity 96.0%; Pred. No. 9.7e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 635 CTCTGTCAACCGAGCTGAGTGACAG 659
|||
DB 4 CTCTGTCAACCGAGCTGAGTGACAG 28

RESULT 333
ACC84463
ID ACC84463 standard; DNA; 28 BP.
XX AC ACC84463;
XX 28-AUG-2003 (first entry)
XX
XX NTP peptide encoding sequence #10.
DE
XX
XX Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
KW neutral thread protein; NTP; tumour; ds.
XX
XX Unidentified.
OS
XX WO2003008443-A2.
XX
XX 30-JAN-2003.
PD
XX
XX 19-JUL-2002; 2002WO-CA001105.
XX
XX 19-JUL-2001; 2001US-0306150P.
XX
XX 19-JUL-2001; 2001US-0306161P.
XX
XX 16-NOV-2001; 2001US-0331477P.
XX
XX (NYMO-) NYMOX CORP.
XX
XX Averbach PA;
XX
XX WPI; 2003-247999/24.
XX
XX P-PSDB; ABR63258.
XX

PT Novel neural thread protein peptide, referred as cell death peptide,
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.

XX
XX
XX Disclosure; Page 17; 77pp; English.

PS
XX
XX The present invention relates to a neural thread protein (NTP) peptide
CC referred to as cell death peptide. Thought to be cytostatic,
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for
CC treating a condition in a patient requiring removal or destruction of
CC cells, for treating a condition such as benign or malignant tumor,
CC inflammatory disease, autoimmune disease and infectious disease. The
CC peptide useful for treatment is derived from the amino acid sequence for
CC a pancreatic chosen protein. The peptide is conjugated, linked or bound
CC to a molecule chosen from antibody or its fragment, antibody-like binding
CC molecule, where the molecule has a higher affinity for binding to a tumor
CC or other target than binding to other cells. Treatment using NTP peptides
CC can remove benign tumors with less risk and fewer of the undesirable side
CC effects of surgery. The present sequence is an NTP encoding sequence

XX SQ Sequence 28 BP; 6 A; 9 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 2.4%; Score 23.4; DB 1; Length 28;
Best Local Similarity 96.0%; Pred. No. 9.7e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 725 CCTGAGTAGCTGGAGCTACAGCGC 749
|||
DB 4 CCTGAGTAGCTGGAGCTACAGCGC 28

RESULT 334
ADP70455
ID ADP70455 standard; DNA; 28 BP.
XX AC ADP70455;
XX
XX 12-AUG-2004 (first entry)
XX
XX RT-PCR primer 2 related to human blood disease-related LRRc8 mutant.
DE
XX
XX LRRc8, B-cell surface membrane; immunosuppressive;
KW non-gamma globulin blood disease; maturation; human; ss; probe;
KW chromosome 9; chromosome 20; translocation.
XX
XX Homo sapiens.
OS
XX
XX JP2004141048-A.
XX
XX 20-MAY-2004.
PD
XX
XX 23-OCT-2002; 2002JP-00308855.
XX
XX 23-OCT-2002; 2002JP-00308855.
XX
XX (OOSA-) ZH OOSAKA SANGYO SHINKO KIKO.
XX
XX (OSAP) OSAKA PREFECTURE.
XX
XX WPI; 2004-382668/36.
XX
XX Novel LRRc8 protein useful as marker for congenital non-gamma globulin
PT blood disease, or for screening B-cell associated disease therapeutic
PT agent or immunosuppressive agent.
XX
XX
XX Disclosure; SEQ ID NO 12; 46pp; Japanese.

CC The invention relates to a novel LRRc8 protein comprising a fully defined
CC sequence as given in the specification, or a receptor protein in which
CC one or more amino acid residues are substituted, added or deleted, that
CC expresses on the B-cell surface membrane of a non-gamma globulin diseased
CC patient. The polypeptide of the invention demonstrates immunosuppressive
CC activity and may be useful for screening a B-cell-associated disease
CC therapeutic agent or immunosuppressive agent, as a marker for congenital

CC non-gamma globulin blood disease or as an agent for maturation of human
CC or mouse B-cells. The current sequence is that of the RT-PCR primer 2 of
CC the invention which is related to the human LRRC8 mutant that is
CC generated by a translocation between chromosomes 9 and 20.

XX Sequence 28 BP; 7 A; 7 C; 7 G; 7 T; 0 U; 0 Other;

SO Query Match 2.4%; Score 23.4; DB 1; Length 28;
Best Local Similarity 96.0%; Pred. No. 9.7e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1018 TCAGCCTCCCAAGACGCTGGATTA 1042
DB 1 TCAGCCTCCCAAGACGCTGGATTA 25

RESULT 335
AAA04010/C
ID AAA04010 standard; DNA; 29 BP.

XX AAA04010;
AC 22-MAY-2000 (first entry)

DE Polymorphic fragment of hypertension associated gene APOC4.

XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
XX Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
XX polycystic kidney disease; von Willebrand's disease; forensic; human;
XX tuberous sclerosis; hereditary hemorrhagica telangiectasia;
XX familial colonic polyposis; osteogenesis imperfecta; porphyria;
XX Ehlers-Danlos syndrome; ss.

XX Homo sapiens.

XX EP955382-A2.

XX 10-NOV-1999.

XX 07-MAY-1999; 99EP-00250150.

XX 07-MAY-1998; 98US-0084641P.

XX 03-MAY-1999; 99US-00304232.

XX (AFY-) AEFYMETRIX INC.

XX (UYCA-) UNIV CASE WESTERN RESERVE.

XX Fan JB, Chakravarti A, Haluska MK;

XX WPI; 2000-107928/10.

XX Novel nucleic acids containing polymorphisms used in the diagnosis of

XX hypertension.

XX Claim 1; Page 22; 53pp; English.

XX The invention provides polymorphic fragments of genes associated with
XX hypertension. The nucleic acids including the polymorphic sites can be
XX used as probes or primers for expressing variant proteins. Detection of
XX the polymorphisms is useful in designing prophylactic and therapeutic
XX regimens customized to underlying abnormalities. The polymorphisms can be
XX used for association studies for hypertension, and in hypertension
XX diagnostic assays. Where the polymorphisms have strong correlation with
XX hypertension, within a gene, they are likely to have a causative role in
XX hypertension. This information can be used to find the precise role of a
XX polymorphism in the disease, and this can be used to identify potential
XX drugs which combat the disease. The polymorphisms can be tested for
XX association with other diseases e.g. agammaglobulinemia, diabetes
XX insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
XX syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
XX kidney disease, hereditary spherocytosis, von Willebrand's disease,
XX tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial

CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
CC acute intermittent porphyria. The polymorphic forms can also be used in
CC forensics to identify individuals

XX Sequence 29 BP; 5 A; 9 C; 8 G; 6 T; 0 U; 1 Other;

SO Query Match 2.4%; Score 23.4; DB 1; Length 29;
Best Local Similarity 88.9%; Pred. No. 9.9e+02;
Matches 24; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 721 GCCTCTGAGTAGCTGGACTACAGGC 747
DB 29 GCCTCTGAGTAGCTGGACTACAGGC 3

RESULT 336
AAH91473/C
ID AAH91473 standard; DNA; 29 BP.

XX AAH91473;

XX 09-OCT-2001 (first entry)

DE Human inflammatory bowel disease associated polymorphic site #548.

XX Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
XX single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
XX chromosome 5q31-33; forensic test; gene therapy; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FT misc_feature 16

XX FT /tag= a

XX /note= "SNP, optionally A or G at this position"

XX WO200142511-A2.

XX 14-JUN-2001.

XX 11-DEC-2000; 2000MO-US033632.

XX 10-DEC-1999; 99US-0170257P.

XX 10-APR-2000; 2000US-0196046P.

XX (WHD) WHITEHEAD INST BIOMEDICAL RES.

XX (ELL-) ELLIPSIS BIOTHERAPEUTICS CORP.

XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;

XX WPI; 2001-367874/38.

XX Testing for the presence of polymorphisms associated with inflammatory

XX bowel disease, using a hybridization assay.

XX Claim 1; Page 61; 463pp; English.

XX The present invention describes a method for detecting the presence of

XX polymorphisms associated with inflammatory bowel diseases such as

XX ulcerative colitis and Crohn's disease. The methods can be used to detect

XX the presence of genetic polymorphisms associated with inflammatory bowel

XX disease and correlating their occurrence with disease states. They may be

XX used in this way for phenotypic correlations, forensics, paternity

XX testing, medicine and genetic analysis. The present sequence is a

XX polymorphic site described in the exemplification of the invention

XX Sequence 29 BP; 9 A; 8 C; 7 G; 4 T; 0 U; 1 Other;

SO Query Match 2.3%; Score 23.2; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1e+03;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1014 TGCTCAGCCTCCCAAGACGCTGGATTA 1042

[illegible]

XX	PCR primer F1209 used to sequence human LDLR DNA.
DE	
XX	discriminant function coefficient; DC; ethnic affiliation; haplotype;
KW	descent predictor; forensic analysis; Alu repeat; hot spot; diversity;
KW	human; low density lipoprotein receptor; LDLR; ss; primer; PCR; F1209.
XX	
OS	Homo sapiens.
XX	
FN	US6544730-B1.
XX	
PD	08-APR-2003.
XX	
PF	27-OCT-1997; 97US-00958009.
XX	
PR	27-OCT-1997; 97US-00958009.
XX	
PA	(DEIN/) DEININGER P.
PA	(KASS/) KASS D.
XX	
P1	Deininger P, Kass D;
XX	
XX	WPI; 2003-566586/53.
XX	
PT	Determining discriminant function coefficient for ethnic affiliation,
PT	comprises comparing haplotypes from donors of known ethnic origin with
PT	expected haplotype frequency and estimating coefficient from obtained
XX	discrepancies.
XX	
PS	Example 2; Col 19; 25pp; English.
XX	
CC	The invention relates to a method which comprises determining
CC	discriminant function coefficient (DC) for ethnic affiliation. This is
CC	achieved via obtaining haplotypes from specific DNA sequence analysis and
CC	comparing haplotypes from human donors of known ethnic origin with
CC	expected haplotype frequency. The DC is used as an ethnic descent
CC	predictor. The method of the invention may be useful for determining a DC
CC	for ethnic affiliation and thus for estimating ethnic affiliation, as
CC	well as for determining an ethnic specific haplotype, estimating genetic
CC	affiliation and during forensic analysis. The 3' A-rich region of the Alu
CC	repeat used within the method is a 'hot spot' for diversity making this
CC	region very useful for forensic analysis. The current sequence is that of
CC	the PCR primer F1209 of the invention which was used to sequence the
CC	human LDLR DNA.
XX	
XX	
SQ	Sequence 23 BP; 5 A; 10 C; 3 G; 5 T; 0 U; 0 Other;
XX	
Query Match	2.3%; Score 23; DB 1; Length 23;
Best Local Similarity	100.0%; Pred. No. 8.9e+02;
Matches 23; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	861 AGTGCTGGGATTACAGGCGTGAG 863
Db	23 AGTGCTGGGATTACAGGCGTGAG 1
XX	
RESULT 339	
AAH91561/c	
ID	AAH91561 standard; DNA; 24 BP.
XX	
AC	AAH91561;
XX	
DT	09-OCT-2001 (first entry)
XX	
DE	Human inflammatory bowel disease associated polymorphic site #636.
XX	
KW	Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW	single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
KW	chromosome 5q31-33; forensic test; gene therapy; ds.
XX	
OS	Homo sapiens.
XX	
PH	Key Location/Qualifiers

[illegible]

XX	10-SEP-2001; 2001US-0318462P.	PR
PR	12-SEP-2001; 2001US-0318770P.	PR
PR	27-SEP-2001; 2001US-0325430P.	PR
PR	27-SEP-2001; 2001US-0325681P.	PR
PR	18-OCT-2001; 2001US-0303808P.	PR
PR	31-OCT-2001; 2001US-0335301P.	PR
PR	14-NOV-2001; 2001US-0332172P.	PR
PR	14-NOV-2001; 2001US-0332271P.	PR
PR	14-NOV-2001; 2001US-0332272P.	PR
PR	14-NOV-2001; 2001US-0333184P.	PR
PR	14-NOV-2001; 2001US-0333272P.	PR
PR	21-NOV-2001; 2001US-0332094P.	PR
PR	03-DEC-2001; 2001US-0337426P.	PR
PR	03-DEC-2001; 2001US-0338092P.	PR
PR	04-DEC-2001; 2001US-0337185P.	PR
PR	03-JAN-2002; 2002US-0345705P.	PR
PR	07-MAR-2002; 2002US-00092900.	PR
XX		
PA	(CURA-) CURAGEN CORP.	
XX		
PI	Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L,	
PI	Zechuau BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda R;	
PI	Patturajan M, Gangolli E, Vernet CAM, Guo X, Tchervnev V;	
PI	Perandura ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y, Anderson D;	
PI	Spederna SK, Catterton E, Burgess C, Leite M, Zhong H, Alebrook JP;	
PI	Lepley DM, Rieger DK;	
XX		
DR	WPI; 2002-723332/78.	
XX		
PT	NOVX polypeptides and polynucleotides, useful for preventing or treating	
PT	a disorder associated with aberrant NOVX expression or activity e.g.,	
PT	cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial	
PT	asthma.	
XX		
PS	Example C; Page 621; 1103pp; English.	
XX		
CC	This invention describes novel human NOVX polypeptides which have	
CC	cytostatic, cardiant, antiarteriosclerotic, antiautomatic and hypotensive	
CC	activity. Pharmaceutical compositions comprising the NOVX proteins or	
CC	nucleic acid molecules or NOVX antibodies are useful for preventing or	
CC	treating a disorder associated with aberrant NOVX expression or activity	
CC	e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial	
CC	asthma. The products of the invention can be used for gene therapy or in	
CC	a vaccine. ABX13460-ABX13462 and ABX97186-ABX971593 represent NOVX	
CC	polynucleotides represented in ABX97008-ABX97185 which encode the	
CC	polypeptides represented in ABU65041-ABU65518. The probes described in	
CC	the invention are modified at the 5'-end by Ter and the 3'-end by TAMRA	
XX		
SO	Sequence 26 BP; 6 A; 9 C; 3 G; 8 T; 0 U; 0 Other;	
XX		
Query Match	2.3%; Score 22.8; DB 1; Length 26;	
Best Local Similarity	92.3%; Pred.No. 9.8e+02;	
Matches	24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
DB		
Qy	573 ATGCACCACTACACCTGGCTAATTTT 598	
1	ATGCACCACTACCTGGCTAATTTT 26	
RESULT 343		
ID	ADN62195	
AC	ADN62195 standard; DNA; 26 BP.	
XX		
DT	01-JUN-2004 (First entry)	
XX		
DE	Human NOV20a RTQ-PCR probe.	
XX		
KM	Human; ss; PCR; NOVX; diabetes; obesity; infectious disease; anorexia;	
KM	cancer-associated cachexia; cancer; neurodegenerative disorder;	
KW	Alzheimer's disease; Parkinson's disease; immune disorder;	

KM	haematopoietic disorder; dyslipidaemia; chronic disease; probe: RTq-PCR
KW	real time quantitative PCR.
XX	
OS	Homo sapiens.
XX	
PN	US2004043382-A1.
PD	
XX	
XX	04-MAR-2004.
PF	
XX	
XX	07-MAR-2002; 2002US-00092900.
PR	
PR	08-MAR-2001; 2001US-0274191P.
PR	08-MAR-2001; 2001US-0274194P.
PR	08-MAR-2001; 2001US-0274281P.
PR	08-MAR-2001; 2001US-0274322P.
PR	09-MAR-2001; 2001US-0274849P.
PR	12-MAR-2001; 2001US-0275235P.
PR	13-MAR-2001; 2001US-0275578P.
PR	13-MAR-2001; 2001US-0275579P.
PR	13-MAR-2001; 2001US-0275601P.
PR	14-MAR-2001; 2001US-0276000P.
PR	16-MAR-2001; 2001US-0276776P.
PR	19-MAR-2001; 2001US-0276994P.
PR	20-MAR-2001; 2001US-0277239P.
PR	20-MAR-2001; 2001US-0277321P.
PR	20-MAR-2001; 2001US-0277327P.
PR	20-MAR-2001; 2001US-0277338P.
PR	21-MAR-2001; 2001US-0277791P.
PR	22-MAR-2001; 2001US-0277833P.
PR	23-MAR-2001; 2001US-0278152P.
PR	26-MAR-2001; 2001US-0278894P.
PR	27-MAR-2001; 2001US-0278999P.
PR	27-MAR-2001; 2001US-0279036P.
PR	28-MAR-2001; 2001US-0279344P.
PR	30-MAR-2001; 2001US-0279999P.
PR	30-MAR-2001; 2001US-0280233P.
PR	02-APR-2001; 2001US-0280802P.
PR	02-APR-2001; 2001US-0280822P.
PR	02-APR-2001; 2001US-0280900P.
PR	04-APR-2001; 2001US-0281444P.
PR	13-APR-2001; 2001US-0283675P.
PR	30-APR-2001; 2001US-0287424P.
PR	02-MAY-2001; 2001US-0288066P.
PR	03-MAY-2001; 2001US-0288342P.
PR	03-MAY-2001; 2001US-0288528P.
PR	15-MAY-2001; 2001US-0291190P.
PR	16-MAY-2001; 2001US-0291099P.
PR	16-MAY-2001; 2001US-0291480P.
PR	30-MAY-2001; 2001US-0294485P.
PR	31-MAY-2001; 2001US-0294889P.
PR	31-MAY-2001; 2001US-0294899P.
PR	18-JUN-2001; 2001US-0299027P.
PR	19-JUN-2001; 2001US-0299303P.
PR	19-JUN-2001; 2001US-0299310P.
PR	10-JUL-2001; 2001US-0304354P.
PR	31-JUL-2001; 2001US-0309198P.
PR	16-AUG-2001; 2001US-0312903P.
PR	10-SEP-2001; 2001US-0318462P.
PR	12-SEP-2001; 2001US-0318770P.
PR	27-SEP-2001; 2001US-0325430P.
PR	27-SEP-2001; 2001US-0325681P.
PR	18-OCT-2001; 2001US-0330380P.
PR	31-OCT-2001; 2001US-0335301P.
PR	14-NOV-2001; 2001US-0335172P.
PR	14-NOV-2001; 2001US-0332771P.
PR	14-NOV-2001; 2001US-0332772P.
PR	14-NOV-2001; 2001US-0333184P.
PR	14-NOV-2001; 2001US-033372P.
PR	21-NOV-2001; 2001US-0332094P.
PR	03-DEC-2001; 2001US-0337426P.
PR	03-DEC-2001; 2001US-0338092P.
PR	04-DEC-2001; 2001US-0337185P.
PR	03-JAN-2002; 2002US-0345705P.

XX (PADIGARU M.,
PA (SPYTEK K. A.,
PA (SHENY S. G.,
PA (TAUPIER R. J.,
PA (PENNA/ C E A.,
PA (LITL/ L. L.,
PA (ZERRH/ ZERRHISEN B. D.,
PA (GUSEV/ GUSEV V. Y.,
PA (JITW/ J. W.,
PA (GORM/ GORMAN L.,
PA (MILL/ MILLER C. E.,
PA (KEKUD/ KEKUDA R.,
PA (PATTRA/ PATTRAJAN M.,
PA (GANG/ GANGOLLI E. A.,
PA (VERN/ VERNET C. A. M.,
PA (GUOX/ GUO X. S.,
PA (TCHER/ TCHERNIEV V. T.,
PA (FERN/ FERNANDES E. R.,
PA (CASW/ CASMAN S. J.,
PA (MAL/ MALYANKAR U. M.,
PA (GERL/ GERLACH V.,
PA (LIUY/ LIU Y.,
PA (ANDE/ ANDERSON D. W.,
PA (SPAD/ SPADERNA S. K.,
PA (CATT/ CATTERTON E.,
PA (LEITE/ LEITE M. W.,
PA (ZHON/ ZHONG H.,
PA (ALSO/ ALSOBROOK J. P.,
PA (LEPL/ LEPLLEY D. M.,
PA (RIEG/ RIEGER D. K.,
PA (BURG/ BURGESS C. E.,
XX
XX Padigaru M., Spytek KA, Shenoy SG, Taupier RJ, Pena CEa, Li L,
PI Zernhusen BD, Gusev VY, Ji W, Gorman L, Miller CE, Guller R, R;
PI Patraurjan M, Gangolli EA, Vernet CAM, Guo XS, Tcherniev VT;
PI Patraurjan ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y;
PI Anderson DW, Spaderna SK, Catterton E, Leite MW, Zhong H;
PI Alsobrook JP, Lepley DW, Rieger DK, Burgess CE;
XX
XX WPI: 2004-225693/21.
DR
XX
XX New NOVX polypeptides and nucleic acid molecules useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. cancer, diabetes,
PT infection or obesity, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX
PS Example C, SEQ ID NO 464; 786bp; English.
XX
XX
XX The invention relates to an isolated polypeptide (designated NOVX, or
CC NOVI-NOVI27) comprising a sequence selected from 178 fully defined amino
CC acid sequences (and their mature forms, variants and fragments). Also
CC included are an isolated nucleic acid molecule encoding NOVX, a vector
CC comprising the nucleic acid, a cell comprising the vector, methods for
CC determining the presence or amount of the polypeptide or the nucleic acid
CC molecule in a sample, methods for determining the presence of or
CC predisposition to a disease associated with altered levels of expression
CC of the above polypeptide or nucleic acid molecule in a first mammalian
CC subject, a method for identifying an agent that binds to the above
CC polypeptide, a method for identifying a potential therapeutic agent for
CC use in the treatment of a pathology that is related to aberrant
CC expression or physiological interactions of the polypeptide, a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide and a method for modulating
CC the activity of the polypeptide cited above. The composition and methods
CC are useful for diagnosing, preventing or treating diseases such as
CC diabetes, obesity, infectious diseases, anorexia, cancer-associated
CC cachexia, cancer, neurodegenerative disorders like Alzheimer's disease or
CC Parkinson's disease, immune disorders, hematopoietic disorders,
CC dyslipidaemias, and other chronic diseases. These may also be used in
CC chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The polypeptides are also useful as vaccines. The
CC present sequence is an RTQ-PCR (real time quantitative PCR) probe used to

CC assay tissue specific expression of a NOVX mRNA.
XX Sequence 26 BP; 6 A; 9 C; 3 G; 8 T; 0 U; 0 Other;
SQ
Query Match 2.3%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 9.8e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 573 ATGCACGACTACCTGGCTAATTT 598
DB 1 ATGCACGACACTCTCGCTAATTT 26
RESULT 344
AAH38083
ID AAH38083 standard; DNA; 27 BP.
XX
AC AAH38083;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 879.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KM SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
KM Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KM polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KM acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KM inflammation; forensic investigation; paternity analysis; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028436.
XX
PR 15-OCT-1999; 99US-0160096P.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
PS Claim 1; Page 54; 83pp; English.
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPs primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic, such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and

CC paternity analysis. The present sequence represents a single nucleotide
CC primer extension (SNPE) primer specific for a human SNP containing DNA
CC sequence
XX
SQ Sequence 27 BP; 5 A; 10 C; 3 G; 8 T; 0 U; 1 Other;
Query Match 2.3%; Score 22.8; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 1e+03;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 699 TTCAGATTATTTCTCTGCCCCAGCCTC 725
DB 1 TTCAGNATTTCTCTGCTCAGCCTC 27
RESULT 345
AAH40487
ID AAH40487 standard; DNA; 27 BP.
XX
AC AAH40487;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 3283.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KM SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
KM Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KM polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KM acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KM inflammation; forensic investigation; paternity analysis; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028436.
XX
PR 15-OCT-1999; 99US-0160096P.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
PS Claim 1; Page 66; 83pp; English.
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPs primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic, such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,

CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a single nucleotide
CC primer extension (SNPE) primer specific for a human SNP containing DNA
CC sequence
CC
SQ Sequence 27 BP; 5 A; 7 C; 7 G; 7 T; 0 U; 1 Other;
XX
XX
Query Match 2.3%; Score 22.8; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 1e+03;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 849 TCGGCTCCCAAGTGTGGATTACA 875
DB 1 TTGGCTCNCACAGTGTGGATTACA 27
RESULT 346
AAH40803
ID AAH40803 standard; DNA; 27 BP.
AC AAH40803;
XX
XX
DT 14-AUG-2001. (first entry)
XX
DE SNP specific SNPE primer SEQ ID 3599.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
XX Leisch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200129262-A2.
XX
XX 26-APR-2001.
XX
XX 13-OCT-2000; 2000MO-US028436.
XX
XX 15-OCT-1999; 99US-0160096P.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX Picoult-Newburg L, Pohl M;
XX
XX WPI; 2001-290930/30.
XX
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
XX
XX Claim 1; Page 68; 83pp; English.
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
XX primer extension (SNPE) primers, and the sequences of regions flanking
XX sites of single nucleotide polymorphisms SNPs. The present invention
XX includes kits for determining the presence or absence of a SNP, using the
XX oligonucleotides of the invention. The PCR primers are used to amplify a
XX SNP flanking sequence, the SNPE primer is used as a genotyping primer.
XX The oligonucleotides are useful for genotyping a nucleic acid sample by
XX performing a single-nucleotide primer extension reaction. The
XX oligonucleotides are useful for determining the presence, absence or
XX identity of a SNP and for genotyping nucleic acid samples, for e.g. to
XX assess by association analysis the genotype of an individual or group of
XX individuals, having a pathological phenotypic trait suspected of being
XX caused by one or more SNPs. Phenotypic traits include diseases e.g.
XX agammaglobulinemia, diabetes insipidus, Leisch-Nyhan syndrome, muscular
XX dystrophy, familial hypercholesterolemia, polycystic kidney disease,
XX osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
XX traits also include symptoms of or susceptibility to multifactorial

CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a single nucleotide
CC primer extension (SNPE) primer specific for a human SNP containing DNA
CC sequence
CC
SQ Sequence 27 BP; 8 A; 6 C; 7 G; 5 T; 0 U; 1 Other;
XX
XX
Query Match 2.3%; Score 22.8; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 1e+03;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 861 AGTGCTGGAATTACAGCGTGAACCA 887
DB 1 AGTGCTGAATTAACAGCGTGAACCA 27
RESULT 347
AAH91322/c
ID AAH91322 standard; DNA; 27 BP.
XX
XX AAH91322;
AC
XX
XX 09-OCT-2001 (first entry)
XX
XX
DE Human inflammatory bowel disease associated polymorphic site #397.
XX
XX Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
XX single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
XX chromosome 5q31-33; forensic test; gene therapy; ds.
XX
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
FH misc_feature 16
FT /*tag= a
FT /note= "SNP, optionally A or G at this position"
XX
XX
XX WO200142511-A2.
XX
XX 14-JUN-2001.
XX
XX 11-DEC-2000; 2000MO-US033632.
XX
XX 10-DEC-1999; 99US-0170257P.
XX 10-APR-2000; 2000US-0196046P.
XX
XX (WHEED) WHITEHEAD INST BIOMEDICAL RES.
XX (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX
XX Daly M, Hudson TJ, Lander ES, Rioux J, Simionovitch K;
XX
XX WPI; 2001-367874/38.
XX
XX
PT Testing for the presence of polymorphisms associated with inflammatory
PT bowel disease, using a hybridization assay.
XX
XX
XX Claim 1; Page 55; 463pp; English.
XX
XX The present invention describes a method for detecting the presence of
XX polymorphisms associated with inflammatory bowel diseases such as
XX ulcerative colitis and Crohn's disease. The methods can be used to detect
XX the presence of genetic polymorphisms associated with inflammatory bowel
XX disease and correlating their occurrence with disease states. They may be
XX used in this way for phenotypic correlations, forensic, paternity
XX testing, medicine and genetic analysis. The present sequence is a
XX polymorphic site described in the exemplification of the invention
XX
SQ Sequence 27 BP; 6 A; 4 C; 11 G; 5 T; 0 U; 1 Other;
XX
XX
Query Match 2.3%; Score 22.8; DB 1; Length 27;

Best Local Similarity 88.9%; Pred. No. 1e+03;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1003 AGCGATTCTCTCTCTCAGCCTCCCA 1029

DB 27 AGCGATTCTCTCTCTCAGCCTCCCA 1

RESULT 348

AAF92843 ID AAF92843 standard; DNA; 24 BP.

XX AAF92843;

XX 17-MAY-2001 (first entry)

DE Human ABC1 transcription factor binding site #6.

XX High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1, ds.

XX Homo sapiens.

XX WO200115676-A2.

XX 08-MAR-2001.

XX 01-SEP-2000; 2000WO-1B001492.

XX 01-SEP-1999; 99US-0151977P.

XX 15-MAR-2000; 2000US-00526193.

XX 23-JUN-2000; 2000US-0213958P.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX (XENON-) XENON GENETICS INC.

XX Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;

XX WPI; 2001-244356/25.

XX Treating a lower than normal high density lipoprotein-cholesterol (HDL-C)

XX level, a higher than normal triglyceride level, or a cardiovascular

XX disease, by administering a compound that modulates LXR- or RXR-mediated

XX transcriptional activity.

XX Disclosure; Fig 3; 317pp; English.

XX The present invention relates to a method for treating a patient

XX diagnosed as having a lower than normal high density lipoprotein-

XX cholesterol (HDL-C) level, a higher than normal triglyceride level, or a

XX cardiovascular disease, involving administering a compound that modulates

XX LXR- or RXR-mediated transcriptional activity or ABC1 expression or

XX activity. The LXR gene product may be used in an assay to identify

XX compounds useful for the treatment of a disease or condition selected a

XX lower than normal HDL cholesterol level, a higher than normal

XX triglyceride level, and a cardiovascular disease

XX Sequence 24 BP; 4 A; 8 C; 6 G; 6 T; 0 U; 0 Other;

XX Query Match 2.3%; Score 22.4; DB 1; Length 24;

XX Best Local Similarity 95.8%; Pred. No. 9.7e+02;

XX Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DT 14-DEC-2001 (first entry)

XX Human transglutaminase 12 PCR primer #1.

XX Human; transglutaminase 12; cytostatic; virucidal; immunomodulatory;

XX antiinflammatory; haemostatic; gene therapy; malignant tumour;

XX haemopathy; HIV infection; immunological disease; inflammation;

XX PCR primer; ss.

XX Homo sapiens.

XX WO200170787-A1.

XX 27-SEP-2001.

XX 26-FEB-2001; 2001WO-CN000243.

XX 10-MAR-2000; 2000CN-0011967.

XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX Mao Y, Xie Y;

XX WPI; 2001-61474/70.

XX Human transglutaminase 12 and encoded polynucleotide, used in diagnosis

XX and treatment of malignant tumors, hemopathy, human immunodeficiency

XX virus infection, immunological diseases and inflammation.

XX Example 2; Page 17; 37pp; Chinese.

XX The present invention relates to human transglutaminase 12 (see

XX CC AAG7882). The transglutaminase and its coding sequence are useful in the

XX diagnosis and treatment of malignant tumors, haemopathy, HIV infection,

XX immunological diseases and various inflammations. The present sequence is

XX a PCR primer which was used in an example from the present invention

XX Sequence 24 BP; 5 A; 8 C; 4 G; 7 T; 0 U; 0 Other;

XX Query Match 2.3%; Score 22.4; DB 1; Length 24;

XX Best Local Similarity 95.8%; Pred. No. 9.7e+02;

XX Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 388 CAAGTGTGCTGATTCAGCGCTG 411

DB 24 CAAGTGTGCTGATTCAGCGCTG 1

RESULT 350

XX AAS00333 standard; DNA; 24 BP.

XX AAS00333;

XX 17-MAY-2001 (first entry)

XX PCR primer #2, used to amplify human RAD51 gene at position -2339.

XX Human; RAD51; breast cancer; BRCA1; BRCA2; PCR primer; ss.

XX Homo sapiens.

XX WO200118254-A2.

XX 15-MAR-2001.

XX 08-SEP-2000; 2000WO-US024786.

XX 10-SEP-1999; 99US-0153288P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang WW, Struwing JP;

XX
DR WPI; 2001-235217/24.
XX
XX New nucleic acids comprising a mutant of the RAD51 gene, useful for
PT diagnosing genetic predisposition or susceptibility to breast cancer.
XX
XX Disclosure; Page 42; 42pp; English.
XX
XX The sequence represents PCR primer #2, used to amplify human RAD51 gene
CC at position -239 upstream of the transcription start site of human RAD51
CC gene. The RAD51 gene is useful in diagnosing genetic predisposition or
CC susceptibility to breast cancer in an individual using the following
CC steps: (1) detecting a mutation in the RAD51 gene in a human subject;
CC comprising analysing a sample from the subject to detect the mutation;
CC (2) assessing the risk of developing breast cancer, comprising: (a)
CC analysing a sample from the subject for the presence of BRCA1 and/or
CC BRCA2 mutations; and (b) if (a) is positive, analysing the sample for a
CC mutation in the RAD51 gene, where the presence of the RAD51 mutation
CC indicates an increased risk in developing breast cancer in the subject as
CC compared to a subject having at least one of the BRCA mutations and a
CC wild-type RAD51 gene. Primers derived from the sequence can be used in a
CC kit for detecting a mutation in the RAD51 gene of a subject, which is
CC associated with a predisposition to breast cancer, comprising at least 2
CC nucleic acid primers derived from the RAD51 gene sequence
XX
SQ Sequence 24 BP; 5 A; 10 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 2.3%; Score 22.4; DB 1; Length 24;
XX Best Local Similarity 95.8%; Pred. No. 9.7e+02;
XX Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 538 CTGCTCAGCGCTCCCAAGTAGCTG 561
DB 1 CTGCTCAGCGCTCCCAAGTAGCTG 24
XX
XX RESULT 351
XX ABZ21100/c
XX ID ABZ21100 standard; DNA; 24 BP.
XX
XX ABZ21100;
XX
XX 25-MAR-2003 (first entry)
XX
XX Zinc finger protein 54.67 PCR primer #2.
XX
XX Zinc finger protein 54.67; tumour; inflammation; immunological disease;
XX haemopathy; HIV infection; cytostatic; anti-HIV; PCR; primer; ss.
XX
XX Unidentified.
XX
XX CN1352015-A.
XX
XX 05-JUN-2002.
XX
XX 06-NOV-2000; 2000CN-00127270.
XX
XX 06-NOV-2000; 2000CN-00127270.
XX
XX (BODE-) BODE GENE DEV CO LTD.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-699446/76.
XX
XX New zinc finger protein 54.67 polypeptide for treating malignant tumors,
XX PT inflammations, immunological diseases, hemopathy and human
XX PT immunodeficiency virus infection.
XX
XX Example 2; Page 16 (Disclosure); 34pp; Chinese.
XX
XX The present invention relates to zinc finger protein 54.67 (ABZ98889).
XX The zinc finger protein can be used for treating various diseases, such

CC as malignant tumours, inflammations, immunological diseases, haemopathy
CC and HIV infection. The present sequence is a PCR primer, which was used
CC in an example from the invention
XX
XX SQ Sequence 24 BP; 4 A; 7 C; 8 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 2.3%; Score 22.4; DB 1; Length 24;
XX Best Local Similarity 95.8%; Pred. No. 9.7e+02;
XX Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 721 GCCTCCTAGTAGCTGGAGACTACA 744
DB 24 GCCTCCTAGTAGCTGGAGACTACA 1
XX
XX RESULT 352
XX ABA96912/c
XX ID ABA96912 standard; DNA; 24 BP.
XX
XX ABA96912;
XX
XX 15-MAY-2002 (first entry)
XX
XX Human arginase 9 RT-PCR primer, SEQ ID NO:3 version #1.
XX
XX Human; arginase 9; recombinant production; arginaemia;
XX arginine metabolism disorder; urea metabolism disorder;
XX developmental disorder; malignant tumour; cancer; gene therapy;
XX immune disorder; inflammatory condition; cytostatic; antiinflammatory;
XX immunomodulator; reverse transcription-PCR; RT-PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200198502-A1.
XX
XX 27-DEC-2001.
XX
XX 14-MAY-2001; 2001WO-CN000788.
XX
XX 19-MAY-2000; 2000CN-00115753.
XX
XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-090440/12.
XX
XX Human arginase 9 and encoding polynucleotide, used in diagnosis and
XX PT treatment of malignant tumors, hemopathy, human immunodeficiency virus
XX PT infection, immunological diseases and inflammation.
XX
XX Example 3; Page 29; 33pp; Chinese.
XX
XX The invention relates to human arginase 9 (AAM49102), nucleic acids
CC encoding it (ABA96911), and a method for the recombinant production of
CC arginase 9. The protein has a molecular weight of 9 kD and has homology
CC over a 60 amino acid stretch to the protein fragment shown in AAM49105.
CC The present invention additionally discloses an antagonist of arginase
CC 9 for therapeutic use, and an antibody which specifically binds to
CC arginase 9. Arginase 9, and nucleotides which encode it may be used
CC for treating a variety of diseases, such as arginaemia, disorders of
CC arginine or urea metabolism, developmental disorders, malignant tumors,
CC immune disorders and inflammatory conditions. The protein may also be
CC used to screen for modulators of its activity or for peptide
CC fingerprinting identification. The polynucleotide can be used as a primer
CC for nucleic acid amplification reactions or as a probe for hybridisation
CC reactions, or in producing gene chips or microarrays. Sequences ABA96912-
CC ABA96913 represent reverse transcription-PCR (RT-PCR) primers used in an
CC exemplification of the invention to isolate human arginase 9 cDNA.
CC Note: The present sequence differs from the sequence also designated SEQ
CC ID NO:3 (ABA96914) which is given on page 12 of the specification
XX
XX Sequence 24 BP; 3 A; 9 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 2.3%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 9.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 868 GGATTACAGCGGTGAGCCACG 891
DB 24 GGATTACAGCGGTGAGCCACGCG 1

RESULT 353
ABQ83933/C
ID ABQ83933 standard; DNA; 24 BP.

XX AC ABQ83933;

DT 04-FEB-2003 (first entry)

DE Human breast susceptible gene protein 10.45 PCR primer 2 SEQ ID NO:4.

XX KW Human; breast susceptible gene coded protein 10.45; tumour;
XX KM embryonic development deformity; PCR primer; 88.

XX OS Homo sapiens.

XX PN CN1342702-A.

XX PD 03-APR-2002.

XX PF 12-SEP-2000; 2000CN-00125173.

XX PR 12-SEP-2000; 2000CN-00125173.

XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX PI Mao Y, Xie Y;

XX DR WPI; 2002-529778/57.

PT A novel human breast susceptible gene coded protein 10.45 polypeptide,
PT and the polynucleotide encoding it, useful for treating several diseases
PT e.g. embryonic development deformity and tumors.

XX PS Example 2; Page 18 (Disclosure); 34pp; Chinese.

CC The present invention describes human breast susceptible gene coded
CC protein 10.45 (I). Also described is a process for preparing (I) using
CC DNA recombination techniques. (I) can be used for treating several
CC diseases e.g. embryonic development deformity and tumours. The present
CC sequence represents a PCR primer for (I), which is used in an example
CC from the present invention

XX SQ Sequence 24 BP; 9 A; 7 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 2.3%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 9.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 192 TTTCATGTTGTCAGGCTGCT 215
DB 24 TTTCATGTTGTCAGGCTGCT 1

RESULT 354
ABT08420

XX ID ABT08420 standard; DNA; 24 BP.

XX AC ABT08420;

DT 27-NOV-2002 (first entry)

DE Human PSF promoter PCR primer SEQ ID NO: 55.

XX KW Human; cyclin-dependent kinase; CDK; cyclin-dependent kinase inhibitor;
XX KW inhibitor; cancer; age-related disease; promoter; atherosclerosis;
XX KW cytosolic; antiarteriosclerotic; neurotropic; neuroprotective;
XX KW nephrotropic; antiarthritic; arthritis; renal disease;
XX KW Alzheimer's disease; amyloidosis; PCR; primer; 88.

XX OS Homo sapiens.

XX PN WO200266681-A2.

XX PD 29-AUG-2002.

XX PF 01-FEB-2002; 2002WO-US002784.

XX PR 01-FEB-2001; 2001US-0265840P.

XX PR 21-MAY-2001; 2001US-00861925.

XX PA (UNIT) UNIT ILLINOIS FOUND.

XX PI Poole J, Robinson IB, Chang B;
XX DR WPI; 2002-674960/72.

PT New recombinant expression construct, useful for identifying compounds
PT that inhibit the induction of genes induced by cyclin-dependent kinase
PT inhibitors for preventing or treating cancer, renal failure or
PT Alzheimer's disease.

XX PS Example 8; Page 130; 137pp; English.

CC The present invention relates to a recombinant expression construct
CC encoding a reporter gene operably linked to a promoter from a mammalian
CC gene induced by a cyclin-dependent kinase (CDK) inhibitor. The construct
CC is useful for identifying compounds that inhibit the induction of genes
CC induced by CDK inhibitors. The compounds are useful for preventing or
CC treating a disease caused by CDK inhibitor induced gene expression, e.g.
CC cancer other than colon cancer, renal failure, Alzheimer's disease,
CC amyloidosis, age-related diseases, atherosclerosis or arthritis. The
CC present sequence is a PCR primer used to amplify a human promoter
CC suitable for use in the construct of the invention

XX SQ Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 2.3%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 9.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 859 AAAGTCTGGATTACAGGCTGA 882
DB 1 AAAGTCTGGATTACAGGCTGA 24

RESULT 355
ACF05122/C

XX ID ACF05122 standard; DNA; 24 BP.

XX AC ACF05122;

DT 06-NOV-2003 (first entry)

DE Human genomic DNA primer A1u.

XX KW Human; alphoid; immunodeficiency virus; HIV; anti-HIV; latency; PCR;
XX KW primer; 88.

XX OS Homo sapiens.

XX PN WO2003054160-A2.

XX PD 03-JUL-2003.

XX PF 18-DEC-2002; 2002WO-US040698.


```
XX 19-DEC-2001; 2001US-0341727P.
XX (REGC ) UNIV CALIFORNIA.
XX
XX Verdin E, Jordan A;
XX WPI; 2003-577369/54.
XX
XX Novel isolated cells that comprise transcription competent
XX immunodeficiency virus e.g. HIV-1, or immunodeficiency virus-based
XX retroviral vector integrated into its genome, useful for identifying
XX latent HIV activators.
XX
XX Example 1; Page 33; 71pp; English.
XX
XX The present sequence is that of primer Alu (EVI255) for human genomic
XX DNA. This primer was used with primer A (see ACC05121) in aliphoid PCR
XX amplifications that demonstrated preferential HIV integration in or near
XX aliphoid DNA in latently infected Jurkat cells. The invention provides
XX isolated cells that harbour a latent immunodeficiency virus that is
XX transcription competent, that can be reactivated, and that is an in vitro
XX model for latent HIV infection in vivo. The cells are useful for
XX investigating the nature of latency, and also in drug screening assays to
XX identify agents that activate latent HIV. Such agents are useful for
XX reducing the reservoir of latent HIV. Methods are provided of treating an
XX immunodeficiency virus infection
XX
XX Sequence 24 BP; 4 A; 7 C; 9 G; 4 T; 0 U; 0 Other;
XX
XX Query Match      2.3%; Score 22.4; DB 1; Length 24;
XX Best Local Similarity 95.8%; Pred. No. 9.7e+02;
XX Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 541 CCTGAGCCTCCGAGTACGCGGA 564
XX      |||||
XX      24 CCTGAGCCTCCGAGTACGCGGA 1
XX
XX RESULT 356
XX ACP35685/c
XX ID ACP35685 standard; DNA; 24 BP.
XX
XX AC ACP35685;
XX
XX DT 13-OCT-2003 (first entry)
XX
XX DE Human TGNP promoter amplifying forward primer.
XX
XX KW Trans-Golgi network integral membrane protein; TGNP; chromosome 2p11.2;
XX cytoskeletal; antiinflammatory; immunomodulator; neuroprotective; human;
XX neurotropic; gene therapy; PCR; primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO2003050302-A2.
XX
XX PD 19-JUN-2003.
XX
XX PF 13-DEC-2002; 2002WO-GB005670.
XX
XX PR 13-DEC-2001; 2001GB-00029846.
XX
XX PA (EIRX-) EIRX THERAPEUTICS LTD.
XX
XX PI Hayes I, Cotter T, Murphy F, Seery L;
XX WPI; 2003-532920/50.
XX
XX DR Detecting apoptosis in a cell, useful for treating cancer, an
XX inflammatory disease, an autoimmune disease or a neurodegenerative
XX disease, comprises detecting a decrease in TGNP activity or expression.
XX
XX Example 11; Page 80; 110pp; English.
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```
XX The invention relates to detecting apoptosis in a cell. The method
XX involves detecting a decrease in trans-Golgi network integral membrane
XX protein (TGNP) activity or expression by detecting the decrease in TGNP
XX polypeptide or its homologue, a nucleic acid encoding the polypeptide, a
XX nucleic acid that hybridizes under stringent conditions to the
XX aforementioned nucleic acid, or their complements. The method,
XX polypeptides, nucleic acids and modulators are useful for treating
XX cancer, an inflammatory disease, an autoimmune disease or a PCR primer
XX for amplifying the human TGNP promoter
XX
XX Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
XX
XX Query Match      2.3%; Score 22.4; DB 1; Length 24;
XX Best Local Similarity 95.8%; Pred. No. 9.7e+02;
XX Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 635 CTCTGACCCGAGGCGTGTGCA 658
XX      |||||
XX      24 CTCTGACCCGAGGCGTGTGCA 1
XX
XX Db
XX
XX RESULT 357
XX ADG28972
XX ID ADG28972 standard; DNA; 24 BP.
XX
XX AC ADG28972;
XX
XX DT 26-FEB-2004 (first entry)
XX
XX DE PCR primer SEQ ID 55 used to amplify human PSF promoter DNA.
XX
XX KW recombinant expression construct; cyclin-dependent kinase inhibitor; CDK;
XX virucide; cytostatic; neuroprotective; neurotropic; antiarteriosclerotic;
XX antiarthritic; nephrotropic; viral infection; cancer; renal;
XX age-related disease; Alzheimer's; atherosclerosis; arthritis;
XX gene therapy; human; ss; PCR; primer; PSF promoter.
XX
XX OS Homo sapiens.
XX
XX PN WO2003073062-A2.
XX
XX PD 04-SEP-2003.
XX
XX PF 29-AUG-2002; 2002WO-US027584.
XX
XX PR 29-AUG-2001; 2001US-0315791P.
XX
XX PA (UNIT ) UNIV ILLINOIS FOUND.
XX
XX PI Robinson IB, Poole J;
XX WPI; 2003-731624/69.
XX
XX DR New recombinant expression construct for identifying and modulating
XX expression of genes regulated by cyclin-dependent kinase inhibitors, such
XX as genes involved in viral infection, cancer, renal diseases or age-
XX related diseases.
XX
XX Example 8; SEQ ID NO 55; 143pp; English.
XX
XX The invention relates to a novel recombinant expression construct
XX encoding a reporter gene operably linked to a promoter from a mammalian
XX viral or cellular gene induced by a cyclin-dependent kinase (CDK)
XX inhibitor. The construct of the invention demonstrates virucide,
XX cytostatic, neuroprotective, neurotropic, antiarteriosclerotic,
XX antiarthritic and nephrotropic activities and may be useful in
XX identifying compounds that inhibit the induction of genes involved in
XX viral infection, cancer, renal diseases or age-related diseases including
XX Alzheimer's disease, atherosclerosis or arthritis, such genes being
XX induced by cyclin-dependent kinase inhibitors. Furthermore, the construct
XX may have gene therapy applications. The current sequence is that of the
```

CC PCR primer which was used in the exemplification of the invention.
XX Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;
SQ

Query Match 2.3%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 9.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 859 AAAGTCTGGATTACAGCGCTGA 882
DB 1 AAAGTCTGGATTACAGCGCTGA 24

RESULT 358
ADQ30417/C
ID ADQ30417 standard; DNA; 24 BP.
XX
AC ADQ30417;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human VRI exon 1d transcription factor binding fragment #136.
XX
KW de; VRI receptor; vanilloid receptor type 1; modulator;
KW pain transmission; primary sensory neuron; transcription factor;
KW detection; MZFL; NKkappaB; NFAT; GATM; sensitivity disorder; analgesia;
KW hyperalgesia; hyperalgesia; neuralgia; myalgia; human.
XX
OS Homo sapiens.
XX
PN WO2004053120-A2.
XX
PD 24-JUN-2004.
XX
PF 01-DEC-2003; 2003WO-BP013522.
XX
PR 09-DEC-2002; 2002DE-01057421.
XX
PA (CHEP) GRENENTHAL GMBH.
XX
PI weine E, Bietler A, Schaefer MKH;
XX
DR WPI; 2004-468868/44.
XX
PT New nucleic acid that modulates expression of the vanilloid receptor-1,
PT useful for control of pain or sensitivity disorders, comprises sequences
PT from control regions of the receptor gene.
XX
PS Disclosure; Page 54; 68pp; German.
XX

This invention describes a novel nucleic acid containing a specific
CC segment having at least one region that modulates expression of the VRI
CC (vanilloid receptor type 1) receptor, or a functional derivative, allele
CC or fragment of this region, or a sequence that hybridises to it under
CC standard conditions. The VRI modulator is derived from one or more of
CC positions 221931-22344 of Genbank AF670399, 31673-36359 of AF663116, or
CC 44731-43231 or 36616-33151 of AF168787 and is involved in transmission of
CC pain, particularly in primary sensory neurons. The invention also
CC describes a vector that contains the VRI modulator, host cells containing
CC this vector (other than human germ or embryonal stem cells) and a method
CC for modulating expression of the VRI receptor by introducing the
CC modulator or the vector into a cell that contains the VRI gene. The
CC products of the invention are used for detecting a transcription factor
CC from its binding to a regulatory sequence (or a double-stranded
CC oligonucleotide fragment of it), e.g. by Western blotting or enzyme-
CC linked immunosorbent assay, particularly for diagnosis of diseases
CC associated with overexpression or underexpression of the transcription
CC factor. The region that modulates VRI receptor expression includes a
CC binding site for a transcription factor, e.g. MZFL, NKkappaB, NFAT or
CC GATM. The nucleic acids of the invention, or vectors containing them,
CC are used for prevention or treatment of pain, also for treating
CC sensitivity disorders, e.g. analgesia, hyperalgesia or hyperalgesia, also
CC neuralgia and myalgia, that are associated with activity of the VRI

CC receptor. This sequence represents a fragment of human VRI exon 1d DNA
CC which is capable of binding to a transcription factor.
XX
SQ Sequence 24 BP; 5 A; 8 C; 6 G; 5 T; 0 U; 0 Other;
XX

Query Match 2.3%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 9.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 387 CCAAGTCTGGATTACAGCGCT 410
DB 24 CCAAGTCTGGATTACAGCGCT 1

RESULT 359
ABX15537
ID ABX15537 standard; DNA; 25 BP.
XX
AC ABX15537;
XX
DT 11-APR-2003 (first entry)
XX
DE Human IL-1 genotyping marker g251g26 primer #1.
XX
KW Human; ss; PCR; primer; interleukin-1; IL-1; marker g251g26; nephropathy;
KW inflammatory disease; Systemic Inflammatory Response; SIRS; genotyping;
KW Alzheimer's disease; arthritis; acute joint inflammation; ophthalmopathy;
KW juvenile chronic arthritis; asthma; bronchial asthma; pulmonary disease;
KW chronic obstructive airways disease; cardiovascular disease; thyroiditis;
KW atherosclerosis; autoimmune carditis; cardiomyopathy; ulcerative colitis;
KW cardiac cell dysfunction; aortic smooth muscle cell activation; trauma;
KW cardiac cell apoptosis; gastrointestinal inflammation; cerebral trauma;
KW inflammatory bowel disease; HIV infection; coronary artery lesion;
KW Kawasaki's syndrome; cervical lymphadenopathy; diabetic nephropathy;
KW glomerulonephritis; diabetic retinopathy; Grave's ophthalmopathy;
KW osteoporosis; bone loss; otitis media; pancreatitis; periodontal disease;
KW chronic lung disease; chronic sinusitis; chronic lymphocytic thyroiditis;
KW urinary tract infection; chronic prostatitis; immunological disorder;
KW chronic pelvic pain syndrome; alopecia areata; Grave's disease;
KW thyroid disease; goiter; struma lymphomatosa; sleep disorder; neoplasia;
KW chronic fatigue syndrome; obesity; infectious disease; Leishmaniasis;
KW Leprosy; myocardial dysfunction; breast cancer; organ transplant;
KW Hodgkin's disease; hormonal regulation; fertility; septicemia.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX
FT modified_base 1..25
FT /*tag= a
FT /mod_base= OTHER
FT misc_difference 5
FT /*tag= b
FT /note= "Given in the specification as the number 7."

US2002146700-A1.
XX
XX 10-OCT-2002.
XX
XX 27-APR-2001; 2001US-00845129.
XX
XX 29-MAY-1997; 97GB-00011040.
XX 30-JUN-1999; 99US-00345217.
XX
XX (INTE-) INTERLEUKIN GENETICS INC.
XX
XX Duff GW, Cox A, Camp NJ, Di Giovine FS;
XX WPI; 1999-080814/07.
XX
XX New method of determining a patient's susceptibility to inflammatory
PT disorders - by detecting the presence of an IL-1 (44112332) haplotype,
PT

PT useful in designing treatment strategies that modulate the activity of
 PT proteins produced by the IL-1 gene cluster.

XX Claim 5, Page 19; 42pp; English.

CC The invention relates to a method for determining whether a subject has
 CC or is predisposed to developing a disease or condition that is associated
 CC with an IL-1 inflammatory haplotype. The method involves detecting at
 CC least one allele of the haplotype, where the presence of the allele
 CC indicates that the subject is predisposed to the development or has the
 CC disease or condition. The invention allows the determination of an
 CC individual's likelihood for developing a particular disease or condition
 CC associated with interleukin 1 (IL-1) polymorphisms without necessarily
 CC determining or characterizing the causative genetic variation. Diseases
 CC such as inflammatory disease e.g. Systemic Inflammatory Response (SIRS),
 CC Alzheimer's disease; arthritis e.g. acute joint inflammation, juvenile
 CC chronic arthritis; asthma e.g. bronchial asthma, chronic obstructive
 CC airways disease; cardiovascular diseases e.g. atherosclerosis, autoimmune
 CC arthritis; cardiomyopathy and cardiac cell dysfunction e.g. aortic smooth
 CC muscle cell activation, cardiac cell apoptosis; gastrointestinal
 CC inflammations e.g. inflammatory bowel disease, ulcerative colitis; HIV
 CC infection; Kawasaki's syndrome e.g. cervical lymphadenopathy, coronary
 CC artery lesions; nephropathies e.g. diabetic nephropathy,
 CC glomerulonephritis; opthalmopathies e.g. diabetic retinopathy, Grave's
 CC opthalmopathy; osteoporosis e.g. bone loss, osteitis media; pancreatitis;
 CC periodontal disease; pulmonary diseases e.g. chronic lung disease,
 CC chronic sinusitis; thyroiditis e.g. chronic lymphocytic thyroiditis;
 CC urinary tract infections e.g. chronic prostatitis, chronic pelvic pain
 CC syndrome; immunological disorders e.g. alopecia areata, Graves disease;
 CC thyroid diseases e.g. goiter, struma lymphomatosa; sleep disorders;
 CC chronic fatigue syndrome; obesity; infectious diseases e.g. Leprosy,
 CC leishmaniasis; trauma e.g. cerebral trauma, myocardial dysfunction;
 CC neoplasias e.g. breast cancer, Hodgkin's disease; hormonal regulation e.g.
 CC fertility, septicemia; organ transplants. This allows for a more
 CC customized approach to preventing the onset or progression of the disease
 CC or condition, e.g. a clinician can more effectively prescribe a therapy
 CC that will address the molecular basis of the disease or condition. The
 CC present sequence represents the sequence of the human IL-1 genotyping
 CC marker g251g26 primer #1

XX Sequence 25 BP; 5 A; 7 C; 10 G; 2 T; 0 U; 1 Other;

XX Query Match 2.3%; Score 22.4; DB 1; Length 25;
 XX Best Local Similarity 92.0%; Pred. NO. 1e+03;

XX Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 867 GGGATTACAGCGCTGAGCCACG 891

DB 1 GGGANTACAGCGCTGAGCCACGCG 25

RESULT 360
 AAH38447/C
 ID AAH38447 standard; DNA; 25 BP.

XX AC AAH38447;

XX DT 14-AUG-2001 (first entry)

XX DE SNP specific SNPE primer SEQ ID 1243.

XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 XX SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
 XX Leech-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
 XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
 XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
 XX inflammation; forensic investigation; paternity analysis; primer; ss.

XX Homo sapiens.

XX MO200129262-A2.

XX 26-APR-2001.

XX 13-OCT-2000; 2000MO-US028436.

XX PR 15-OCT-1999; 99US-0160096P.

XX (ORCH-) ORCHID BIOSCIENCES INC.

XX Picoult-Newburg L, Pohl M;

XX WPI; 2001-290930/30.

PT New genotyping oligonucleotide, useful for detecting the presence,
 PT absence or identity of single polynucleotide polymorphism in a nucleic
 PT acid sample.

XX Claim 1, Page 56; 83pp; English.

CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC primer extension (SNPE) primers, and the sequences of regions flanking
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC includes kits for determining the presence or absence of a SNP, using the
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC performing a single-nucleotide primer extension reaction. The
 CC oligonucleotides are useful for determining the presence, absence or
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC assess by association analysis the genotype of an individual or group of
 CC individuals, having a pathological phenotypic trait suspected of being
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC agammaglobulinemia, diabetes insipidus, Leech-Nyhan syndrome, muscular
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC traits also include symptoms of or susceptibility to multifactorial
 CC disease of which a component is or may be genetic such as autoimmune
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,
 CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC microorganism. The method is also useful in forensic investigations and
 CC paternity analysis. The present sequence represents a single nucleotide
 CC primer extension (SNPE) primer specific for a human SNP containing DNA
 CC sequence

XX Sequence 25 BP; 6 A; 2 C; 13 G; 4 T; 0 U; 0 Other;

XX Query Match 2.3%; Score 22.4; DB 1; Length 25;
 XX Best Local Similarity 95.8%; Pred. NO. 1e+03;

XX Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 531 CATCTCTCTGCTCCAGCTCCCA 554

DB 24 CATCTCTCTGCTCCAGCTCCCA 1

RESULT 361
 ADB04744
 ID ADB04744 standard; DNA; 25 BP.

XX AC ADB04744;

XX DT 20-NOV-2003 (first entry)

XX DE Human MD27 scanning oligonucleotide SEQ ID 5730.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
 XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
 XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 XX developmental disorder; ss.

XX Homo sapiens.

XX EPI281758-A2.

XX 05-FEB-2003.

```
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5730; 103bp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 25 BP; 5 A; 1 C; 9 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 2.3%; Score 22.4; DB 1; Length 25;
XX Best Local Similarity 95.8%; Pred. No. 1e+03;
XX Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 771 TTTGATTTTGTAGTAGAGATGGG 794
XX |||||
XX 1 TTTGATTTTGTAGTAGAGACGGG 24
XX
XX Db
XX
XX RESULT 362
XX ADB04742
XX ID ADB04742 standard; DNA; 25 BP.
XX
XX ADB04742;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MD27 scanning oligonucleotide SEQ ID 5728.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EP1281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX PI
```

```
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5728; 103bp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 25 BP; 6 A; 1 C; 7 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 2.3%; Score 22.4; DB 1; Length 25;
XX Best Local Similarity 95.8%; Pred. No. 1e+03;
XX Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 770 TTTGATTTTGTAGTAGAGATGGG 793
XX |||||
XX 2 TTTGATTTTGTAGTAGACGGG 25
XX
XX Db
XX
XX RESULT 363
XX ADO12082/C
XX ID ADO12082 standard; DNA; 27 BP.
XX
XX ADO12082;
XX
XX 15-JUL-2004 (first entry)
XX
XX Single multiplex PCR primer #1454.
XX
XX ss; primer; simultaneous amplification;
XX single multiplex polymerase chain reaction; multifactorial disease;
XX genetic alteration; pharmacogenetic reaction; genotyping; polymorphism;
XX gene expression profiling.
XX
XX Synthetic.
XX
XX WO2004033649-A2.
XX
XX 22-APR-2004.
XX
XX 07-OCT-2003; 2003WO-US031874.
XX
XX 07-OCT-2002; 2002US-0417009P.
XX
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
XX LI H, LI J;
XX
XX WPI; 2004-340914/31.
XX
XX Designing primers for simultaneous amplification of target DNA fragments
XX in a single multiplex polymerase chain reaction, for high throughput
XX multiplex DNA sequence amplification, comprises aligning two primers.
XX
XX Disclosure; Page 39; 120pp; English.
XX
XX PS
```

XX The invention relates to a method of designing primers for simultaneous
CC amplification of target DNA fragments in a single multiplex polymerase
CC chain reaction by aligning a first primer and a second primer. The method
CC comprises: (a) aligning a first primer and a second primer; and (b)
CC selecting the first primer where the first primer at its 3' end does not
CC contain four or more bases that are perfectly matching to the 3' end
CC sequence of the first primer or a second primer, the first primer at its
CC 3' end does not contain seven or more bases that are perfectly matching
CC except one mismatch to the 3' end sequence of the first primer or the
CC second primer, the first primer at its 3' end does not contain six or
CC more bases that are perfectly matching to a sequence anywhere of the
CC first primer or the second primer, and the first primer at its 3' end
CC does not contain eleven or more bases that are perfectly matching except
CC one mismatch to a sequence anywhere of the first primer or the second
CC primer. The method is useful for designing primers for simultaneous
CC amplification of target DNA fragments in a single multiplex polymerase
CC chain reaction. It is also useful in the identification of multiple genes
CC related to multifactorial diseases, the genome-scale detection of genetic
CC alterations, the studies in pharmacogenetic reactions, the genotyping
CC genetic polymorphisms in a large population, the gene expression
CC profiling in various samples and high throughput genotyping technologies.
CC This sequence corresponds to an example of a primer of the invention.
XX
SQ Sequence 27 BP; 5 A; 6 C; 11 G; 5 T; 0 U; 0 Other;
Query Match 2.2%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 1.1e+03;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 661 GGCGCAATCTTGGCTCAGTCAACCTC 687
Db 27 GGCGCACTCTCGGCTCAGTCAACCTC 1
RESULT 364
AD012035
ID AD012035 standard; DNA; 27 BP.
XX
AC AD012035;
XX
DT 15-JUL-2004 (first entry)
XX
DE Single multiplex PCR primer #1407.
XX
KW as; primer; simultaneous amplification;
KW single multiplex polymerase chain reaction; multifactorial disease;
KW genetic alteration; pharmacogenetic reaction; genotyping; polymorphism;
KW gene expression profiling.
XX
OS Synthetic.
XX
PN WO2004033649-A2.
XX
PD 22-APR-2004.
XX
PF 07-OCT-2003; 2003WO-US031874.
XX
PR 07-OCT-2002; 2002US-0417009P.
XX
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI L4 H, L4 J;
XX
DR WPI; 2004-340914/31.
XX
PT Designing primers for simultaneous amplification of target DNA fragments
PT in a single multiplex polymerase chain reaction, for high throughput
PT multiplex DNA sequence amplification, comprises aligning two primers.
XX
PS Disclosure; Page 39; 120pp; English.
XX
CC The invention relates to a method of designing primers for simultaneous

CC amplification of target DNA fragments in a single multiplex polymerase
CC chain reaction by aligning a first primer and a second primer. The method
CC comprises: (a) aligning a first primer and a second primer; and (b)
CC selecting the first primer where the first primer at its 3' end does not
CC contain four or more bases that are perfectly matching to the 3' end
CC sequence of the first primer or a second primer, the first primer at its
CC 3' end does not contain seven or more bases that are perfectly matching
CC except one mismatch to the 3' end sequence of the first primer or the
CC second primer, the first primer at its 3' end does not contain six or
CC more bases that are perfectly matching to a sequence anywhere of the
CC first primer or the second primer, and the first primer at its 3' end
CC does not contain eleven or more bases that are perfectly matching except
CC one mismatch to a sequence anywhere of the first primer or the second
CC primer. The method is useful for designing primers for simultaneous
CC amplification of target DNA fragments in a single multiplex polymerase
CC chain reaction. It is also useful in the identification of multiple genes
CC related to multifactorial diseases, the genome-scale detection of genetic
CC alterations, the studies in pharmacogenetic reactions, the genotyping
CC genetic polymorphisms in a large population, the gene expression
CC profiling in various samples and high throughput genotyping technologies.
CC This sequence corresponds to an example of a primer of the invention.
XX
SQ Sequence 27 BP; 5 A; 11 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 2.2%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 1.1e+03;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 661 GGCGCAATCTTGGCTCAGTCAACCTC 687
Db 1 GGCGCACTCTCGGCTCAGTCAACCTC 27
RESULT 365
AAV29285
ID AAV29285 standard; cDNA; 22 BP.
XX
AC AAV29285;
XX
DT 21-AUG-1998 (first entry)
XX
DE Nucleotide sequence of PCR primer P2.
XX
KW Human; tumorigenesis gene; T-gene; PLAG2; PLAG1; CTNNB1; antibody;
KW benign tumour; malignant tumour; leukaemia; lymphoma; cancer; inhibition;
KW PCR; amplification; primer; ss.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
PN BP825198-A1.
XX
PD 25-FEB-1998.
XX
PF 17-JAN-1997; 97EP-00200130.
XX
PR 22-AUG-1996; 96EP-00202339.
XX
PA (KULE-) KU LEUVEN RES & DEV.
PA (UYGO-) UNIV GOETTERBORGS HOLDINGBOUAGET AB.
XX
PI Van De Ven WJM, Stenman KGD, Kas KP, Voz ML;
XX
DR WPI; 1998-132252/13.
XX
PT New tumorigenesis T-genes and proteins - useful for, e.g. preparing
PT antibodies for clinically diagnosing cells having non-physiological
PT proliferative capacity such as lipodlastomas.
XX
PS Example 1; Page 6; 71pp; English.
XX
CC This is the nucleotide sequence of the PCR primer P2 used for
CC amplification in the method of the invention, which involves isolation of

CC the tumorigenesis genes (T-gene), in the form of PLAG1, PLAG2, and
CC CTNNB1 genes. Their proteins can be used as a starting point for
CC preparing antibodies for clinically/medically diagnosing cells having a
CC non-physiological proliferative capacity as compared to wild type cells,
CC where the former cells are selected from both benign and malignant
CC tumours, as well as leukaemia and lymphomas. Derivatives of the T-gene
CC are also used in the diagnosis and preparation of therapeutical
CC compositions for the treatment of cancers, such as nucleic acid
CC derivatives, and antibodies. The T-gene may be used as a starting point
CC for designing suitable expression-modulating compounds or techniques for
CC the treatment of non-physiological proliferation phenomena in humans or
CC animals. Expression inhibitors of the T-gene can be used in the treatment
CC of diseases involving benign or malignant tumours
CC
CC
SQ Sequence 22 BP; 6 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 2.2%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 385 TCCCAAGTGTGGATTACAG 406
1 TCCCAAGTGTGGATTACAG 22
DB
RESULT 366
AAZ07500
ID AAZ07500 standard; DNA; 22 BP.
AC AAZ07500;
DT 26-NOV-1999 (first entry)
DE AHRCASEPO transgene specific primer 220.
XX Erythropoietin; EPO; mammalian milk; transgenic animal; lactation;
XX ectopic expression; growth factor; cytokine; enzyme; transgene; human;
XX PCR primer; ss.
OS Synthetic.
XX US959171-A.
XX 28-SEP-1999.
XX 17-AUG-1994; 94US-00291074.
XX 17-AUG-1994; 94US-00291074.
XX (PHAR-) PHARMING BV.
XX Jaenne J, Hyttinen J, Korhonen V;
XX WPI; 1999-561081/47.
XX
XX Producing biologically active polypeptides in mammalian milk.
XX Example 1; Col 7; 10pp; English.
XX
XX The invention relates to a new process for producing biologically active
XX polypeptides (e.g. erythropoietin (EPO)) in mammalian milk as fusion
XX proteins that are less active (or non-active) than the free polypeptides.
XX The process may be used for the recombinant expression of proteins
XX (especially EPO) in the milk of transgenic animals such as sheep and
XX cows. The protein is expressed and secreted into the milk as a fusion
XX protein that has reduced biological activity. The animal is then milked
XX and the fusion protein is then cleaved (chemically or enzymatically) to
XX release the desired active protein which may then be isolated and
XX utilized. The use of to recombinantly produce polypeptides in milk
XX minimizes health problems in the animal and prevents side effects
XX associated with ectopic expression or leakage of the protein into
XX surrounding tissues and the circulation. These side effects are a
XX particular risk when producing potent polypeptides such as growth

CC factors, cytokines and enzymes. This means the transgenic animal remains
CC healthy, viable and able to lactate for longer. Sequences AAZ07499-500
CC represent AHRCASEPO transgene specific primers used for screening GO
CC mice. AHRCASEPO is a gene construct designed to secrete biologically
CC active free human EPO in transgenic mouse milk
CC
CC
SQ Sequence 22 BP; 4 A; 4 C; 8 G; 6 T; 0 U; 0 Other;
Query Match 2.2%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 480 GTGCAGTGTGTGATCACAGCT 501
1 GTGCAGTGTGTGATCACAGCT 22
DB
RESULT 367
AAC87596
ID AAC87596 standard; DNA; 22 BP.
AC AAC87596;
DT 16-MAR-2001 (first entry)
DE Human Alu sequence PCR primer, CL1.
XX Human; keratinocyte growth factor; KGF; chromosome 9p11; abnormality;
XX cancer; miscarriage; spontaneous abortion; genetic susceptibility;
XX diagnosis; Alu sequence; PCR primer; ss.
OS Homo sapiens.
XX JP2000287684-A.
XX 17-OCT-2000.
XX 31-JAN-2000; 2000JP-00022688.
XX 05-FEB-1999; 99JP-00028705.
XX (ASAK) ASAKI BREWERIES LTD.
XX WPI; 2001-065570/08.
XX
XX The base sequence of 9p11 chromosomal region participating to cancer and
XX abortion.
XX
XX Example 3; Page 5; 88pp; Japanese.
XX
XX The invention relates to human chromosomal region 9p11 (AAC87588).
XX Abnormalities in this region of the short arm of chromosome 9 is thought
XX to be associated with miscarriage and cancer, as an ovarian cancer
XX patient with a history of miscarriage was found to have a chromosomal
XX inversion inv(9) (p11;q13). The 9p11 region contains the gene encoding
XX keratinocyte growth factor (KGF), and the invention also specifically
XX claims the KGF PCR primers AAC87589 and AAC87590 for use in detecting all
XX or part of the KGF gene. The nucleic acid sequences can be used to detect
XX abnormalities in chromosomal region 9p11 and thus give an indication of
XX an individual's risk of developing a 9p11-associated condition. Sequences
XX AAC87596-C87597 represent human Alu sequence PCR primers used in an
XX exemplification to the invention
XX
SQ Sequence 22 BP; 6 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 2.2%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 385 TCCCAAGTGTGGATTACAG 406
1 TCCCAAGTGTGGATTACAG 22
DB

```

RESULT 368
AAF88160
ID AAF88160 standard; DNA; 22 BP.
XX
XX AAF88160;
AC
XX 17-JUL-2001 (first entry)
DT
XX
XX Human thyroid malfunction-associated protein RITA PCR primer #1.
DE
XX KRAB domain; hyperplasia; thyroid; tumor; zinc finger motif; primer;
KW cystostatic; antithyroid; gene therapy; chromosome 19; 19q13; ss.
XX
XX Homo sapiens.
OS
XX WO200127265-A1.
PN
XX 19-APR-2001.
PD
XX
XX 11-OCT-2000; 2000WO-DE003600.
PF
XX
XX 12-OCT-1999; 99DB-01049179.
PR
XX (UYBR-) UNITV BREMEN.
PA
XX Bullerdiel J, Rippe V, Meiboom M, Belge G;
PI
XX WPI; 2001-290723/30.
DR
XX
XX New nucleic acid useful for the diagnosis and treatment of thyroid
PT disorders, e.g. tumors.
XX
XX Example 8; Page 29; 59pp; German.
PS
XX
XX This invention describes a novel nucleic acid (N1) encoding a polypeptide
CC which comprises a KRAB-domain and/or at least one zinc finger motif. The
CC products of the invention have cytosstatic and antithyroid activity and
CC can be used in gene therapy. Nucleic acids, polypeptides, and antibodies
CC of the invention may be used in the diagnosis and/or the therapy of the
CC malfunction of the thyroid and/or hyperplasias of the thyroid and/or
CC thyroid tumors. They may also be used in the production of medicaments.
CC (N1) can also be used to diagnose thyroid tumors which are located on
CC chromosome 19 at band 19q13. This sequence represents a PCR primer used
CC in the isolation of the thyroid malfunction-associated protein, RITA
CC which is described in the method of the invention
XX
XX Sequence 22 BP; 6 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 2.2%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 385 TCCCAAGTCTGGATTACAG 406
DB 1 TCCCAAGTCTGGATTACAG 22

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PN WO2003008443-A2.
XX
XX 30-JAN-2003.
PD
XX
XX 19-JUL-2002; 2002WO-CA001105.
PF
XX
XX 19-JUL-2001; 2001US-0306150P.
PR 19-JUL-2001; 2001US-0306161P.
PR 16-NOV-2001; 2001US-0331477P.
XX
XX (NYMO-) NYMOX CORP.
PA
XX
XX Averbach PA;
PI
XX
XX WPI; 2003-247999/24.
DR
XX P-PSDB; ABR63259.
DR
XX
XX Novel neural thread protein peptide, referred as cell death peptide,
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.
XX
XX Disclosure; Page 18; 77pp; English.
PS
XX
XX The present invention relates to a neural thread protein (NTP) peptide
CC referred to as cell death peptide. Thought to be cytosstatic,
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for
CC treating a condition in a patient requiring removal or destruction of
CC cells, for treating a condition such as benign or malignant tumor,
CC inflammatory disease, autoimmune disease and infectious disease. The
CC peptide useful for treatment is derived from the amino acid sequence for
CC a pancreatic thread protein. The peptide is conjugated, linked or bound
CC to a molecule chosen from antibody or its fragment, antibody-like binding
CC molecule, where the molecule has a higher affinity for binding to a tumor
CC or other target than binding to other cells. Treatment using NTP peptides
CC can remove benign tumors with less risk and fewer of the undesirable side
CC effects of surgery. The present sequence is an NTP encoding sequence
XX
XX Sequence 22 BP; 5 A; 5 C; 9 G; 3 T; 0 U; 0 Other;
SQ
Query Match 2.2%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 728 GAGTACTGGGACTACAGGCGC 749
DB 1 GAGTACTGGGACTACAGGCGC 22

```

```

RESULT 369
ACC84464
ID ACC84464 standard; DNA; 22 BP.
XX
XX ACC84464;
AC
XX 28-AUG-2003 (first entry)
DT
XX
XX NTP peptide encoding sequence #11.
DE
XX
XX Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
KW neural thread protein; NTP; tumour; ds.
XX
XX Unidentified.
OS
XX

```

```

RESULT 370
AAH44054/C
ID AAH44054 standard; DNA; 24 BP.
XX
XX AAH44054;
AC
XX 11-SEP-2001 (first entry)
DT
XX
XX Mouse SMN 5' untranslated region PCR primer SEQ ID NO:5.
DE
XX
XX Mouse; survival motor neuron; SMN; knockout; spinal muscular atrophy;
KW SMA; diagnosis; detection; PCR primer; ss.
XX
XX Mus SP.
OS
XX
XX US6245963-B1.
PN
XX
XX 12-JUN-2001.
PD
XX
XX 25-MAY-2000; 2000US-00578656.
PF
XX
XX 28-MAY-1999; 99US-0136520P.
PR
XX
XX (SINI-) ACAD SINICA.
PA
XX

```

PI Li H, Hsieh-Li H, Chang J;
XX MPI; 2001-380517/40.
XX
PT New transgenic mouse having a genome comprising a homozygous disruption
PT of an Smn gene, useful e.g. as a model for human spinal muscular atrophy,
PT or for testing the efficacy of present or future treatments for spinal
PT muscular atrophy.
XX
PS Disclosure; Col 7; 12pp; English.
XX
CC The present invention describes a transgenic mouse whose genome comprises
CC a homozygous disruption of an Smn (Survival motor neuron) gene which does
CC not produce functional Smn protein. The mouse genome additionally
CC comprises a DNA sequence encoding human SMN protein, where expression of
CC the DNA sequence encoding the human SMN protein makes the mouse viable.
CC The mouse shows one or more neurological defects similar to the
CC pathological features of an SMN patient. The transgenic mouse is useful
CC as a model for human spinal muscular atrophy (SMA); in developing and
CC evaluating methods for diagnosing and treating SMA; for testing the
CC accuracy and sensitivity of diagnostic methods for SMA; for testing the
CC efficacy of various present and future therapeutic methods for SMA; and
CC as a convenient positive control necessary for developing and testing any
CC diagnostic methods for SMA. The present sequence represents a PCR primer
CC which is used in the identification of transgenic mice by probing the 5'
CC untranslated region of Smn
XX
SQ Sequence 24 BP; 7 A; 8 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 2.2%; Score 22; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 TTGTCAGGCTGCTCGAAGT 223
DB 23 TTGTCAGGCTGCTCGAAGT 2

RESULT 371
AAH38407
ID AAH38407 standard; DNA; 25 BP.
XX
AC AAH38407;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 1203.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028436.
XX
PR 15-OCT-1999; 99US-0160096P.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR MPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic

PT acid sample.
XX
XX Claim 1; Page 56; 83pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a single nucleotide
CC primer extension (SNPE) primer specific for a human SNP containing DNA
CC sequence
XX
SQ Sequence 25 BP; 6 A; 5 C; 7 G; 6 T; 0 U; 1 Other;

Query Match 2.2%; Score 22; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1e+03;
Matches 22; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 724 TCTTGAGTACTGGGACTACAGC 747
DB 1 TCTTGAGTACTGGGACTACAGC 24

RESULT 372
ADB04745
ID ADB04745 standard; DNA; 25 BP.
XX
AC ADB04745;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5731.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR MPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder

PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
PS Example 8; SEQ ID NO 5731; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
XX
SQ Sequence 25 BP; 5 A; 1 C; 9 G; 10 T; 0 U; 0 Other;
Query Match 2.2%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 772 TTGTATTTTGTAGAGATGGGCTT 796
DB 1 TTGTATTTTGTAGAGACGGGGT 25
RESULT 373
ADB04579
ID ADB04579 standard; DNA; 25 BP.
XX
XX ADB04579;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX Human MDZ7 scanning oligonucleotide SEQ ID 5565.
DE
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX EP1281758-A2.
PN
XX
XX 05-FEB-2003.
PD
XX
XX 30-JUL-2002; 2002EP-00016874.
PF
XX
XX 02-AUG-2001; 2001US-00922181.
PR
XX
XX (AEOM-) AEOMICA INC.
PA
XX
XX Shannon M, Gu Y, Nguyen C;
PI
XX
XX WPI; 2003-423107/40.
DR
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5565; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,

CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
XX
SQ Sequence 25 BP; 4 A; 2 C; 4 G; 15 T; 0 U; 0 Other;
Query Match 2.2%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 607 TTTTATTTTGTGACAGACTCT 631
DB 1 TTTTATTTTGTGACAGACTCT 25
RESULT 374
ADB04741
ID ADB04741 standard; DNA; 25 BP.
XX
XX ADB04741;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX Human MDZ7 scanning oligonucleotide SEQ ID 5727.
DE
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX EP1281758-A2.
PN
XX
XX 05-FEB-2003.
PD
XX
XX 30-JUL-2002; 2002EP-00016874.
PF
XX
XX 02-AUG-2001; 2001US-00922181.
PR
XX
XX (AEOM-) AEOMICA INC.
PA
XX
XX Shannon M, Gu Y, Nguyen C;
PI
XX
XX WPI; 2003-423107/40.
DR
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5727; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross

CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 25 BP; 6 A; 1 C; 6 G; 12 T; 0 U; 0 Other;

QY Query Match 2.2%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 768 TTTTGTATTTTGTAGTAGAGATGG 792
1 TATTTGTATTTTGTAGTAGACGG 25

RESULT 375
ADJ33167/C
ID ADJ33167 standard; DNA; 25 BP.

XX AC ADJ33167;

DT 15-APR-2004 (first entry)

XX Primer sequence R2, seq id 34.

XX Antiinflammatory; nephrotoxic; hepatotoxic; neuroprotective; nootropic;
XX gynecological; cytostatic; antiallergic; immunosuppressive; antithyroid;
XX antiparkinsonian; antidiabetic; monocarboxylic acid; transport protein;
XX inhibitor; potentiator; organic ion; TCH131; TCH182; TCH120;
XX respiratory disease; aschma; kidney disease; kidney failure;
XX nervous system disease; Alzheimer's disease; muscle disease;
XX muscle wasting; allergic disease; meningitis; autoimmune disease;
XX multiple sclerosis; allergic disease; hayfever; spleen disease;
XX immune deficiency disease; leukopenia; liver disease; hepatitis;
XX digestive disease; Crohn's disease; genital disease;
XX ovarian hypofunction; cancer; PCR; primer; ss.

XX Unidentified.

XX WO2003040184-A1.

XX 15-MAY-2003.

XX 06-NOV-2002; 2002WO-JP011559.

XX 07-NOV-2001; 2001JP-00342139.

XX 16-NOV-2001; 2001JP-00351086.

XX 20-NOV-2001; 2001JP-00354971.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Nakanishi A, Sagiya Y, Hikichi Y, Nishimura A;

XX WPI; 2003-441528/41.

XX Monocarboxylic acid and organic ion transport proteins and compounds
XX modifying their activity or expression for treatment, prevention and
XX diagnosis of respiratory, inflammatory, autoimmune, allergic and kidney
XX diseases and cancer.

XX Example 5; SEQ ID NO 34; 209pp; Japanese.

XX The invention relates to proteins TCH131 (human, mouse and rat), TCH182
XX (human) and TCH120 (human) and their salts and partial peptides, and
XX similar proteins with equivalent activity. Also disclosed are
XX polynucleotides (including DNA) encoding the proteins. Proteins of the
XX invention are useful in the prevention, treatment and diagnosis of
XX respiratory diseases (including asthma and bronchitis), kidney diseases
XX (including kidney failure and nephritis), nervous system diseases
XX (including Alzheimer's, Parkinson's and schizophrenia), metabolic
XX acidosis, muscle diseases (including muscle wasting), allergic diseases
XX (including pneumonia, meningitis and myocarditis), autoimmune diseases

CC (including muscular dystrophy and multiple sclerosis), allergic diseases
CC (including hayfever), spleen diseases (including spleen hyperfunction),
CC immune deficiency diseases (including leukopenia), liver diseases
CC (including hepatitis), digestive diseases (including Crohn's disease),
CC genital diseases (including ovarian hypofunction) and cancer (including
CC pancreas cancer, lung cancer, non-small cell lung cancer, kidney cancer,
CC liver cancer, ovarian cancer, prostate cancer, stomach cancer, breast
CC cancer, bladder cancer and colon cancer). The sequences given in records
CC ADJ33167-ADJ33242 include proteins of the invention and those related to
CC the invention, polynucleotides encoding these proteins, and primers and
CC probes for the amplification and detection of DNA encoding them.

XX Sequence 25 BP; 7 A; 4 C; 11 G; 3 T; 0 U; 0 Other;

QY Query Match 2.2%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 535 CTCCTGCTCAGCCTCCCACTAGC 559
25 CTCCTGCTCAGCCTCCCATGTAGC 1

RESULT 376
AAH91005
ID AAH91005 standard; DNA; 26 BP.

XX AC AAH91005;

DT 09-OCT-2001 (first entry)

XX Human inflammatory bowel disease associated polymorphic site #80.

XX Human, inflammatory bowel disease; Crohn's disease; ulcerative colitis;
XX single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
XX chromosome 5q11-33; forensic test; gene therapy; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX misc_feature 13

XX /*tag= a

XX /note= "SNP, optionally C or T at this position"

XX WO200142511-A2.

XX 14-JUN-2001.

XX 11-DEC-2000; 2000WO-US033632.

XX 10-DEC-1999; 99US-0170257P.

XX 10-APR-2000; 2000US-0196046P.

XX (WHEED) WHITEHEAD INST BIOMEDICAL RES.

XX (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.

XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;

XX WPI; 2001-367874/38.

XX Claim 1; Page 42; 463pp; English.

XX The present invention describes a method for detecting the presence of
XX polymorphisms associated with inflammatory bowel diseases such as
XX ulcerative colitis and Crohn's disease. The methods can be used to detect
XX the presence of genetic polymorphisms associated with inflammatory bowel
XX disease and correlating their occurrence with disease states. They may be
XX used in this way for phenotypic correlations, forensics, paternity
XX testing, medicine and genetic analysis. The present sequence is a
XX polymorphic site described in the exemplification of the invention

XX Sequence 26 BP; 6 A; 4 C; 9 G; 6 T; 0 U; 1 Other;
SQ
Query Match 2.2%; Score 21.8; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 862 GTGCTGGATTACAGCGCTGAGCCAC 887
DB 1 GTGCTGGATTACAGCGCTGAGCCAC 26
RESULT 377
AAH91096/c
ID AAH91096 standard; DNA; 26 BP.
XX AAH91096;
AC
XX
XX
XX 09-OCT-2001 (first entry)
XX
XX
XX Human inflammatory bowel disease associated polymorphic site #171.
DE
XX
XX Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
KW chromosome 5q31-33; forensic test; gene therapy; ds.
XX
XX Homo sapiens.
OS
XX
XX
XX Key Location/Qualifiers
FH misc_feature 12
FT /tag= a
FT /note= "SNP, optionally C or T at this position"
XX
XX
XX WO200142511-A2.
XX
XX 14-JUN-2001.
XX
XX 11-DEC-2000; 2000WO-US033632.
XX
XX 10-DEC-1999; 99US-0170257P.
PR 10-APR-2000; 2000US-0196046P.
XX
XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (ELI-) ELIPSIS BIOTHERAPEUTICS CORP.
XX
XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
PI
XX
XX WPI; 2001-367874/38.
XX
XX
XX Testing for the presence of polymorphisms associated with inflammatory
PT bowel disease, using a hybridization assay.
XX
XX Claim 1; Page 46; 463pp; English.
XX
XX The present invention describes a method for detecting the presence of
CC polymorphisms associated with inflammatory bowel diseases such as
CC ulcerative colitis and Crohn's disease. The methods can be used to detect
CC the presence of genetic polymorphisms associated with inflammatory bowel
CC disease and correlating their occurrence with disease states. They may be
CC used in this way for phenotypic correlations, forensics, paternity
CC testing, medicine and genetic analysis. The present sequence is a
CC polymorphic site described in the exemplification of the invention
XX
SQ Sequence 26 BP; 6 A; 10 C; 5 G; 4 T; 0 U; 1 Other;
Query Match 2.2%; Score 21.8; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 862 GTGCTGGATTACAGCGCTGAGCCAC 887
DB 26 GTGCTGGATTACAGCGCTGAGCCAC 1

RESULT 378
AAH38507/c
ID AAH38507 standard; DNA; 27 BP.
XX
XX AAH38507;
AC
XX
XX 14-AUG-2001 (first entry)
XX
XX
XX SNP specific SNPE primer SEQ ID 1303.
DE
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; primer; ss.
XX
XX
XX Homo sapiens.
OS
XX
XX
XX WO200129262-A2.
XX
XX 26-APR-2001.
XX
XX 13-OCT-2000; 2000WO-US028436.
PR 15-OCT-1999; 99US-0160096P.
XX
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
PA
XX
XX Picoult-Newburg L, Pohl M;
PI
XX
XX WPI; 2001-290930/30.
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polymorphic polymorphism in a nucleic
PT acid sample.
XX
XX
XX Claim 1; Page 56; 83pp; English.
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a single nucleotide
CC primer extension (SNPE) primer specific for a human SNP containing DNA
XX
SQ Sequence 27 BP; 8 A; 6 C; 8 G; 3 T; 0 U; 2 Other;
Query Match 2.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 85.2%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 671 TGGCTACTGCAACCTCTGCTCCCG 697
DB TGGCTACTGCAACCTCTGCTCCCG 1

```
Db          27 TGGCTCACTGNAACCTGACTGCTGG 1
RESULT 379
AAH37975/C
ID          AAH37975 standard; DNA; 27 BP.
XX
XX
AC          AAH37975;
XX
XX
DT          14-AUG-2001 (first entry)
XX
XX
DE          SNP specific SNPE primer SEQ ID 771.
XX
XX
DE          Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX
XX
KM          SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
XX
XX
KM          Leisch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX
XX
KM          polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX
XX
KM          acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX
XX
KM          inflammation; forensic investigation; paternity analysis; primer; ss.
XX
XX
OS          Homo sapiens.
XX
XX
PN          WO200129262-A2.
XX
XX
PD          26-APR-2001.
XX
XX
PF          13-OCT-2000; 2000WO-US028436.
XX
XX
PR          15-OCT-1999; 99US-0160096P.
XX
XX
XX          (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX
PI          Picoult-Newburg L, Pohl M;
XX
XX
DR          WPI; 2001-290930/30.
XX
XX
PT          New genotyping oligonucleotide, useful for detecting the presence,
XX
XX
PT          absence or identity of single polynucleotide polymorphism in a nucleic
XX
XX
PT          acid sample.
XX
XX
PS          Claim 1; Page 53; 83pp; English.
XX
XX
CC          Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
XX
XX
CC          primer extension (SNPE) primers, and the sequences of regions flanking
XX
XX
CC          sites of single nucleotide polymorphisms SNPs. The present invention
XX
XX
CC          includes kits for determining the presence or absence of a SNP, using the
XX
XX
CC          oligonucleotides of the invention. The PCR primers are used to amplify a
XX
XX
CC          SNP flanking sequence, the SNPE primer is used as a genotyping primer.
XX
XX
CC          The oligonucleotides are useful for genotyping a nucleic acid sample by
XX
XX
CC          performing a single-nucleotide primer extension reaction. The
XX
XX
CC          oligonucleotides are useful for determining the presence, absence or
XX
XX
CC          identity of a SNP and for genotyping nucleic acid samples, for e.g. to
XX
XX
CC          assess by association analysis the genotype of an individual or group of
XX
XX
CC          individuals, having a pathological phenotypic trait suspected of being
XX
XX
CC          caused by one or more SNPs. Phenotypic traits include diseases e.g.
XX
XX
CC          agammaglobulinaemia, diabetes insipidus, Leisch-Nyhan syndrome, muscular
XX
XX
CC          dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
XX
XX
CC          osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
XX
XX
CC          traits also include symptoms of or susceptibility to multifactorial
XX
XX
CC          disease of which a component is or may be genetic such as autoimmune
XX
XX
CC          diseases, including, rheumatoid arthritis, multiple sclerosis,
XX
XX
CC          inflammation, cancer, nervous system diseases and infection by pathogenic
XX
XX
CC          microorganism. The method is also useful in forensic investigations and
XX
XX
CC          paternity analysis. The present sequence represents a single nucleotide
XX
XX
CC          primer extension (SNPE) primer specific for a human SNP containing DNA
XX
XX
CC          sequence
XX
XX
SQ          Sequence 27 BP; 6 A; 6 C; 8 G; 5 T; 0 U; 2 Other;
```

```
Query Match          2.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 85.2%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY          485 GTGGTGTGATCAAGCTCACTGACGCC 511
Db          27 GTGGTGTGATCAAGCTCACTGANNCC 1
RESULT 380
AAH91552/C
ID          AAH91552 standard; DNA; 27 BP.
XX
XX
AC          AAH91552;
XX
XX
DT          09-OCT-2001 (first entry)
XX
XX
DE          Human inflammatory bowel disease associated polymorphic site #627.
XX
XX
XX          Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
XX
XX
KM          single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
XX
XX
KM          chromosome 5q31-33; forensic test; gene therapy; ds.
XX
XX
OS          Homo sapiens.
XX
XX
XX
XX
FH          Key          Location/Qualifiers
XX
XX
FT          misc_feature          15
XX
XX
FT          /tag= a
XX
XX
FT          /note= "SNP, optionally T or C at this position"
XX
XX
XX          WO200142511-A2.
XX
XX
XX          14-JUN-2001.
XX
XX
XX          11-DEC-2000; 2000WO-US033632.
XX
XX
XX          10-DEC-1999; 99US-0170257P.
XX
XX
PR          10-APR-2000; 2000US-0196046P.
XX
XX
XX          (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
XX
PA          (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX
XX
PI          Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
XX
XX
XX          WPI; 2001-367874/38.
XX
XX
XX          Testing for the presence of polymorphisms associated with inflammatory
XX
XX
XX          bowel disease, using a hybridization assay.
XX
XX
PS          Claim 1; Page 65; 463pp; English.
XX
XX
XX          The present invention describes a method for detecting the presence of
XX
XX
XX          polymorphisms associated with inflammatory bowel diseases such as
XX
XX
XX          ulcerative colitis and Crohn's disease. The methods can be used to detect
XX
XX
XX          the presence of genetic polymorphisms associated with inflammatory bowel
XX
XX
XX          disease and correlating their occurrence with disease states. They may be
XX
XX
XX          used in this way for phenotypic correlations, forensics, paternity
XX
XX
XX          testing, medicine and genetic analysis. The present sequence is a
XX
XX
XX          polymorphic site described in the exemplification of the invention
XX
XX
XX
XX
SQ          Sequence 27 BP; 7 A; 6 C; 7 G; 6 T; 0 U; 1 Other;
```

```
Query Match          2.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 88.5%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
RESULT 381
AAH83037/C
ID          AAH83037 standard; DNA; 23 BP.
XX
XX
AC          AAH83037;
XX
```


CC various diseases such as malignant tumours, haemopathy, human
CC immunodeficiency virus (HIV) infection, immunological diseases, and
CC various inflammations. The present sequence represents a reverse
CC transcriptase (RT)-PCR primer used to isolate cDNA encoding human zinc
CC finger protein 10.01
XX
SQ Sequence 24 BP; 3 A; 8 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 2.2%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 1.1e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 868 GGATTACAGCGGTGAGCCACCAC 890
Db 24 GGATTACAGCGGTGAGCCACCAC 2
RESULT 384
ABS58184/C
ID ABS58184 standard; DNA; 24 BP.
XX
AC ABS58184;
XX
DT 26-FEB-2003 (first entry)
XX
DE RT-PCR primer #2 for cDNA encoding human zinc finger protein 10.01.
XX
KW Human; zinc finger protein 10.01; malignant tumour; haemopathy;
KW human immunodeficiency virus infection; HIV infection; inflammation;
KW immunological disease; RT-PCR; primer; reverse transcriptase-PCR; ss.
XX
OS Homo sapiens.
XX
PN CN1352110-A.
XX
PD 05-JUN-2002.
XX
PF 06-NOV-2000; 2000CN-00127241.
XX
PR 06-NOV-2000; 2000CN-00127241.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-692406/75.
XX
PT New human zinc finger protein 10.01 polypeptide for treating malignant
PT tumors, hemopathy, human immunodeficiency virus infection, immunological
PT diseases and various inflammations.
XX
PS Example 2; Page 17 (disclosure); 33pp; Chinese.
XX
CC The present invention relates to the isolation of human zinc finger
CC protein 10.01, and the polynucleotide sequence encoding it. Also
CC described is the process for preparing the protein by DNA recombination
CC and the application of the polypeptide and polynucleotide in treating
CC various diseases such as malignant tumours, haemopathy, human
CC immunodeficiency virus (HIV) infection, immunological diseases, and
CC various inflammations. The present sequence represents a reverse
CC transcriptase (RT)-PCR primer used to isolate cDNA encoding human zinc
CC finger protein 10.01
XX
SQ Sequence 24 BP; 6 A; 5 C; 9 G; 4 T; 0 U; 0 Other;
Query Match 2.2%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 1.1e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 997 GGCTCAGCGATTCTCTGCTC 1019
Db 23 GGCTCAGCGATTCTCTGCTC 1

RESULT 385
ABA04737
ID ABA04737 standard; DNA; 24 BP.
XX
AC ABA04737;
XX
DT 22-FEB-2002 (first entry)
XX
DE Human alkylation DNA protein cysteine methyltransferase 11 PCR primer #2.
XX
KW Human; alkylation DNA protein cysteine methyltransferase 11; cytostatic;
KW haemostatic; virucide; immunomodulatory; antiinflammatory; gene therapy;
KW tumour; haemopathy; HIV infection; immunological disease; inflammation;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200188146-A1.
XX
PD 22-NOV-2001.
XX
PF 26-MAR-2001; 2001WO-CN000464.
XX
PR 28-MAR-2000; 2000CN-00115226.
XX
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-055701/07.
XX
DE Human alkylation-DNA-protein cysteine methyltransferase and encoding
PT polynucleotide, used in diagnosis and treatment of malignant tumors,
PT hemopathy, human immunodeficiency virus infection, immunological diseases
PT and inflammation.
XX
PS Example 2; Page 19; 40pp; Chinese.
XX
CC The present invention relates to human alkylation-DNA-protein cysteine
CC methyltransferase (see ABA47739). The protein and its coding sequence are
CC useful in the diagnosis and treatment of malignant tumours, haemopathy,
CC HIV infection, immunological diseases and various inflammations. The
CC present sequence is a PCR primer, which was used in an example from the
CC present invention
XX
SQ Sequence 24 BP; 4 A; 0 C; 4 G; 16 T; 0 U; 0 Other;
Query Match 2.2%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 1.1e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 767 TTTTGTGATTTTGTAGTGA 789
Db 2 TTTTGTGATTTTGTAGTGA 24
RESULT 386
AAL45771/C
ID AAL45771 standard; DNA; 24 BP.
XX
AC AAL45771;
XX
DT 28-JUN-2002 (first entry)
XX
DE Human acid phosphatase family protein 11 cDNA PCR primer #2.
XX
KW Human; acid phosphatase family protein 11; cancer; haemopathy;
KW cytostatic; haemostatic; virucide; immunomodulatory; antiinflammatory;
KW immune disease; HIV infection; phlogosis; gene therapy; PCR; primer; ss.
XX
OS Homo sapiens.
XX

PN WO200220579-A1.
XX
PD 14-MAR-2002.
XX
PF 19-JUN-2001; 2001WO-CN001011.
XX
PR 21-JUN-2000; 2000CN-00116667.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-329869/36.
XX
PT Homo acid phosphatase family protein 11 and encoding polynucleotide, used
XX in diagnosis and treatment of malignant tumors, hemopathy, human
XX immunodeficiency virus infection, immunological diseases and
XX inflammation.
XX
PS Example 2; Page 12; 39pp; Chinese.
XX
CC The present invention provides the protein and coding sequences of human
XX acid phosphatase family protein 11. The sequences can be used in the
XX treatment of cancer, haemopathy, HIV infection, immune diseases and
XX phlogosis. The present sequence is a PCR primer for the coding sequence
XX of the invention
SQ Sequence 24 BP; 5 A; 3 C; 11 G; 5 T; 0 U; 0 Other;
XX
QY Query Match 2.2%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 1.1e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
DB 675 TCACCTGCACCTCTGCTCCCGG 697
24 TCACTGCACCTCTGCTCCCGG 2
XX
RESULT 387
AAD50373/C
ID AAD50373 standard; DNA; 24 BP.
XX
AC AAD50373;
XX
DT 24-MAR-2003 (first entry)
XX
DE PCR primer #1 used to illustrate the method of the invention.
XX
KM Stutter reduction; microsatellite amplification; genetic analysis; PCR;
XX primer; ss.
XX
OS Unidentified.
XX
PN WO200290562-A2.
XX
PD 14-NOV-2002.
XX
PF 06-MAY-2002; 2002WO-US014189.
XX
PR 07-MAY-2001; 2001US-00850514.
XX
PA (BIOW) APPLIED BIOSYSTEMS INC.
XX
PI Coticone SR, Bloch W;
XX
DR WPI; 2003-111983/10.
XX
PT Reducing stutter in the amplification of a microsatellite for genetic
XX analysis by contacting the sample comprising a microsatellite with an
XX enzyme with nucleic acid polymerase activity and incubating the sample
XX with the enzyme.
PS Disclosure; Page 29; 60pp; English.

XX
CC The present invention relates to a method of reducing stutter in the
XX amplification of a microsatellite. The method involves providing a sample
XX comprising a microsatellite of interest; contacting the sample with at
XX least one enzyme having nucleic acid polymerase activity and incubating
XX the sample with the enzyme for amplifying the microsatellite. The method
XX is useful for reducing stutter in the amplification of a microsatellite
XX for genetic analysis. The present sequence is a PCR primer used to
XX illustrate the method of the invention
SQ Sequence 24 BP; 7 A; 3 C; 9 G; 5 T; 0 U; 0 Other;
XX
QY Query Match 2.2%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 1.1e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
DB 966 AATCTGGCTCACTGCACCTCT 988
23 AATCTGGCTCACTGCACCTCT 1
XX
RESULT 388
ADL06343/C
ID ADL06343 standard; DNA; 24 BP.
XX
AC ADL06343;
XX
DT 06-MAY-2004 (first entry)
XX
DE RT-PCR primer #1 for cDNA encoding human protein-13.2.
XX
KM Human; protein-13.2; site-specific recombinase;
XX growth development disorder; tumour; reverse transcriptase-PCR; RT-PCR;
XX primer; ss.
XX
OS Homo sapiens.
XX
PN CN1393548-A.
XX
PD 29-JAN-2003.
XX
PF 29-JUN-2001; 2001CN-00113178.
XX
PR 29-JUN-2001; 2001CN-00113178.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2003-422181/40.
XX
PT Polypeptide-human protein-13.2 containing site specific recombinase
XX characteristic sequence fragment and polynucleotide for coding it.
XX
PS Example 3; SEQ ID NO 3; 32pp; Chinese.
XX
CC The present invention relates to the isolation of human protein-13.2
XX containing a site-specific recombinase characteristic sequence fragment,
XX and the polynucleotide sequence encoding it. Also disclosed is a process
XX for preparing the polypeptide by a DNA recombination technique and
XX application of the polypeptide and polynucleotide in treating diseases
XX such as growth development disorders and tumours. The present sequence
XX represents a reverse transcriptase-PCR primer used in the examples of the
XX present invention.
SQ Sequence 24 BP; 6 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
XX
QY Query Match 2.2%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 1.1e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
DB 1005 CGATTCTCCGTGCTCAGCTCCG 1027
|||||

DB 24 CGATTCTCCTGCTCAGCCTCCC 2
 RESULT 389
 AAH38671
 ID AAH38671 standard; DNA, 25 BP.
 AC AAH38671;
 DT 14-AUG-2001 (first entry)
 DE SNP specific SNPE primer SEQ ID 1467.
 XX
 XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 KM SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
 KM Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
 KM polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
 KM acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
 KM inflammation; forensic investigation; paternity analysis; primer; ss.
 XX
 XX Homo sapiens.
 OS
 PN WO200129262-A2.
 PD 26-APR-2001.
 XX
 XX 13-OCT-2000; 2000WO-US028436.
 PF
 XX 15-OCT-1999; 99US-0160096P.
 PR
 XX (ORCH-) ORCHID BIOSCIENCES INC.
 XX
 XX Picoult-Newburg L, Pohl M;
 PI
 XX WPI; 2001-290930/30.
 DR
 XX
 XX New genotyping oligonucleotide, useful for detecting the presence,
 PT absence or identity of single polynucleotide polymorphism in a nucleic
 PT acid sample.
 XX
 XX Claim 1; Page 57; 83pp; English.
 PS
 XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC primer extension (SNPE) primers, and the sequences of regions flanking
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC includes kits for determining the presence or absence of a SNP, using the
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC performing a single-nucleotide primer extension reaction. The
 CC oligonucleotides are useful for determining the presence, absence or
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC assess by association analysis the genotype of an individual or group of
 CC individuals, having a pathological phenotypic trait suspected of being
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC traits also include symptoms of or susceptibility to multifactorial
 CC disease of which a component is or may be genetic such as autoimmune
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,
 CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC microorganism. The method is also useful in forensic investigations and
 CC paternity analysis. The present sequence represents a single nucleotide
 CC primer extension (SNPE) primer specific for a human SNP containing DNA
 CC sequence
 XX
 XX Sequence 25 BP; 7 A; 1 C; 5 G; 12 T; 0 U; 0 Other;
 SQ

Query Match 2.2%; Score 21.4; DB 1; Length 25;
 Best Local Similarity 95.7%; Pred. No. 1.1e+03;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 769 TTTTGTATTTTAGTAGAGATG 791
 DB 3 TTTTGTATTTTAGTAGAGAG 25
 RESULT 390
 AAH38231
 ID AAH38231 standard; DNA, 25 BP.
 AC AAH38231;
 DT 14-AUG-2001 (first entry)
 DE SNP specific SNPE primer SEQ ID 1027.
 XX
 XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 KM SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
 KM Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
 KM polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
 KM acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
 KM inflammation; forensic investigation; paternity analysis; primer; ss.
 XX
 XX Homo sapiens.
 OS
 PN WO200129262-A2.
 PD 26-APR-2001.
 XX
 XX 13-OCT-2000; 2000WO-US028436.
 PF
 XX 15-OCT-1999; 99US-0160096P.
 PR
 XX (ORCH-) ORCHID BIOSCIENCES INC.
 XX
 XX Picoult-Newburg L, Pohl M;
 PI
 XX WPI; 2001-290930/30.
 DR
 XX
 XX New genotyping oligonucleotide, useful for detecting the presence,
 PT absence or identity of single polynucleotide polymorphism in a nucleic
 PT acid sample.
 XX
 XX Claim 1; Page 55; 83pp; English.
 PS
 XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC primer extension (SNPE) primers, and the sequences of regions flanking
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC includes kits for determining the presence or absence of a SNP, using the
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC performing a single-nucleotide primer extension reaction. The
 CC oligonucleotides are useful for determining the presence, absence or
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC assess by association analysis the genotype of an individual or group of
 CC individuals, having a pathological phenotypic trait suspected of being
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC traits also include symptoms of or susceptibility to multifactorial
 CC disease of which a component is or may be genetic such as autoimmune
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,
 CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC microorganism. The method is also useful in forensic investigations and
 CC paternity analysis. The present sequence represents a single nucleotide
 CC primer extension (SNPE) primer specific for a human SNP containing DNA
 CC sequence
 XX
 XX Sequence 25 BP; 7 A; 1 C; 5 G; 12 T; 0 U; 0 Other;
 SQ

Query Match 2.2%; Score 21.4; DB 1; Length 25;
 Best Local Similarity 95.7%; Pred. No. 1.1e+03;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 769 TTTTGTATTTTGTAGAGAG 791
 |||||
 DB 3 TTTTGTATTTTGTAGAGAG 25

RESULT 391
 AA245143/C
 ID AA245143 standard; DNA; 26 BP.
 AC AA245143;
 DT 28-FEB-2000 (first entry)
 XX
 XX Oligonucleotide used to determine the function of MMP-9 polymorphism.
 DE Matrix metalloproteinase-9; MMP-9; polymorphism; endopeptidase; detect;
 XX inflammatory disease; diagnose; atherosclerosis; tumour; metastasis;
 KW neurologic disease; multiple sclerosis; arthritis; ss.
 KM
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX WO9597315-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-GB001447.
 XX
 XX 07-MAY-1998; 98GB-00009764.
 XX
 XX (ISIS-) ISIS INNOVATION LTD.
 PA
 XX Zhang BP, Ye S, Henney A;
 PI
 DR WPI; 2000-052977/04.
 XX
 PT Detection of matrix metalloproteinase 9 gene polymorphisms for diagnosis or
 PT prognosis of diseases characterized by metalloproteinase mediated
 PT remodelling.
 PT
 XX
 XX Example 3; Page 14; 29pp; English.
 PS
 XX Oligonucleotides AA245143-245144 are used to determine the function of
 CC the matrix metalloproteinase-9 (MMP-9) gene -1562 (C/T) polymorphic site.
 CC MMP-9 is a zinc-dependent endopeptidase, and is located on chromosome 20.
 CC MMP activity is associated with inflammatory diseases and MMP-9 is
 CC implicated in the pathology of multiple sclerosis. Certain polymorphic
 CC sequences in the MMP-9 promoter, coding sequence and 3' untranslated
 CC region of the human MMP-9 gene (see AA245145) can affect the severity of
 CC atherosclerosis. The invention relates to the presence or absence of one
 CC variant form of a MMP-9 gene polymorphism (-1562 Cytosine/Threonine),
 CC detection of this polymorphism using oligonucleotides AA245137-245140 can
 CC be used for disease prognosis. The invention shows that the MMP-9 C-1562T
 CC polymorphism is a regulatory functional polymorphism. The methods and
 CC oligonucleotides are used to detect polymorphisms in the MMP-9 gene. They
 CC are useful for the diagnosis and prognosis of diseases characterized by
 CC metalloproteinase mediated remodelling, such as atherosclerosis, tumour
 CC invasion and metastasis, inflammatory disease, and neurological diseases,
 CC particularly those involving demyelination such as multiple sclerosis,
 CC and arthritic disease. Proteins encoded by the MMP-9 gene variants may be
 CC used for screening compounds that bind specifically to a molecule encoded
 CC by one variant of a polymorphic sequence, thus identifying compounds
 CC which modulate the activity of the enzyme. Such compounds can then be
 CC used for rational drug design
 CC
 XX
 SQ Sequence 26 BP; 5 A; 7 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 2.1%; Score 21.2; DB 1; Length 26;
 Best Local Similarity 88.5%; Pred. No. 1.2e+03;
 Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 870 ATTACAGCGTGAGCCACCGCCG 895
 |||||
 DB 26 ATTATAGCGTGCGCCACCGCCCTG 1

RESULT 392
 ABK61474/C
 ID ABK61474 standard; DNA; 26 BP.
 AC ABK61474;
 DT 18-JUN-2002 (first entry)
 XX
 XX Human NOV3 Exon linking PCR primer #2.
 DE
 XX
 XX Human; ss; NOVX; gene therapy; cardiomyopathy; atherosclerosis;
 KW cell signal processing disorder; metabolic pathway modulation disorder;
 KW diabetes; cancer; adenocarcinoma; lymphoma; prostate cancer; primer;
 KW uterus cancer; immune response; graft-versus-host disease; Exon linking;
 KW acquired immunodeficiency syndrome; AIDS; asthma; Crohn's disease;
 KW hypertension; congenital heart defects; multiple sclerosis; inflammation;
 KW Albright hereditary osteodystrophy.
 XX
 XX
 OS Homo sapiens.
 XX
 XX WO200216599-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 27-AUG-2001; 2001WO-US026510.
 XX
 XX 25-AUG-2000; 2000US-0228191P.
 XX
 XX 08-FEB-2001; 2001US-0267300P.
 XX
 XX 20-FEB-2001; 2001US-0269961P.
 XX
 XX 20-MAR-2001; 2001US-0277337P.
 XX
 XX (CURA-) CURAGEN CORP.
 PA (COR-) COR THERAPEUTICS INC.
 PI Burgess CE, Conley PB, Grose WM, Hart M, Kekuda R, Shinkets RA;
 PI Spytek KA, Szekeres ES, Tomlinson JE, Topper JN, Yang R;
 XX
 DR WPI; 2002-280937/32.
 XX
 PT New polypeptides for treating or preventing a disorder associated with
 PT them, in humans, e.g. cardiomyopathy, atherosclerosis or cancers.
 PT
 XX
 XX Example 1; Page 204; 263pp; English.
 PS
 XX The invention relates to an isolated polypeptide (NOVX) a mature form of
 CC NOVX, a NOVX variant (differing by no more than 15%), the nucleotide
 CC encoding NOVX (or its complement, fragment or variant). NOVX is NOV1-14,
 CC 15a, 15b, 16a, and 16b. The NOVX polypeptide, nucleic acid encoding it
 CC and antibody against it, are useful for treating or preventing (e.g. by
 CC gene therapy) a NOVX-associated disorder in humans, e.g. cardiomyopathy,
 CC atherosclerosis, a disorder related to cell signal processing and
 CC metabolic pathway modulation, diabetes or cancers. The NOVX polypeptide
 CC and nucleic acids are also useful for determining the presence of
 CC predisposition to the diseases. The NOVX nucleic acid and polypeptide are
 CC especially useful in therapeutic or prophylactic applications for
 CC disorders associated with aberrant NOVX expression or activity, e.g.
 CC cancers (e.g. adenocarcinoma, lymphoma, prostate cancer or uterus
 CC cancer), immune response, graft-versus-host disease, acquired
 CC immunodeficiency syndrome (AIDS), asthma, Crohn's disease, hypertension,
 CC congenital heart defects, multiple sclerosis, inflammation or Albright
 CC hereditary osteodystrophy and many other diseases listed in the
 CC specification. The DNA encoding the protein is useful in gene therapy for
 CC treating the conditions. This is also useful in detection assays,
 CC chromosome mapping, tissue typing, diagnostic or prognostic assays, or
 CC for developing a powerful assay system for functional analysis of various
 CC human disorders, as well as in diagnostic applications. The present
 CC sequence is a primer used to isolate DNA encoding a NOVX protein by the
 CC technique of exon linking

XX SQ Sequence 26 BP; 7 A; 5 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 2.1%; Score 21.2; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 1.2e+03;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 535 CTCCTGCTCAGCTCCCAAGTAGCT 560
DB 26 CTCCTGCTCAGCTCCCAAGTAGCT 1

RESULT 393

ABK67128
ID ABK67128 standard; DNA; 26 BP.

XX AC ABK67128;

XX DT 02-JUL-2002 (first entry)

XX DE Human gene specific PCR primer #1216.

XX KW Primer; ss; DNA microarray; differential expression analysis; human.

XX OS Homo sapiens.

XX PN US6352829-B1.

XX PD 05-MAR-2002.

XX PF 05-JAN-1999; 99US-00225928.

XX PR 21-MAY-1997; 97US-00859998.

XX PA (CLON-) CLONTECH LAB INC.

XX PI Chenchik A, Jokhadze G, Bibilashvili R;

XX DR WPI; 2002-314699/35.

PT Producing sub-population of labeled nucleic acids, useful for analyzing
PT differences in RNA profiles between several different physiological
PT sources, using set of distinct gene specific primers.

PS Example 3; SEQ ID NO 1216; 11pp; English.

XX CC The invention relates to producing a sub-population of labeled nucleic
XX acids (NAs) comprising contacting a NA sample from a physiological
XX source, with a pool of 50 distinct gene specific primers under suitable
XX conditions to enzymatically generate sub-population of NAs, where each
XX gene specific primer has a sequence complementary to a distinct mRNA, and
XX each labeled NA is generated using a single gene specific primer. The
XX method is useful for producing a sub-population of labeled NAs which is
XX useful for analyzing the differences in the RNA profiles between several
XX different physiological sources, where the method comprises producing
XX subpopulation of labeled NAs for the different physiological sources,
XX comprising the populations for each physiological source to identify
XX differences in the population, where the comparison is preferably
XX performed by hybridizing the labeled NAs for each of the distinct
XX physiological sources to an array of probe NAs stably associated with the
XX surface of a substrate to produce a hybridisation pattern for each of the
XX sources, and comparing the patterns for each of the sources, where
XX differential gene expression assays are utilised in differential
XX expression analysis of diseased a normal tissue e.g. neoplastic a normal
XX tissue, or different tissue or sub-tissue types. The present sequence is a
XX human gene specific PCR primer used in the method of the invention. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from USPTO
XX at <http://wipo.segdata.uspto.gov/sequence.html?docID=6352829B1>

SQ Sequence 26 BP; 7 A; 5 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 2.1%; Score 21.2; DB 1; Length 26;

Best Local Similarity 88.5%; Pred. No. 1.2e+03;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 867 GGGATTACAGGCGTGGAGCCACCGC 892
DB 1 GGGATTACAGGCGTGGAGCCACCGC 26

RESULT 394

ABZ22656/C
ID ABZ22656 standard; DNA; 26 BP.

XX AC ABZ22656;

XX DT 31-MAR-2003 (first entry)

XX DE Human PEPT1 PCR primer PEPT1#1 R.

XX KW Human; PEPT1; PEPT2; intestinal peptide transporter; transport;
KW transporter; PCR primer; ss.

XX OS Homo sapiens.

XX PN WO2002100172-A1.

XX PD 19-DEC-2002.

XX PF 11-JUN-2002; 2002WO-US018686.

XX PR 11-JUN-2001; 2001US-0297732P.

XX PR 01-MAR-2002; 2002US-0361002P.

XX PA (XENO-) XENOPORT INC.

XX PI Zerangue N, Dias T, Dower WJ;

XX DR WPI; 2003-148722/14.

PT Screening for agents, conjugates or their moieties for transport by PEPT2
PT transporter, by contacting cell expressing transporter with the agent,
PT and detecting their passage pass into and/or through the transporter.

PS Example; Page 23; 43pp; English.

XX CC The present invention describes a method (M1) of screening for agents,
XX conjugates or conjugate moieties (I), for transport by PEPT2 (an
XX intestinal peptide transporter) transporter (II), comprising providing a
XX cell expressing (II), contacting the cell with (I), and determining if
XX (I) passes into and/or through the cell by the way of (II). Also
XX described: (i) a conjugate (III), comprising an agent linked to a
XX conjugate moiety that is a substrate for (II), where the conjugate shows
XX a Vmax of at least 1 % of Gly-Sar for (II), where the agent has a
XX pharmaceutical activity without the conjugate moiety, and the conjugate
XX has a greater Vmax for PEPT2 than the agent without the conjugate moiety;
XX and (2) manufacturing (M2) a pharmaceutical composition, by linking an
XX agent to a conjugate moiety to form a conjugate, where the conjugate is
XX transported by (II) with a Vmax of at least 1 % of the Vmax of the
XX substrate Gly-Sar, and formulating the conjugate with a carrier as a
XX pharmaceutical composition. (III) is useful for treatment, by orally
XX administering (III) to a patient, where the agent exerts a
XX pharmacological effect in the patient who is free of a disease of brain,
XX kidney, lung or spleen. The present sequence represents a PCR primer for
XX human PEPT1, which is used in an example from the present invention

SQ Sequence 26 BP; 5 A; 9 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 2.1%; Score 21.2; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 1.2e+03;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 867 GGGATTACAGGCGTGGAGCCACCGC 892

DB 26 GGGATTACAGGCGTGGAGCCACCGC 1


```
FT      /*tag= a
FT      /standard_name="single nucleotide polymorphism"
XX
XX
XX      WO200118250-A2.
XX
XX      15-MAR-2001.
XX
XX      07-SEP-2000; 2000WO-US024503.
XX
XX      10-SEP-1999; 99US-0153357P.
XX      26-JUL-2000; 2000US-0220947P.
XX      16-AUG-2000; 2000US-0225724P.
XX
XX      (MHED ) WHITEHEAD INST BIOMEDICAL RES.
XX      (MILL-) MILLENNIUM PHARM INC.
XX
XX      Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
XX      WPI; 2001-226749/23.
XX
XX      Nucleic acids comprising single nucleotide polymorphisms, useful in
XX      applications such as forensics, paternity testing, medicine, genetic
XX      analysis and phenotype correlations to diseases such as diabetes and
XX      atherosclerosis.
XX
XX      Example; Page 83; 242pp; English.
XX
XX      The present invention provides a method of diagnosing a vascular disease
XX      in an individual, involving determining the sequence at various
XX      polymorphic sites within the human chromosome 1 and thrombospondin 4
XX      genes. The sequences at a number of polymorphic sites are also provided
XX      in the specification. In particular, the method can be used in the
XX      diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX      disease, stroke, peripheral vascular diseases, venous thrombembolism and
XX      pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX      useful in forensics, paternity testing, genetic analysis and phenotype
XX      correlations to diseases. The present sequence is an example of one of
XX      the human gene SNPs shown in the specification
XX
XX      Sequence 21 BP; 5 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX      Query Match      2.1%; Score 21; DB 1; Length 21;
XX      Best Local Similarity 100.0%; Pred. No. 1e+03;
XX      Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      383 CCTCCCAAGTGTGGGATTA 403
XX      |||||||||||||||||||
XX      DB      1 CCTCCCAAGTGTGGGATTA 21
XX
XX      RESULT 398
XX      AAH24567/C
XX      ID      AAH24567 standard; DNA; 21 BP.
XX
XX      AAH24567;
XX
XX      07-AUG-2001 (first entry)
XX
XX      Human Alu sequence-specific primer Alu-Sense.
XX
XX      Human; Alu; metastatic potential determination; cancer;
XX      chorionallantoic membrane; CAM; avian embryo; intravasation;
XX      cell migration; drug screening; PCR primer; ss.
XX
XX      Homo sapiens.
XX
XX      US6228345-B1.
XX
XX      08-MAY-2001.
XX
XX      04-AUG-1999; 99US-00366840.
XX
XX      04-AUG-1999; 99US-00366840.
XX
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XX
XX      (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
XX      Osowski L;
XX
XX      WPI; 2001-342659/36.
XX
XX      Determining the metastatic potential of cancer cells and measuring
XX      invasion, comprises introducing cancer cells into the upper
XX      PT chorionallantoic membrane (CAM) and detecting cancer cell migration from
XX      the upper CAM to the lower CAM.
XX
XX      Example; Col 11; 24pp; English.
XX
XX      The invention relates to a method for determining the metastatic
XX      potential of cancer cells derived from a subject with cancer. The method
XX      comprises introducing a cancer cell sample into the upper chorionallantoic
XX      membrane (CAM) of an avian embryo into which an artificially generated
XX      air pocket has been created, incubating the embryo for intravasation to
XX      occur, and detecting migration of the cancer cells from the upper CAM to
XX      the lower CAM. The present sequence was used to selectively amplify human
XX      specific Alu repeat sequences, which will be present in the cancer cell
XX      DNA but not in the DNA of the CAM. This procedure enables detection of
XX      the migration of inoculated cancer cells into the lower CAM. The method
XX      is useful for measuring the metastatic potential of cancer cells, for
XX      measuring the ability of the cancer cells to invade blood vessels, and as
XX      a drug screening assay for the identification of agents having anti-
XX      metastatic activity and thereby modulating the metastatic potential of
XX      cancer cells. The method may also be used to screen for agents capable of
XX      inhibiting cancer cell intravasation, and to detect phenotypic changes
XX      effected by genetic manipulation of cancer cells that result in changes
XX      in metastatic potential
XX
XX      Sequence 21 BP; 5 A; 8 C; 3 G; 5 T; 0 U; 0 Other;
XX
XX      Query Match      2.1%; Score 21; DB 1; Length 21;
XX      Best Local Similarity 100.0%; Pred. No. 1e+03;
XX      Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      390 AAGTCTGGGATTAAGGCGT 410
XX      |||||||||||||||||||
XX      DB      21 AAGTCTGGGATTAAGGCGT 1
XX
XX      ABS98163
XX      ID      ABS98163 standard; DNA; 21 BP.
XX
XX      ABS98163;
XX
XX      23-DEC-2002 (first entry)
XX
XX      Human multidrug resistance gene polymorphic sequence #65.
XX
XX      Human; ds; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1;
XX      cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTP;
XX      adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR112;
XX      aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
XX      cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
XX      epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
XX      glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
XX      HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
XX      NADPH quinone oxidoreductase 2; NQO2; sulfoxidoreductase thermolabile; STM;
XX      UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
XX      UGT2B7; UDP-glucuronosyl transferase; UGT2B15; uridine kinase receptor; URA;
XX      multidrug resistance 1; lactoferrin; orphan nuclear receptor;
XX      acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
XX      altered drug metabolism; cardiovascular function; colorectal tumour;
XX      central nervous system; pulmonary; immunological; SNP;
XX      single nucleotide polymorphism.
XX
XX      Homo sapiens.
XX
XX      OS
```

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XX WO200257410-A2.
PN
XX
XX 25-JUL-2002.
PD
XX
XX 28-NOV-2001; 2001WO-US044838.
PF
XX
XX 28-NOV-2000; 2000US-00724389.
PR
XX
XX (DNAS-) DNA SCI LAB INC.
PA
XX
XX Guida M, Hall J;
PI
XX
XX WPI; 2002-698522/75.
DR
XX
XX
XX Isolated nucleic acid molecules having polymorphisms in known human genes
PT e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT for locating, identifying and characterizing the genes responsible for
PT disorder-related traits.
XX
XX Example 22; Page 144; 714pp; English.
PS
XX
XX This invention relates to the sequence of an isolated nucleic acid
CC molecule comprising at least one base variation from that of a known
CC human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),
CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
CC inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating
CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC transferase (HNMT), (kallikrein 2) KLK2, nicotinamide-N-methyl
CC sulfoltransferase thermolabile (STM), UDP-glucuronosyl transferase 284
CC (UGT2B4), UDP-glucuronosyl transferase 287 (UGT2B7), UDP-glucuronosyl
CC transferase (UGT2B5), uronkinase receptor (UPR), multidrug resistance 1
CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC The polymorphisms in the human genes cited in the invention are useful as
CC genetic linkage markers for locating and characterizing the genes that
CC are responsible for specific traits within the genome and eventually
CC identifying the genes responsible for a variety of disorder-related
CC traits as a result of their e.g., overexpression, constitutive
CC expression, mutation or underexpression, which may be used in diagnosing
CC and/or treating the disorders. The nucleic acid molecules comprising the
CC polymorphic sequences contained in CYP450A1, CYP450A2, CYP4502E1,
CC AHRNT, EPHX2, GST12, NNMT, NOO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B5, AHR,
CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,
CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC used to screen for altered cardiovascular function, in COX2 for altered
CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC nervous system function, in FLAP and HNMT for altered pulmonary,
CC immunological or haematological function, in KLK2 for altered serine
CC protease activity in the prostate, in LTF for altered immunological or
CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC peripheral nervous system function. The present sequence represents a
CC polymorphic DNA sequence of the invention
XX
XX Sequence 21 BP; 5 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 2.1%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 1e+03;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 868 GGATTACAGCGCTGAGCCACC 888
DB 1 GGATTACAGCGCTGAGCCACC 21
```

```
ID ADF38789 standard; DNA; 21 BP.
XX
XX ADF38789;
AC
XX
XX 12-FEB-2004 (first entry)
DT
XX
XX Human TNF-alpha induced apoptosis-related DNA - SEQ ID 17.
DE
XX
XX tumour necrosis factor; TNF-alpha; apoptosis; antiapoptotic;
XX antisense gene therapy; human; ds.
XX
XX Homo sapiens.
OS
XX
XX JP2003289866-A.
EN
XX
XX 14-OCT-2003.
PD
XX
XX 01-APR-2002; 2002JP-00098130.
PF
XX
XX 01-APR-2002; 2002JP-00098130.
PR
XX
XX (GENO-) GENO FUNCTION KK.
PA (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIUTTSU SO.
PA (TAHT/) TAHIRA K.
PA (KAWA/) KAWASAKI H.
XX
XX WPI; 2004-038428/04.
DR
XX
XX Novel polynucleotide encoding protein involved in tumor necrosis factor
PT induced apoptosis, useful as probe to acquire perfect length cDNA of gene
PT related to TNF-alpha induced apoptosis.
XX
XX Claim 1; SEQ ID NO 17; 18pp; Japanese.
PS
XX
XX The invention relates to a novel polynucleotide which encodes a protein
CC involved in tumour necrosis factor (TNF)-alpha induced apoptosis. The
CC polynucleotide of the invention demonstrates antiapoptotic activity and
CC may be useful during gene therapy as an antisense polynucleotide for
CC suppressing the expression of the protein involved in TNF-alpha induced
CC apoptosis and for elucidating the mechanism of TNF-alpha induced
CC apoptosis. The current sequence is that of the human TNF-alpha induced
CC apoptosis-related DNA of the invention.
XX
XX Sequence 21 BP; 9 A; 7 C; 0 G; 5 T; 0 U; 0 Other;
SQ
XX
XX Query Match 2.1%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 1e+03;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 776 ATTTTAGTAGAGATGGGGTT 796
DB 21 ATTTTAGTAGAGATGGGGTT 1
XX
XX RESULT 401
XX ADO55495 standard; DNA; 21 BP.
ID
XX
XX ADO55495;
AC
XX
XX 26-AUG-2004 (first entry)
DT
XX
XX HIV gene expression analysis primer SB704 following siRNA inhibition.
DE
XX
XX sg; primer; anti-HIV; virucide; gene therapy; small interfering RNA;
XX siRNA; HIV; genome; diagnosis.
XX
XX Human immunodeficiency virus 1.
OS
XX
XX WO2004047764-A2.
EN
XX
XX 10-JUN-2004.
PD
XX
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PF 24-NOV-2003; 2003WO-US037860.
XX
XX 22-NOV-2002; 2002US-0428631P.
PR 04-FEB-2003; 2003US-0444893P.
XX
XX (UTMA-) UNIV MASSACHUSETTS.
XX
XX Stevenson M, Jacque J;
XX
XX WPI; 2004-441081/41.
XX
XX New small interfering RNA (siRNA) comprising a sequence complementary to
XX a portion of the HIV genome to mediate RNA interference (RNAi), useful
XX for diagnosing, preventing and/or treating HIV infections.
XX
XX Disclosure; SEQ ID NO 18; 59pp; English.
XX
XX The invention relates to a small interfering RNA (siRNA) comprising a
XX sequence complementary to a portion of the HIV genome to mediate RNA
XX interference (RNAi). The methods and compositions of the present
XX invention are useful for the diagnosis, prevention and/or treatment of
XX HIV infections. This sequence corresponds to a PCR primer to carry out
XX real time PCR to determine gene expression after expression interference
XX by the siRNAs of the invention.
XX
XX Sequence 21 BP; 4 A; 3 C; 9 G; 5 T; 0 U; 0 Other;
SQ
XX
XX Query Match 2.1%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 1e+03;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 863 TGCTGGATTACAGCGCTGAG 883
DB 1 TGCTGGATTACAGCGCTGAG 21
XX
XX RESULT 402
XX ADH13395/C
XX ID ADH13395 standard; DNA; 23 BP.
XX
XX ADH13395;
XX
XX 11-MAR-2004 (first entry)
XX
XX Human malignant neoplasia-related PCR primer SeqID244.
XX
XX malignant neoplasia; cytostatic; breast cancer; ovarian cancer;
XX gastric cancer; colon cancer; oesophageal cancer; mesenchymal cancer;
XX bladder cancer; non-small cell lung cancer; human; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX EPI365034-A2.
XX
XX 26-NOV-2003.
XX
XX 09-MAY-2003; 2003EP-00010447.
XX
XX 21-MAY-2002; 2002EP-00010291.
XX
XX 13-FEB-2003; 2003EP-00003112.
XX
XX (FARB ) BAYER AG.
XX
XX Wirtz R, Munnes M, Kallabis H;
XX
XX WPI; 2004-073279/08.
XX
XX Predicting, diagnosing or prognosing malignant neoplasia by detecting at
XX least two markers, where the markers are genes from one or more
XX chromosomal regions altered in malignant neoplasia,.
XX
XX Disclosure; SEQ ID NO 244; 267pp; English.
XX
```

```
CC This invention relates to a novel method for the prediction, diagnosis,
CC or prognosis of malignant neoplasia by the detection of at least two
CC markers. The invention may also be useful for the development of
CC cytostatic compounds through the regulation of the expression of a gene
CC or activity of a protein associated with malignant neoplasia. The method
CC is useful for prediction, diagnosis or prognosis of malignant neoplasia
CC such as breast cancer, ovarian cancer, gastric cancer, colon cancer,
CC oesophageal cancer, mesenchymal cancer, bladder cancer or non-small cell
CC lung cancer. The polynucleotides and polypeptides defined in the
CC specification, antisense polynucleotides targeting the polynucleotides,
CC antibodies targeting either one of the polynucleotides or polypeptides,
CC and compounds identified by the screening methods are useful for
CC preventing or treating malignant neoplasia. The disease treated is
CC preferably breast cancer. The present sequence is that of a PCR primer
CC which was used in the exemplification of the invention.
XX
XX Sequence 23 BP; 6 A; 3 C; 9 G; 4 T; 0 U; 1 Other;
SQ
XX
XX Query Match 2.1%; Score 21; DB 1; Length 23;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 667 ATCTTGCTCTCTGCAACCTC 687
DB 23 ATCTTGCTCTCTGCAACCTC 3
XX
XX RESULT 403
XX AAV19046/C
XX ID AAV19046 standard; DNA; 24 BP.
XX
XX AAV19046;
XX
XX 28-JUL-1998 (first entry)
XX
XX Alu PCR primer 3.
XX
XX PCR; primer; amplification; Alu repeat sequence; vector;
XX circular yeast artificial chromosome; YAC; ss.
XX
XX Saccharomyces sp.
XX
XX WO9801573-A1.
XX
XX 15-JAN-1998.
XX
XX 09-JUL-1996; 96WO-US011478.
XX
XX 09-JUL-1996; 96WO-US011478.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Resnick MA, Lationov VL, Kouprina NY, Perkins EL;
XX
XX WPI; 1998-110234/10.
XX
XX Preparation of yeast artificial chromosomes - by in vivo recombination
XX using vector comprising yeast centromere, marker, yeast telomere and
XX nucleic acid for recombination.
XX
XX Example 2; Page 61; 117pp; English.
XX
XX This is the nucleotide sequence for the PCR primer used in the
XX amplification of the 3' fragment of the Alu repeat sequence, which is
XX used as a probe in the method of the invention. It involves the creation
XX and use of circular yeast artificial chromosome (YAC) to selectively
XX clone specific nucleic acids from a background of mixed nucleic acids by
XX introducing the vector(s) into E. coli cells. They can be used to rapidly
XX isolate human DNA where only a part of the sequence of DNA is known.
XX Using the methods large fragments of DNA can be easily cloned and
XX analysed
XX
```



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XX AC AAF24627;
XX XX
XX PD 20-APR-2001 (first entry)
XX DT
XX XX
XX DE Primer for a polymorphism at base 1962 of HMG-CoA reductase gene.
XX XX
XX XX 3-hydroxy-3-methylglutaryl-coenzyme A reductase gene; dyslipidemia;
XX KM HMG-CoA reductase gene; genetic marker; cardiovascular disease;
XX KM myocardial infarction; stroke; PCR primer; ss.
XX XX
XX OS Homo sapiens.
XX PN WO20079003-A1.
XX PD 28-DEC-2000.
XX XX
XX PF 19-JUN-2000; 2000WO-GB002396.
XX PR 22-JUN-1999; 99GB-00014440.
XX PA (ASTR ) ASTRAZENECA UK LTD.
XX PI March RE, Thornton SM;
XX DR WPI; 2001-102732/11.
XX DR
XX PT Novel polymorphisms in human 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-
XX PT CoA) gene useful for diagnosis and treatment of HMG-CoA reductase-
XX PT mediated diseases such as dyslipidemia and other cardiovascular diseases.
XX PS Example 1; Page 31; 45pp; English.
XX XX
XX CC PCR primers AAF24627-28 were used to detect a polymorphism in the human 3
XX CC -hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase gene. The
XX CC polymorphism is present in the promoter region, exon 15, introns 2, 5, 15
XX CC or 18. HMG-CoA reductase polymorphisms are useful as genetic markers in
XX CC linkage studies. Detection of the presence of the polymorphisms is useful
XX CC for assessing the pharmacogenetics of therapeutic compounds in the
XX CC treatment of HMG-CoA reductase mediated diseases. The polymorphisms are
XX CC useful for diagnosis of HMG-CoA reductase mediated diseases such as
XX CC dyslipidemia and other cardiovascular diseases such as myocardial
XX CC infarction and stroke. HMG-CoA reductase antagonist drugs are used to
XX CC treat dyslipidemia and other cardiovascular diseases such as myocardial
XX CC infarction and stroke
XX CC
XX SQ Sequence 24 BP; 5 A; 8 C; 8 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 2.1%; Score 20.8; DB 1; Length 24;
XX Best Local Similarity 91.7%; Pred. No. 1.2e+03;
XX Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 931 CTCACCTGCTTACCCAGGCTGAG 954
XX DB 24 CTCACCTGCTGAGCCAGGCTGAG 1
XX
XX RESULT 407
XX AAF24635/C
XX ID AAF24635 standard; DNA; 24 BP.
XX AC AAF24635;
XX XX
XX DT 20-APR-2001 (first entry)
XX XX
XX DE Primer for polymorphism at base 37 of human HMG-CoA reductase gene.
XX XX
XX XX 3-hydroxy-3-methylglutaryl-coenzyme A reductase gene; dyslipidemia;
XX KM HMG-CoA reductase gene; genetic marker; cardiovascular disease;
XX KM myocardial infarction; stroke; PCR primer; ss.
XX XX
XX OS Homo sapiens.
XX XX

```

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PN WO20079003-A1.
XX XX
XX PD 28-DEC-2000.
XX XX
XX PF 19-JUN-2000; 2000WO-GB002396.
XX PR 22-JUN-1999; 99GB-00014440.
XX PA (ASTR ) ASTRAZENECA UK LTD.
XX PI March RE, Thornton SM;
XX DR WPI; 2001-102732/11.
XX DR
XX PT Novel polymorphisms in human 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-
XX PT CoA) gene useful for diagnosis and treatment of HMG-CoA reductase-
XX PT mediated diseases such as dyslipidemia and other cardiovascular diseases.
XX PS Example 1; Page 32; 45pp; English.
XX XX
XX CC PCR primers AAF24635-36 were used to detect a polymorphism in the human 3
XX CC -hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase gene. The
XX CC polymorphism is present in the promoter region, exon 15, introns 2, 5, 15
XX CC or 18. HMG-CoA reductase polymorphisms are useful as genetic markers in
XX CC linkage studies. Detection of the presence of the polymorphisms is useful
XX CC for assessing the pharmacogenetics of therapeutic compounds in the
XX CC treatment of HMG-CoA reductase mediated diseases. The polymorphisms are
XX CC useful for diagnosis of HMG-CoA reductase mediated diseases such as
XX CC dyslipidemia and other cardiovascular diseases such as myocardial
XX CC infarction and stroke. HMG-CoA reductase antagonist drugs are used to
XX CC treat dyslipidemia and other cardiovascular diseases such as myocardial
XX CC infarction and stroke
XX CC
XX SQ Sequence 24 BP; 5 A; 8 C; 8 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 2.1%; Score 20.8; DB 1; Length 24;
XX Best Local Similarity 91.7%; Pred. No. 1.2e+03;
XX Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 931 CTCACCTGCTTACCCAGGCTGAG 954
XX DB 24 CTCACCTGCTGAGCCAGGCTGAG 1
XX
XX RESULT 408
XX AAH75870
XX ID AAH75870 standard; DNA; 24 BP.
XX AC AAH75870;
XX XX
XX DT 26-OCT-2001 (first entry)
XX XX
XX DE Human reverse transcriptase 13 coding sequence PCR primer #2.
XX XX
XX XX Human; reverse transcriptase 13; cytosolic; virucide; immunomodulatory;
XX KM antiinflammatory; haemostatic; gene therapy; malignant tumour;
XX KM haemopathy; HIV infection; immunological disease; inflammation;
XX KM developmental disorder; PCR primer; ss.
XX XX
XX OS Homo sapiens.
XX PN WO200164893-A1.
XX PD 07-SEP-2001.
XX PF 26-FEB-2001; 2001WO-CN000280.
XX PR 02-MAR-2000; 2000CN-00111806.
XX PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX PI Mao Y, Xie Y;
XX XX

```


DR WPI; 2001-550183/61.
XX
XX New human reverse transcriptase 13 for diagnosing and treating
PT developmental disorders; malignant tumor; hemopathy; human
PT immunodeficiency virus infection; immunological diseases and
PT inflammations.
XX
XX Example 3; Page 12; 34pp; Chinese.
XX
CC The present invention relates to human reverse transcriptase 13 and its
CC coding sequence (see AA175868 and AA66428). The reverse transcriptase
CC and its coding sequence are useful in the diagnosis and treatment of
CC malignant tumour, haemopathy, HIV infection, immunological diseases,
CC various inflammations and developmental disorders. The present sequence
CC is a PCR primer, which was used in an example from the present invention
XX
SQ Sequence 24 BP; 4 A; 9 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.1%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 926 GGAACTCACTCTGTACCCAGGC 949
DB 1 GGAGTCTCACTGTCCACCCAGGC 24

RESULT 409
AA12447
ID AA12447 standard; DNA; 24 BP.
XX
AC AA12447;
XX
DT 18-DEC-2001 (first entry)
XX
DE Ribosome s19e protein 11, RT-PCR primer #2.
XX
KM Human; ribosome s19e protein 11; cytosolic; virucidal; immunomodulatory;
KM antiinflammatory; haemostatic; malignant tumour; haemopathy; ss;
KM human immunodeficiency virus; HIV; immunological disease; inflammation;
KM PCR primer.
XX
OS Homo sapiens.
XX
PN WO200164866-A1.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-CN000219.
XX
PR 02-MAR-2000; 2000CN-00111831.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2001-582156/65.
XX
XX Ribosome s19e protein 11 and encoded polynucleotide for diagnosis and
PT treatment of malignant tumors, hemopathy, HIV infection, immunological
PT diseases and inflammations.
XX
PS Example 2; Page 12; 34pp; Chinese.
XX
CC The invention relates to an isolated polypeptide of ribosome s19e protein
CC 11 and its corresponding coding sequence. The polypeptide and encoded
CC polynucleotide are applicable in diagnosis and treatment of malignant
CC tumours, haemopathy, human immunodeficiency virus (HIV) infection,
CC immunological diseases and various inflammations. The present sequence
CC represents the reverse transcriptase (RT) PCR primer #2 used in analysis
CC of ribosome s19e protein 11
XX
SQ Sequence 24 BP; 4 A; 4 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 2.1%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 181 TAGAGATGAGTTTCTCCATGTTG 204
DB 1 TAGACATGGGGTTTCTCCATGTTG 24

RESULT 410
AA16532
ID AA16532 standard; DNA; 24 BP.
XX
AC AA16532;
XX
DT 11-DEC-2001 (first entry)
XX
XX Human pterin-molybdenum oxidoreductase 10 cDNA PCR primer #2.
DE
XX Human; pterin-molybdenum oxidoreductase 10; cancer; hemopathy;
KM immunological disease; HIV infection; inflammation; gene therapy;
KM PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200172788-A1.
XX
PD 04-OCT-2001.
XX
PF 23-MAR-2001; 2001WO-CN000393.
XX
PR 24-MAR-2000; 2000CN-00115110.
XX
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2001-602841/68.
XX
XX New polypeptide for the diagnosis and treatment of malignant neoplasm,
PT hemopathy, HIV infection, immunological diseases and inflammations,
PT comprises the human pterin-molybdenum oxidoreductase 10 protein.
XX
PS Example 2; Page 17; 36pp; Chinese.
XX
CC The present invention provides the protein and coding sequences of human
CC pterin-molybdenum oxidoreductase 10. The sequences can be used in the
CC treatment of cancer, haemopathy, HIV infection, immunological diseases
CC and inflammation. The present sequence is a PCR primer for the coding
CC sequence of the invention
XX
SQ Sequence 24 BP; 5 A; 5 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 2.1%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 638 TGTCAACCAGGCTGGAGTGACGTG 661
DB 1 TGTCAATCAGGCTGGAGTACAGTG 24

RESULT 411
AA171673/C
ID AA171673 standard; DNA; 24 BP.
XX
AC AA171673;
XX
DT 15-JAN-2002 (first entry)
XX
DE Human myosin heavy chain 12-14 coding sequence PCR primer #1.
XX

KW Human; myosin heavy chain 12-14; Prader Willi syndrome; PCR primer;
KW Klinefelter syndrome; inflammation; kinetic illness; gene therapy; ss.
OS Homo sapiens.
FN WO200185752-A1.
XX
PD 15-NOV-2001.
XX
PF 28-APR-2001; 2001WO-CN000670.
XX
PR 29-APR-2000; 2000CN-00115544.
XX
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2001-648982/74.
XX
PT Peptide-human myosin heavy chain 12-14 and encoded polynucleotide, used
PT in diagnosis and treatment of Prader Willi syndrome, and Klinefelters
PT syndrome.
XX
PS Example 2; Page 17; 39pp; Chinese.
XX
CC The present invention provides the protein and coding sequences of human
CC myosin heavy chain 12-14. The sequences can be used in the treatment of
CC Prader Willi syndrome, Klinefelter syndrome, kinetic illnesses and
CC inflammation. The present sequence is a PCR primer for the coding
CC sequence of the invention
XX
SQ Sequence 24 BP; 5 A; 5 C; 11 G; 3 T; 0 U; 0 Other;
XX
Query Match 2.1%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 969 CTCGGCTCACTGCAACCTCTGCCT 992
DB 24 CTCGGCTCACTGCAACCTCTGCCT 1
XX
RESULT 412
AAf69722
ID AAF69722 standard; DNA; 24 BP.
XX
AC AAF69722;
XX
DT 18-APR-2001 (first entry)
XX
DE Human IL4Ralpha gene PCR primer #58.
XX
KW Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;
KW allergic disease; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200104270-A1.
XX
PD 18-JAN-2001.
XX
PF 13-JUL-2000; 2000WO-US019094.
XX
PR 13-JUL-1999; 99US-0143435P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
PI Windemuth AK;
XX
DR WPI; 2001-103078/11.
XX
PT New isolated polynucleotide useful for the identification of therapeutics

PT in allergic diseases is new.
XX
PS Example 1; Page 62; 188pp; English.
XX
CC The present invention relates to polymorphisms of the human interleukin 4
CC receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference
CC sequence). Polynucleotides comprising polymorphic gene variants are
CC useful for therapeutic purposes. For example, where a patient may benefit
CC from expression of a particular IL4Ralpha protein isoform, an expression
CC vector encoding the isoform may be administered to the patient. It may
CC desirable to decrease or block expression of a particular IL4Ralpha
CC isogene, which may be done by turning off by transforming a targeted
CC organ, tissue or cell population with an expression vector that expresses
CC high levels of untranslatable mRNA for the isogene. Specific therapeutics
CC identified by these methods may be useful for allergic diseases. The
CC present sequence is a PCR primer for human IL4R-alpha
XX
SQ Sequence 24 BP; 4 A; 9 C; 4 G; 7 T; 0 U; 0 Other;
XX
Query Match 2.1%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1002 AAGGATTCTCTGCTCAGCCTC 1025
DB 1 AAGGATTCTCTGCTCAGCCTC 24
XX
RESULT 413
AAI68386
ID AAI68386 standard; DNA; 24 BP.
XX
AC AAI68386;
XX
DT 03-JAN-2002 (first entry)
XX
DE Human ATP-dependent hydrolase serine 9 PCR primer SEQ ID NO 4.
XX
KW Human; ATP-dependent hydrolase serine 9; cytosolic; viral; viral;
KW immunomodulatory; anti-inflammatory; haemostatic; malignant tumour; HIV;
KW infection; human immunodeficiency virus; gene therapy;
KW immunological disease; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200175042-A2.
XX
PD 11-OCT-2001.
XX
PF 26-MAR-2001; 2001WO-CN000434.
XX
PR 27-MAR-2000; 2000CN-00115164.
XX
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2001-626418/72.
XX
PT Human ATP-dependent serine hydrolase 9 and encoded polynucleotide, used
PT in diagnosis and treatment of malignant tumors, hemopathy, human
PT immunodeficiency virus infection, immunological diseases and
PT inflammation.
XX
PS Example 2; Page 17; 39pp; Chinese.
XX
CC The invention relates to human ATP-dependent serine hydrolase 9 with
CC cytosolic, viral, immunomodulatory, anti-inflammatory and haemostatic
CC activity. The protein and encoding polynucleotide are used in diagnosis
CC and treatment of malignant tumour, haemopathy, human immunodeficiency
CC virus (HIV) infection, immunological diseases and various inflammations.
CC The polynucleotide is useful in gene therapy. The present sequence is
CC that of a PCR primer, useful to the invention

XX Sequence 24 BP; 5 A; 8 C; 5 G; 6 T; 0 U; 0 Other;
SQ

Query Match 2.1%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 924 ATGGAATCTACTCTGTATCCGAG 947
Db 1 ATGAGCTCTACTCTGTATCCGAG 24

RESULT 414
ABAB2841/c
ID ABA82841 standard; DNA; 24 BP.

XX ABA82841;

XX 07-FEB-2002 (first entry)

XX Human protective DNA sequence CNI-00746 fragment #6.

XX Human; protective sequence; cell death; cancer; autoimmune disease;

KW neurological disorder; stroke; cytostatic; neuroprotective; gene therapy;

KW ds.

OS Homo sapiens.

XX W0200176457-A2.

XX 18-OCT-2001.

XX 09-APR-2001; 2001WO-US011663.

XX 11-APR-2000; 2000US-00547735.

XX (COGE-) COGENT NEUROSCIENCE INC.

XX Thomas MB, Portbury SD, Putnam K, Katz LC, Lo DC, Barney S;

XX WPI; 2002-025874/03.

XX P-PSDB; ABB44743.

XX Claim 2; Fig 11; 283pp; English.

XX The present invention relates to protective sequence proteins (ABB44624-

CC ABB44830) and their coding sequences (ABA82701-ABA82937). The sequences,

CC when introduced into a cell either predisposed to undergo cell death or

CC in the process of undergoing cell death, prevent, delay or rescue the

CC cell from death, hence, these sequences are named "protective sequences".

CC The sequences are useful for treating and/or ameliorating cancer,

CC autoimmune diseases and neurological disorders e.g. stroke. Further

CC examples of diseases which may be treated by the present invention are

CC given in the specification

XX Sequence 24 BP; 7 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

XX Query Match 2.1%; Score 20.8; DB 1; Length 24;

XX Best Local Similarity 91.7%; Pred. No. 1.2e+03;

XX Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 177 TTACTAGAGATGAGATTTCAT 200

Db 24 TTACTAGAGATGAGATTTCAT 1

ID ABL59102 standard; DNA; 24 BP.

XX ABL59102;

XX 27-SEP-2002 (first entry)

XX PCR primer used to amplify an 82 bp Alu probe.

XX Yeast artificial chromosome; YAC; pPD39;

KW transformation-associated recombination; PCR; primer; ss.

XX Synthetic.

XX US6391642-B1.

XX 21-MAY-2002.

XX 14-APR-1998; 98US-00060023.

XX 09-JUL-1996; 96WO-US011478.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Resnick MA, Lariouov VL, Kouprina NY, Perkins EL,

XX WPI; 2002-498777/53.

XX Preparing yeast artificial chromosomes, useful e.g. for cloning specific

XX human nucleic acid, comprises recombination in yeast cells between a

XX nucleic acid and a yeast vector.

XX Example 2; Col 35; 50pp; English.

XX The specification describes a method for making a yeast artificial

XX chromosome (YAC) that includes an origin of replication (ori). The method

XX comprises incorporating into yeast cells: a population of mammalian

XX nucleic acid; and a vector that comprises a yeast centromere, selection

XX marker, yeast telomere and a sequence that recombines with a region of

XX the nucleic acid, so that in vivo recombination to a YAC occurs. This

XX method, designated transformation-associated recombination, eliminates

XX the need for an in vitro ligation step, and makes possible selective

XX cloning of cDNAs for which only the 3'-sequence is known. The method is

XX used for making a YAC. The method is also used for selective cloning of

XX mammalian, specifically human, nucleic acid from a population,

XX particularly radiation hybrids that contain only a small fragment of a

XX human chromosome. PCR primers ABL59102-03 were used to amplify an 82 bp

XX Alu probe from the pPD39 plasmid containing an Alu consensus sequence.

XX The probe was used to identify human YACs, generated using the method of

XX the invention

SQ Sequence 24 BP; 4 A; 6 C; 11 G; 3 T; 0 U; 0 Other;

XX Query Match 2.1%; Score 20.8; DB 1; Length 24;

XX Best Local Similarity 91.7%; Pred. No. 1.2e+03;

XX Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 675 TCACGCAACCTCTGCTCCCGG 698

Db 24 TCACGCAACCTCTGCTCCCGG 1

RESULT 416

ABK14186

ID ABK14186 standard; DNA; 24 BP.

XX ABK14186;

XX 21-MAY-2002 (first entry)

XX Human splicing factor 9.24 cDNA RT-PCR primer #2.

XX Human; splicing factor 9.24; ss; cytostatic; gene therapy; cancer;

KW tumour; foetus deforming; protein metabolic disturbance related disease;

XX

KW RT-PCR; reverse transcription-PCR; primer.
XX Homo sapiens.
OS WO200212302-A1.
XX
XX 14-FEB-2002.
XX
XX 18-JUN-2001; 2001WO-CN000982.
XX
XX 19-JUN-2000; 2000CN-00116576.
XX
XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-172132/22.
XX
XX Human splicing factor 9.24 polypeptide and encoding polynucleotide, used
PT in diagnosis and treatment of tumors and protein metabolic disturbance
PT related disease.
XX
XX Example 2; Page 12; 38pp; Chinese.
XX
XX The invention relates to the human splicing factor 9.24 polypeptide and
CC the DNA sequence encoding it. The DNA and protein sequences are used in
CC diagnosis and treatment of tumors, foetus deforming and protein
CC metabolic disturbance related diseases. This sequence represents a
CC reverse transcription-PCR (RT-PCR) primer used in isolation of cDNA
CC encoding the human splicing factor 9.24 polypeptide of the invention
XX
XX Sequence 24 BP; 5 A; 5 C; 7 G; 7 T; 0 U; 0 Other;
SQ
XX
XX Query Match 2.1%; Score 20.8; DB 1; Length 24;
XX Best Local Similarity 91.7%; Pred. No. 1.2e+03;
XX Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 633 AACTCTGTACCCAGCTGAGTGTG 656
DB 1 AACTTGTACCTAGCTGAGTGTG 24
XX
XX RESULT 417
XX ABK12860
XX ID ABK12860 standard; DNA; 24 BP.
XX
XX AC ABK12860;
XX
XX 18-JUN-2002 (first entry)
XX
XX Human topoisomerase I 9.79 protein, RT-PCR primer1.
DE
XX Human; topoisomerase I 9.79; teratogenesis; tumour; primer; ss; RT-PCR;
KW reverse transcriptase PCR.
XX
XX Homo sapiens.
OS
XX CN1328155-A.
XX
XX 26-DEC-2001.
XX
XX 14-JUN-2000; 2000CN-00116475.
XX
XX 14-JUN-2000; 2000CN-00116475.
XX
XX 14-JUN-2000; 2000CN-00116475.
XX
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-281738/33.
XX
XX Human topoisomerase I 9.79 polypeptide and the polynucleotide encoding
PT it, for treating teratogenesis and tumors.

XX
XX Example 2; Page 18 (Disclosure); 32pp; Chinese.
XX
XX The present invention relates to a new human topoisomerase I 9.79
CC polypeptide, the polynucleotide encoding it and a DNA recombination
CC process used to produce the polypeptide. The invention also discloses the
CC agonist resisting the polypeptide. The polypeptide and its antagonist are
CC useful for treating teratogenesis and tumors. The present nucleic acid
CC sequence represents a reverse transcriptase (RT)-PCR primer that was used
CC in the methods of the invention to isolate the coding sequence of the
CC human topoisomerase I 9.79 protein of the invention
XX
XX Sequence 24 BP; 3 A; 8 C; 9 G; 4 T; 0 U; 0 Other;
SQ
XX
XX Query Match 2.1%; Score 20.8; DB 1; Length 24;
XX Best Local Similarity 91.7%; Pred. No. 1.2e+03;
XX Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 540 GCCTGAGCTTCCCAAGTGTGG 563
DB 1 GCCTGAGCTTCCCAAGTGTGG 24
XX
XX RESULT 418
XX ABZ25248/C
XX ID ABZ25248 standard; DNA; 24 BP.
XX
XX AC ABZ25248;
XX
XX 24-APR-2003 (first entry)
XX
XX Human peroxidase 9.90 PCR primer #2.
DE
XX Human; peroxidase 9.90; enzyme; cancer; HIV infection; cytostatic;
KW anti-HIV; PCR; primer; ss.
XX
XX Homo sapiens.
OS
XX CN1360029-A.
XX
XX 24-JUL-2002.
XX
XX 20-DEC-2000; 2000CN-00135148.
XX
XX 20-DEC-2000; 2000CN-00135148.
XX
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-733654/80.
XX
XX Polypeptide-human peroxidase protein 9.90 and polynucleotide for coding
PT it.
XX
XX Example 2; Page 16 (Disclosure); 31pp; Chinese.
XX
XX The present invention relates to human peroxidase 9.90 (see ABP59112).
CC The peroxidase is useful for treating diseases such as cancer and HIV
CC infection. The present sequence is a PCR primer, which was used in an
CC example from the invention
XX
XX Sequence 24 BP; 7 A; 5 C; 8 G; 4 T; 0 U; 0 Other;
SQ
XX
XX Query Match 2.1%; Score 20.8; DB 1; Length 24;
XX Best Local Similarity 91.7%; Pred. No. 1.2e+03;
XX Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1099 CACCATATTTGTGAGCTGTCTC 1122
DB 24 CACCATATTTGTGAGCTGTCTC 1

RESULT 419

ABA02134

ID ABA02134 standard; DNA; 24 BP.

XX ABA02134;

AC ABA02134;

XX 08-FEB-2002 (first entry)

DT 08-FEB-2002 (first entry)

XX Human zinc ion transport protein 26 RT-PCR primer, SEQ ID NO:3.

DE Human zinc ion transport protein 26; rat Znt-1 homologue;

XX Human; zinc ion transport protein 26; rat Znt-1 homologue;

XX zinc transporter; recombinant production; malignant tumour; cancer;

XX blood disease; HIV infection; human immunodeficiency virus;

XX immune disorder; inflammatory condition; embryonic development disorder;

XX developmental disorder; growth disorder; cytostatic; anti-HIV;

XX anti-inflammatory; immunomodulator; reverse transcription-PCR;

XX RT-PCR primer; 88.

XX Homo sapiens.

XX MO200181539-A2.

XX 01-NOV-2001.

XX 23-APR-2001; 2001WO-CN000610.

XX 27-APR-2000; 2000CN-00115461.

XX (BIOW-) B10MINDOW GENE DEV INC SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2002-026163/03.

XX Human zinc ion transport protein 26 and encoded polynucleotide, used in

XX diagnosis and treatment of malignant tumors, hemopathy, human

XX immunodeficiency virus infection, immunological diseases and

XX inflammation.

XX Example 3; Page 11; 31pp; Chinese.

XX The invention relates to human zinc ion transport protein 26 (AA052621),

XX nucleic acids encoding it (ABA02133), and a method for the recombinant

XX production of zinc ion transport protein 26. The protein has a molecular

XX weight of 26 kD, and has 35% identity and 54% homology over a 210 amino

XX acid stretch with the rat zinc transporter Znt-1 (GenBank accession

XX number U71713). The present invention additionally discloses an

XX antagonist of zinc ion transport protein 26 for therapeutic use, and an

XX antibody which specifically binds to zinc ion transport protein 26. Zinc

XX ion transport protein 26, and nucleotides which encode it may be used for

XX treating a variety of diseases, such as malignant tumours, blood

XX diseases, HIV (human immunodeficiency virus) infection, immune disorders,

XX inflammatory conditions, embryonic development disorders, and development

XX and growth disorders. The protein may also be used to screen for

XX modulators of its activity or for peptide fingerprinting identification.

XX The polynucleotide can be used as a primer for nucleic acid amplification

XX reactions or as a probe for hybridisation reactions, or in producing gene

XX chips or microarrays. Sequences ABA02134-ABA02135 represent reverse

XX transcription-PCR (RT-PCR) primers used in an exemplification of the

XX invention to isolate human zinc ion transport protein 26 cDNA

XX

XX Sequence 24 BP; 4 A; 6 C; 6 G; 8 T; 0 U; 0 Other;

SQ

Query Match 2.1%; Score 20.8; DB 1; Length 24;

Best Local Similarity 91.7%; Pred. No. 1.2e+03;

Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1096 TTTCACCATATTTGTGACGCTGCT 1119

DB 1 TTTCACCATATTTGCGCAGGCTGCT 24

RESULT 420

AA016055/c

ID AA016055 standard; DNA; 24 BP.

XX AA016055;

AC AA016055;

XX 29-JUN-2002 (first entry)

DT 29-JUN-2002 (first entry)

XX Human microtubulin 11 RT-PCR primer #2.

DE Human microtubulin 11; cancer; haemopathy; PCR primer;

XX Human; ss; microtubulin 11; cancer; haemopathy; PCR primer;

XX human immunodeficiency virus infection; immunological disease;

XX inflammation; embryonic development disorder; nervous system disorder;

XX growth disorder; cytostatic; virucidal; immunomodulatory; anti-inflammatory;

XX haemostatic.

XX Homo sapiens.

XX MO200174128-A2.

XX 11-OCT-2001.

XX 26-FEB-2001; 2001WO-CN000226.

XX 02-MAR-2000; 2000CN-00111820.

XX (BIOW-) B10MINDOW GENE DEV INC SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2002-025780/03.

XX Human microtubulin 11 and encoded polynucleotide, applicable in diagnosis

XX and treatment of e.g. developmental disorders, cancer, hemopathy, HIV

XX infection, immunological diseases and various inflammations.

XX Example 2; Page 11; 31pp; Chinese.

XX The invention relates to an isolated polypeptide of human microtubulin

XX CC 11, the nucleic acid encoding it, a fragment, analogue or derivative of

XX CC it, a transformed cell expressing the protein from an expression vector,

XX CC antibodies against the protein and antagonists of the protein. The

XX CC polypeptide and encoded polynucleotide are applicable in diagnosis and

XX CC treatment of cancer, haemopathy, human immunodeficiency virus infection,

XX CC immunological diseases, various inflammations, embryonic development

XX CC disorders, disorders of the nervous system and growth disorders. The

XX CC present sequence is an RT-PCR (reverse transcriptase PCR) primer used to

XX CC isolate a nucleic acid encoding human microtubulin 11

XX

XX Sequence 24 BP; 5 A; 9 C; 5 G; 5 T; 0 U; 0 Other;

SQ

Query Match 2.1%; Score 20.8; DB 1; Length 24;

Best Local Similarity 91.7%; Pred. No. 1.2e+03;

Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 645 CAGCTGAGTGTGACGCTGCTAT 668

DB 24 CAGACTGAGTGTGACGCTGCTAT 1

RESULT 421

AB057470/c

ID AB057470 standard; DNA; 24 BP.

XX AB057470;

AC AB057470;

XX 27-FEB-2003 (first entry)

DT 27-FEB-2003 (first entry)

XX Human plasminogen activator inhibitor 2-9.9 cDNA RT-PCR primer #1.

XX Human; plasminogen activator inhibitor 2-9.9; primer; ss; thrombosis;

XX KM haemorrhagic disease; cerebral infarction; myocardial infarction; tumour;

XX KM haemopathy; human immunodeficiency virus; HIV; inflammation; cancer;

XX RT-PCR; reverse transcriptase.

```
XX Homo sapiens.
OS
XX CN1352101-A.
PN
XX 05-JUN-2002.
PD
XX 06-NOV-2000; 2000CN-00127230.
PF
XX 06-NOV-2000; 2000CN-00127230.
PR
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
PA
XX Mao Y, Xie Y;
PI
XX WPI; 2002-675822/73.
DR
XX New human plasminogen activator inhibitor 2-9.9 polypeptide for treating
PT e.g. hemorrhagic disease, thrombosis, cerebral infarction, various
PT tumors, hemopathy, human immunodeficiency virus infection, and
PT inflammations.
XX
PS Example 2; Page 17 (Disclosure); 33pp; Chinese.
XX
CC The invention relates to the human plasminogen activator inhibitor 2-9.9
CC polypeptide, the polynucleotide encoding the polypeptide and a DNA
CC recombination process used to produce the polypeptide. The polypeptide
CC and polynucleotide are used for treating various diseases, such as
CC haemorrhagic disease, thrombosis, cerebral infarction, myocardial
CC infarction, various tumors, haemopathy, human immunodeficiency virus
CC (HIV) infection and inflammations. This sequence represents a reverse
CC transcriptase PCR (RT-PCR) primer used for isolation of cDNA encoding
CC human plasminogen activator inhibitor 2-9.9
XX
SQ Sequence 24 BP; 2 A; 9 C; 9 G; 4 T; 0 U; 0 Other;
XX
Query Match 2.1%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 873 ACAGCGGTGAGCCACGAGCCCGG 896
Db 24 ACAGCGGTGAGCCACGAGCCCGTGG 1
XX
RESULT 422
AB221093
ID AB221093 standard; DNA; 24 BP.
XX
XX AB221093;
AC
XX 25-MAR-2003 (first entry)
DT
XX Starch precursor protein binding protein 13.42 PCR primer #2.
DE
XX Starch precursor protein binding protein 13.42; Alzheimer's disease;
KM tumour; development disorder; inflammation; immunological disease;
KM haemopathy; HIV infection; cytostatic; anti-HIV; PCR; primer; ss.
XX
XX Unidentified.
OS
XX CN1352014-A.
PN
XX 05-JUN-2002.
PD
XX 06-NOV-2000; 2000CN-00127264.
PF
XX 06-NOV-2000; 2000CN-00127264.
PR
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
PA
XX Mao Y, Xie Y;
PI
XX
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DR WPI; 2002-699445/76.
XX
XX New starch precursor protein binding protein 13.42 polypeptide for
PT treating e.g. Alzheimer's disease, malignant tumors, inflammations,
PT immunological diseases, hemopathy and human immunodeficiency virus
PT infection.
XX
XX Example 2; Page 17 (Disclosure); 34pp; Chinese.
XX
CC The present invention relates to starch precursor protein binding protein
CC 13.42 (see AB98887). The protein can be used for treating various
CC diseases, such as Alzheimer's disease, malignant tumors, development
CC disorders, inflammations, immunological diseases, haemopathy and HIV
CC infection. The present sequence is a PCR primer, which was used in an
CC example from the invention
XX
SQ Sequence 24 BP; 3 A; 6 C; 7 G; 8 T; 0 U; 0 Other;
XX
Query Match 2.1%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 932 TCACCTGTTACCCAGCGCTGAGT 955
Db 1 TCACCTGTTGTCCAGCGCTGAGT 24
XX
RESULT 423
ACA90126
ID ACA90126 standard; DNA; 24 BP.
XX
XX ACA90126;
AC
XX 10-JUN-2003 (first entry)
DT
XX Human kinesin gene(s) antisense oligonucleotide #9.
DE
XX
XX Human; ss; antisense; kinesin; CENP-B; Eg5; MCAK; colon cancer; stroke;
KM T cell cancer; B cell lymphoma; pancreatic cancer; breast cancer;
KM leukaemia; bladder cancer; stomach cancer; brain cancer; bone cancer;
KM oesophageal cancer; liver cancer; adrenal carcinoma; lung cancer;
KM testicular cancer; heart cancer; ovarian cancer; uterine cancer;
KM head/neck cancer; cervical cancer; gall bladder cancer; spleen cancer;
KM parathyroid cancer; penile cancer; prostate cancer; skin cancer;
KM thymus cancer; thyroid cancer; muscle cancer; ganglial cancer; melanoma;
KM myeloma sarcoma; teratocarcinoma; digestive cancer; ischaemia; epilepsy;
KM autoimmune disorder; viral infection; neurological disorder; meningitis;
KM liver disease; pancreatic disease; myocardial infarction; cerebral palsy;
KM Alzheimer's disease; Huntington's disease; Parkinson's disease;
KM amyotrophic lateral sclerosis; motor neuron disorder; multiple sclerosis;
KM retinitis pigmentosa; demyelinating disease; prion disease;
KM Creutzfeldt-Jakob disease; muscular dystrophy; schizophrenia; amnesia;
KM diabetic neuropathy; Tourette's disease; cystic fibrosis; infection;
KM diabetic mellitus; Grave's disease; gastrointestinal disorder;
KM ulcerative colitis; AIDS; allergic reactions; inflammatory bowel disease;
KM myasthenia gravis; rheumatoid arthritis; osteoarthritis; scleroderma;
KM Sjgren's syndrome; systemic lupus erythematosus; toxic shock syndrome.
XX
XX Homo sapiens.
OS
XX WO2003030832-A2.
PN
XX 17-APR-2003.
PD
XX 11-OCT-2002; 2002WO-US032596.
PF
XX 12-OCT-2001; 2001US-0328444P.
PR
XX (CHIR ) CHIRON CORP.
PA
XX Reinhard C, Walter A;
PI
XX WPI; 2003-381676/36.
XX
```

XX Treatment of disease e.g. cancer, rheumatoid arthritis, Alzheimer's
 PT disease and Parkinson's disease involves administration of antisense
 PT oligonucleotide.
 PS Claim 5, Page 6, 57pp: English.
 XX
 CC The invention relates to treatment of disease involving administering an
 CC antisense oligonucleotide. The oligonucleotide inhibits the expression of
 CC human kinesin gene. The human kinesin gene is CENP-B, human Eg5 or MCAK.
 CC Also included are the antisense oligonucleotides appearing as ACA90118-
 CC ACA90135, combination therapy involving administration of at least one
 CC chemotherapeutic or radionuclide and further involves administration of
 CC at least one anti-sense oligonucleotide (the oligonucleotide is
 CC administered either separately or in combination) and a pharmaceutical
 CC composition comprising the AS oligonucleotide and a carrier. The human
 CC kinesin gene-targeting antisense oligonucleotides are useful for
 CC treatment of disease having aberrant cell proliferation such as cancer
 CC e.g. colon cancer, T and B cell lymphoma, pancreatic cancer, breast
 CC cancer, leukaemia, bladder cancer, stomach cancer, brain cancer,
 CC oesophageal cancer, liver cancer, adrenocarcinoma, lung cancer,
 CC testicular cancer, heart cancer, ovarian cancer, uterine cancer, head and
 CC neck cancer, bone cancer, cervical cancer, prostate cancer, skin cancer, spleen
 CC parathyroid cancer, penile cancer, prostate cancer, skin cancer, spleen
 CC cancer, thymus cancer, thyroid cancer, muscle cancer, ganglial cancer,
 CC melanoma, myeloma sarcoma and teratocarcinomas, digestive cancer,
 CC lymphoma, autoimmune disorder, viral infection, neurological disorder,
 CC condition associated with ischaemia and liver or pancreatic disease,
 CC myocardial infarction, stroke, epilepsy, ischaemic cerebrovascular
 CC disease, cerebral neoplasm, Alzheimer's disease, Pick's disease,
 CC Huntington's disease, dementia, Parkinson's disease, extrapyramidal
 CC disorder, amyotrophic lateral sclerosis, motor neuron disorders,
 CC progressive neural muscular atrophy, retinitis pigmentosa, hereditary
 CC ataxia, suppurative intracranial thrombophlebitis, multiple sclerosis,
 CC demyelinating disease, bacterial and viral meningitis, brain abscess,
 CC subdural empyema, myelitis, paralytic, viral central nervous system
 CC disease, prion disease including kuru, Creutzfeldt-Jakob disease,
 CC Gerstmann-Strausler-Scheinker syndrome, insomnia, neurofibromatosis,
 CC mental retardation, cerebral palsy, autonomic nervous system disorder,
 CC muscular dystrophy, peripheral nervous system disorders, dermatomyositis,
 CC anxiety, schizophrenia, amnesia, diabetic neuropathy, tardive dyskinesia,
 CC Tourette's disease, cystic fibrosis, hypercholesterolaemia, diabetic
 CC mellitus, hyper- and hypoglycaemia, Grave's disease, neuralgia, Cushing's
 CC disease, Addison's disease, gastrointestinal disorders e.g. ulcerative
 CC colitis, duodenal ulcer, AIDS, allergic reactions, autoimmune haemolytic
 CC anaemia, proliferative glomerulonephritis, inflammatory bowel disease,
 CC myasthenia gravis, rheumatoid arthritis, osteoarthritis, scleroderma,
 CC Sjogren's syndrome, systemic lupus erythematosus, toxic shock syndrome,
 CC viral, bacterial, fungal, helminthic and protozoal infections. The
 CC present sequence is a human kinesin gene-targeting antisense
 CC oligonucleotide of the invention
 XX
 SQ Sequence 24 BP; 6 A; 11 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 2.1%; Score 20.8; DB 1; Length 24;
 Best Local Similarity 91.7%; Pred. No. 1.2e+03;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 359 GCTCAGAGCTCCACCTCCTCAG 362
 DB 1 GCTCAGAGCTCCACCTCCTCAG 24
 RESULT 424
 ACA90127 standard; DNA, 24 BP.
 ID ACA90127
 AC ACA90127;
 XX
 XX 10-JUL-2003 (first entry)
 DT
 XX
 DE Human kinesin gene(s) antisense oligonucleotide #10.

KW Human; ss; antisense; kinesin; CENP-B; Eg5; MCAK; colon cancer; stroke;
 KW T cell cancer; B cell lymphoma; pancreatic cancer; breast cancer;
 KW leukaemia; bladder cancer; stomach cancer; brain cancer; bone cancer;
 KW oesophageal cancer; liver cancer; adrenalcarcinoma; lung cancer;
 KW testicular cancer; heart cancer; ovarian cancer; uterine cancer;
 KW head/neck cancer; cervical cancer; gall bladder cancer; spleen cancer;
 KW parathyroid cancer; penile cancer; prostate cancer; skin cancer;
 KW thymus cancer; thyroid cancer; muscle cancer; ganglial cancer; melanoma;
 KW myeloma sarcoma; teratocarcinoma; digestive cancer; ischaemia; epilepsy;
 KW autoimmune disorder; viral infection; neurological disorder; meningitis;
 KW liver disease; pancreatic disease; myocardial infarction; cerebral palsy;
 KW Alzheimer's disease; Huntington's disease; Parkinson's disease;
 KW amyotrophic lateral sclerosis; motor neuron disorder; multiple sclerosis;
 KW retinitis pigmentosa; demyelinating disease; prion disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; schizophrenia; amnesia;
 KW diabetic neuropathy; Tourette's disease; cystic fibrosis; infection;
 KW diabetic mellitus; Grave's disease; gastrointestinal disorder;
 KW ulcerative colitis; AIDS; allergic reactions; inflammatory bowel disease;
 KW myasthenia gravis; rheumatoid arthritis; osteoarthritis; scleroderma;
 KW Sjogren's syndrome; systemic lupus erythematosus; toxic shock syndrome.
 XX
 OS Homo sapiens.
 XX
 PN MO2003030832-A2.
 XX
 PD 17-APR-2003.
 XX
 PF 11-OCT-2002; 2002WC-US032596.
 XX
 PR 12-OCT-2001; 2001US-032844P.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Reinhard C, Walter A;
 XX
 DR WPI; 2003-381676/36.
 XX
 PT Treatment of disease e.g. cancer, rheumatoid arthritis, Alzheimer's
 PT disease and Parkinson's disease involves administration of antisense
 PT oligonucleotide.
 PS Claim 5, Page 6, 57pp: English.
 XX
 CC The invention relates to treatment of disease involving administering an
 CC antisense oligonucleotide. The oligonucleotide inhibits the expression of
 CC human kinesin gene. The human kinesin gene is CENP-B, human Eg5 or MCAK.
 CC Also included are the antisense oligonucleotides appearing as ACA90118-
 CC ACA90135, combination therapy involving administration of at least one
 CC chemotherapeutic or radionuclide and further involves administration of
 CC at least one anti-sense oligonucleotide (the oligonucleotide is
 CC administered either separately or in combination) and a pharmaceutical
 CC composition comprising the AS oligonucleotide and a carrier. The human
 CC kinesin gene-targeting antisense oligonucleotides are useful for
 CC treatment of disease having aberrant cell proliferation such as cancer
 CC e.g. colon cancer, T and B cell lymphoma, pancreatic cancer, breast
 CC cancer, leukaemia, bladder cancer, stomach cancer, brain cancer,
 CC oesophageal cancer, liver cancer, adrenocarcinoma, lung cancer,
 CC testicular cancer, heart cancer, ovarian cancer, uterine cancer, head and
 CC neck cancer, bone cancer, cervical cancer, prostate cancer, skin cancer,
 CC parathyroid cancer, penile cancer, prostate cancer, skin cancer, spleen
 CC cancer, thymus cancer, thyroid cancer, muscle cancer, ganglial cancer,
 CC melanoma, myeloma sarcoma and teratocarcinomas, digestive cancer,
 CC lymphoma, autoimmune disorder, viral infection, neurological disease,
 CC condition associated with ischaemia and liver or pancreatic disease,
 CC myocardial infarction, stroke, epilepsy, ischaemic cerebrovascular
 CC disease, cerebral neoplasm, Alzheimer's disease, Pick's disease,
 CC Huntington's disease, dementia, Parkinson's disease, extrapyramidal
 CC disorder, amyotrophic lateral sclerosis, motor neuron disorders,
 CC progressive neural muscular atrophy, retinitis pigmentosa, hereditary
 CC ataxia, suppurative intracranial thrombophlebitis, multiple sclerosis,
 CC demyelinating disease, bacterial and viral meningitis, brain abscess,
 CC subdural empyema, myelitis, paralytic, viral central nervous system
 CC disease, prion disease including kuru, Creutzfeldt-Jakob disease,

CC Gerstmann-Strausler-Scheinker syndrome, insomnia, neurofibromatosis,
CC mental retardation, cerebellar palsy, autonomic nervous system disorder,
CC muscular atrophy, peripheral nervous system disorders, dermatomyositis,
CC anxiety, schizophrenia, amnesia, diabetic neuropathy, tardive dyskinesia,
CC Tourette's disease, cystic fibrosis, hypercholesterolemia, diabetic
CC mellitus, hyper- and hypoglycaemia, Grave's disease, neuralgia, Cushing's
CC disease, Addison's disease, gastrointestinal disorders e.g. ulcerative
CC colitis, duodenal ulcer, AIDS, allergic reactions, autoimmune haemolytic
CC anaemia, proliferative glomerulonephritis, inflammatory bowel disease,
CC myaesthesia gravis, rheumatoid arthritis, osteoarthritis, scleroderma,
CC Sjogren's syndrome, systemic lupus erythematosus, toxic shock syndrome,
CC viral, bacterial, fungal, helminthic and protozoal infections. The
CC present sequence is a human kinesin gene-targeting antisense
CC oligonucleotide of the invention
CC
SQ Sequence 24 BP; 6 A; 7 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 2.1%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 867 GGGATTACAGCGGTGAGCCACC 890
1 GGGATTACAGCGCATGAGCCACCGC 24

RESULT 425
ACCS7313
ID ACCS7313 standard; DNA; 24 BP.

AC ACCS7313;
DT 27-JUN-2003 (first entry)

DE Zinc finger protein 11.55 related PCR primer #SEQ ID 3.
XX
XX Zinc finger protein, 11.55; human immunodeficiency virus; HIV; cancer;
KM PCR; primer; ss.
XX
XX Unidentified.
OS
XX
XX CN1363594-A.
PD 14-AUG-2002.
XX
XX 05-JAN-2001; 2001CN-00105078.
PF
XX
XX 05-JAN-2001; 2001CN-00105078.
PR
XX
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
PA
XX
XX Mao Y, Xie Y;
PI
XX
XX WPI; 2003-000323/01.
DR
XX
XX Polypeptide-zinc finger protein 11.55 and polynucleotide encoding it.
PT
XX
XX Example 2; Page 17 (disclosure); 33pp; Chinese.
PS
XX
XX The invention relates to a novel zinc finger protein designated 11.55.
CC Also disclosed are the polynucleotide encoding it, and a process for
CC preparing the polypeptide using DNA recombination techniques. The
CC application of the polypeptide is in treating diseases such as cancer and
CC human immunodeficiency virus (HIV) infection. The current sequence
CC represents a zinc finger protein 11.55 related PCR primer
XX
XX
SQ Sequence 24 BP; 5 A; 6 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 2.1%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 198 CATGTTGTCAGGCTGCTCGAA 221

Db 1 CATGTTGTCAGGCTGCTCGAA 24
1 CATGTTGTCAGGCTGCTCGAA 24

RESULT 426
ADG83872
ID ADG83872 standard; DNA; 24 BP.
XX
XX ADG83872;
AC
XX
XX 11-MAR-2004 (first entry)
DT
XX
XX Human SLCA14 forward PCR primer SEQ ID NO:13.
DE
XX
XX differentiation; ulcerative colitis; Crohn's disease;
KM target genetic marker gene; human; PCR primer; ss.
XX
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WQ2004001073-A1.
XX
XX 31-DEC-2003.
PD
XX
XX 25-JUN-2003; 2003WO-SE001105.
PF
XX
XX 25-JUN-2002; 2002SE-00001954.
PR 25-JUN-2002; 2002SE-00001956.
PR 15-JUL-2002; 2002US-0395629P.
PR 15-JUL-2002; 2002US-0395631P.
PR 18-JUL-2002; 2002SE-00002251.
PR 18-JUL-2002; 2002SE-00002252.
PR 18-JUL-2002; 2002US-00002256.
PR 04-SEP-2002; 2002US-0407682P.
PR 04-SEP-2002; 2002US-0407713P.
PR 10-SEP-2002; 2002US-0409213P.
XX
XX (INDE-) INDEX PHARM AB.
XX
XX Dieckmann A, Loeffberg R, Von Stein O, Von Stein P;
PI
XX
XX WPI; 2004-071745/07.
DR
XX
XX Differentiating between ulcerative colitis and Crohn's disease based on
PT the analysis of gene expression profiles in biopsy samples comprises
PT determining the expression levels of at least two of a number of marker
PT genes.
XX
XX Claim 7; SEQ ID NO 13; 30pp; English.
PS
XX
XX The present invention describes a method for differentiating between
CC ulcerative colitis and Crohn's disease based on the analysis of gene
CC expression profiles in biopsy samples obtained from inflamed and
CC optionally non-inflamed areas in the intestines of the patient. The
CC method comprises determining the expression levels of at least two of a
CC number of marker genes chosen from any of the 7 sequences SEQ ID NO:1 to
CC 7 (see ADG83886, ADG83887, ADG83888, ADG83889, ADG83890, ADG83891 and
CC ADG83892). The method can be used for differentiating between ulcerative
CC colitis and Crohn's disease based on the analysis of gene expression
CC profiles in biopsy samples obtained from inflamed and optionally non-
CC inflamed areas in the intestines of the patient. The present sequence
CC represents a PCR primer for a target genetic marker gene sequence which
CC is used in the exemplification of the present invention.
XX
XX
SQ Sequence 24 BP; 5 A; 4 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 2.1%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 862 GTGCTGGATTACAGCGGTGAGCC 885
1 GTGCTGAGATTACAGGTGTAGCC 24


```
RESULT 427
AAAX24391
ID AAAX24391 standard; DNA; 25 BP.
XX
XX AAAX24391;
XX
XX 07-JUN-1999 (first entry)
XX
XX Chemokine receptor CCR8 PCR primer CY6.
XX
XX Chemokine receptor; CCR8; human; G protein coupled receptor; HIV;
XX infection; therapy; immunomodulator; chemotaxis; apoptosis; PCR; primer;
XX ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO9906561-A2.
XX
XX 11-FEB-1999.
XX
XX 29-JUL-1998; 98WO-US015730.
XX
XX 29-JUL-1997; 97US-0054094P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Tiffany HL, Murphy PM, Berger EA, Alkhatib G, Bazan H, Bonner TI;
XX Lauteus L;
XX
XX WPI; 1999-153791/13.
XX
XX New isolated chemokine receptor CCR8 - used to develop agents for
XX modulating immune responses or agents for the prevention or treatment of
XX HIV infection.
XX
XX Example 1; Page 53; 81bp; English.
XX
XX This oligonucleotide, termed primer CY6, was used with primer CY6B (see
XX AAAX24390) in a PCR amplification of novel human CC chemokine receptor
XX CCR8 cDNA (see also AAAX24385). Radiation hybrid mapping was performed bp
XX PCR using these primers. The CCR8 gene was mapped to human chromosome
XX 3p22-p23. CCR8 (see AAW97868) is a G protein coupled receptor that plays
XX an essential role in the membrane fusion step of HIV infection.
XX Establishment of stable, non-human cell lines and transgenic mammals
XX having cells that coexpress CD4 and CCR8 provides valuable tools for
XX research on HIV infection. Antibodies which bind to CCR8, CCR8 variants,
XX and CCR8-binding agents capable of blocking membrane fusion between HIV
XX and target cells represent potential anti-HIV therapeutics
XX
XX Sequence 25 BP; 8 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
XX
XX
XX Query Match 2.1%; Score 20.8; DB 1; Length 25;
XX Best Local Similarity 91.7%; Pred. No. 1.2e+03;
XX Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 864 GCTGGGATTTCAGGCGTGAGCCAC 887
XX |||||
XX 1 GCTAGGATTACAGGCATGAGCCAC 24
XX
XX
XX RESULT 428
XX ADB04739
XX ID ADB04739 standard; DNA; 25 BP.
XX
XX ADB04739;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MDZ7 scanning oligonucleotide SEQ ID 5725.
XX
XX
```

```
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EP1281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5725; 103bp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
XX encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
XX MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
XX 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 25 BP; 8 A; 1 C; 4 G; 12 T; 0 U; 0 Other;
XX
XX
XX Query Match 2.1%; Score 20.8; DB 1; Length 25;
XX Best Local Similarity 91.7%; Pred. No. 1.2e+03;
XX Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 766 ATTTTGTGATTTTGTAGTAGAGA 789
XX |||||
XX 1 AATATTTTGTATTTTGTAGTAGAGA 24
XX
XX
XX RESULT 429
XX ADB04618
XX ID ADB04618 standard; DNA; 25 BP.
XX
XX ADB04618;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MDZ7 scanning oligonucleotide SEQ ID 5604.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EP1281758-A2.
XX
XX
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XX 05-FEB-2003.
PD
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5604; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 25 BP; 5 A; 6 C; 10 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 2.1%; Score 20.8; DB 1; Length 25;
XX Best Local Similarity 91.7%; Pred. No. 1.2e+03;
XX Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 647 GGCTGAGTGCAGTGGCGCATCT 670
XX |||||
XX 1 GGCTGAGTGCAGTGGCGCATCT 24
XX
XX RESULT 430
XX ADB04738
XX ID ADB04738 standard; DNA; 25 BP.
XX
XX ADB04738;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MD27 scanning oligonucleotide SEQ ID 5724.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EPI281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
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XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5724; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 25 BP; 8 A; 0 C; 4 G; 13 T; 0 U; 0 Other;
XX
XX Query Match 2.1%; Score 20.8; DB 1; Length 25;
XX Best Local Similarity 91.7%; Pred. No. 1.2e+03;
XX Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 766 ATTTTGTATTCTTACTAGAGA 789
XX |||||
XX 2 AATTATTGTATTCTTACTAGAGA 25
XX
XX RESULT 431
XX ADB04740
XX ID ADB04740 standard; DNA; 25 BP.
XX
XX ADB04740;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MD27 scanning oligonucleotide SEQ ID 5726.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EPI281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX
```

PT MD24, MD27 or MD212, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5726; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded in therapy,
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 25 BP; 7 A; 1 C; 5 G; 12 T; 0 U; 0 Other;
QY
Query Match 2.1%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
DB 768 TTTTGTATTTTGTAGAGATG 791
2 TATTTGTATTTTGTAGAGACG 25
RESULT 432
ADB04617
ID ADB04617 standard; DNA; 25 BP.
AC ADB04617;
XX
XX 20-NOV-2003 (first entry)
DT
DE Human MD27 scanning oligonucleotide SEQ ID 5603.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX EP1281758-A2.
PN
XX
XX 05-FEB-2003.
PD
XX
XX 30-JUL-2002; 2002EP-00016874.
PF
XX
XX 02-AUG-2001; 2001US-00922181.
PR
XX
XX (AEOM-) AEOMICA INC.
PA
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XX Shannon M, Gu Y, Nguyen C;
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XX WPI; 2003-423107/40.
DR
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX PT associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
PT
XX
XX Example 8; SEQ ID NO 5603; 103pp; English.
PS
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome

CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 25 BP; 4 A; 6 C; 11 G; 4 T; 0 U; 0 Other;
QY
Query Match 2.1%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
DB 647 GGCTGAGTGCAGTGGCGCATCT 670
2 GGCTGAGTGCAGTGGCGCATCT 25
RESULT 433
ADB04578
ID ADB04578 standard; DNA; 25 BP.
AC ADB04578;
XX
XX 20-NOV-2003 (first entry)
DT
DE Human MD27 scanning oligonucleotide SEQ ID 5564.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX EP1281758-A2.
PN
XX
XX 05-FEB-2003.
PD
XX
XX 30-JUL-2002; 2002EP-00016874.
PF
XX
XX 02-AUG-2001; 2001US-00922181.
PR
XX
XX (AEOM-) AEOMICA INC.
PA
XX
XX Shannon M, Gu Y, Nguyen C;
PI
XX
XX WPI; 2003-423107/40.
DR
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX PT associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
PT
XX
XX Example 8; SEQ ID NO 5564; 103pp; English.
PS
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are

CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 25 BP; 4 A; 2 C; 4 G; 15 T; 0 U; 0 Other;

Query Match 2.1%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 607 TTTTAAATTTTGGACAGAGCTC 630
DB 2 TTTTATTTTGGACAGAGCTC 25

RESULT 434

ID ADB04746 standard; DNA; 25 BP.

AC ADB04746;

DT 20-NOV-2003 (first entry)

DE Human MD27 scanning oligonucleotide SEQ ID 5732.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;

XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;

XX developmental disorder; ss.

XX Homo sapiens.

OS

PN EPI281758-A2.

PD 05-FEB-2003.

PF 30-JUL-2002; 2002EP-00016874.

PR 02-AUG-2001; 2001US-00922181.

PA (AEOM-) AEOMICA INC.

PI Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

DR

XX

PT New zinc finger-containing proteins and nucleic acids, useful in

PT manufacturing a medicament for treating or preventing a disorder

PT associated with decreased or increased expression or activity of MD23,

PT MD24, MD27 or MD212, e.g. cancer.

XX

PS Example 8; SEQ ID NO 5732; 103bp; English.

XX

CC The present invention relates to novel human zinc finger-containing

CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is

CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,

CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome

CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,

CC or in manufacturing a medicament for treating or preventing a disorder

CC associated with decreased or increased expression or activity of MD23,

CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic

CC acids caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic

CC acids can also be used as probes to detect and characterize gross

CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are

CC useful in constructing microarrays for measuring gene expression. The

CC proteins are useful as therapeutic agents for gene therapy or as

CC vaccines. The present sequence was used to illustrate the invention.

XX

SEQ Sequence 25 BP; 5 A; 1 C; 9 G; 10 T; 0 U; 0 Other;

Query Match 2.1%; Score 20.8; DB 1; Length 25;

Best Local Similarity 91.7%; Pred. No. 1.2e+03;

Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 773 TGTATTTAGTAGAGTGGGTT 796
DB 1 TGTATTTAGTAGAGCGGGCT 24

RESULT 435
ID ADB04580 standard; DNA; 25 BP.

AC ADB04580;

DT 20-NOV-2003 (first entry)

DE Human MD27 scanning oligonucleotide SEQ ID 5566.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;

XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;

XX developmental disorder; ss.

XX Homo sapiens.

OS

PN EPI281758-A2.

PD 05-FEB-2003.

PF 30-JUL-2002; 2002EP-00016874.

PR 02-AUG-2001; 2001US-00922181.

PA (AEOM-) AEOMICA INC.

PI Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

DR

XX

PT New zinc finger-containing proteins and nucleic acids, useful in

PT manufacturing a medicament for treating or preventing a disorder

PT associated with decreased or increased expression or activity of MD23,

PT MD24, MD27 or MD212, e.g. cancer.

XX

PS Example 8; SEQ ID NO 5566; 103bp; English.

XX

CC The present invention relates to novel human zinc finger-containing

CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is

CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,

CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome

CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,

CC or in manufacturing a medicament for treating or preventing a disorder

CC associated with decreased or increased expression or activity of MD23,

CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic

CC acids caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic

CC acids can also be used as probes to detect and characterize gross

CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are

CC useful in constructing microarrays for measuring gene expression. The

CC proteins are useful as therapeutic agents for gene therapy or as

CC vaccines. The present sequence was used to illustrate the invention.

XX

SEQ Sequence 25 BP; 4 A; 2 C; 5 G; 14 T; 0 U; 0 Other;

Query Match 2.1%; Score 20.8; DB 1; Length 25;

Best Local Similarity 91.7%; Pred. No. 1.2e+03;

Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 608 TTTTAAATTTTGGACAGAGCTC 631
DB 1 TTTTATTTTGGACAGAGCTC 24

RESULT 436

AD011741
ID AD011741 standard; DNA, 25 BP.
XX
AC AD011741;
XX
XX 15-JUL-2004 (first entry)
XX
DE Single multiplex PCR primer #1113.
XX
KW ss; primer: simultaneous amplification;
KW single multiplex polymerase chain reaction; multifactorial disease;
KW genetic alteration; pharmacogenetic reaction; genotyping; polymorphism;
KW gene expression profiling.
XX
OS Synthetic.
XX
PN WO2004033649-A2.
XX
PD 22-APR-2004.
XX
PF 07-OCT-2003; 2003WO-US031874.
XX
PR 07-OCT-2002; 2002US-0417009P.
XX
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI Li H, Li J,
XX
DR WPI, 2004-340914/31.
XX
PT Designing primers for simultaneous amplification of target DNA fragments
PT in a single multiplex polymerase chain reaction, for high throughput
PT multiplex DNA sequence amplification, comprises aligning two primers.
XX
XX Disclosure; Page 38; 120pp; English.
XX
XX The invention relates to a method of designing primers for simultaneous
XX amplification of target DNA fragments in a single multiplex polymerase
XX chain reaction by aligning a first primer and a second primer. The method
XX comprises: (a) aligning a first primer and a second primer; and (b)
XX selecting the first primer where the first primer at its 3' end does not
XX contain four or more bases that are perfectly matching to the 3' end
XX of the first primer or a second primer, the first primer at its
XX 3' end does not contain seven or more bases that are perfectly matching
XX except one mismatch to the 3' end sequence of the first primer or the
XX second primer, the first primer at its 3' end does not contain six or
XX more bases that are perfectly matching to a sequence anywhere of the
XX first primer or the second primer, and the first primer at its 3' end
XX does not contain eleven or more bases that are perfectly matching except
XX one mismatch to a sequence anywhere of the first primer or the second
XX primer. The method is useful for designing primers for simultaneous
XX amplification of target DNA fragments in a single multiplex polymerase
XX chain reaction. It is also useful in the identification of multiple genes
XX related to multifactorial diseases, the genome-scale detection of genetic
XX alterations, the studies in pharmacogenetic reactions, the genotyping
XX genetic polymorphisms in a large population, the gene expression
XX profiling in various samples and high throughput genotyping technologies.
XX This sequence corresponds to an example of a primer of the invention.
XX
SQ Sequence 25 BP; 5 A; 4 C; 8 G; 8 T; 0 U; 0 Other;
XX
XX
Query Match 2.1%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 181 TAGAGATGAGCTTCTCCATGTTG 204
DB 1 TAGAGATGAGCTTCCACCGTGTG 24
XX
XX
RESULT 437
AAZ25152
ID AAZ25152 standard; DNA, 22 BP.

XX
AC AAZ25152;
XX
XX 13-DEC-1999 (first entry)
XX
XX Human short interspersed repetitive element PCR primer #10.
XX
DE Human; short interspersed repetitive element; SINE; PCR; primer;
KW Oncorhynchus; restriction primer; short interspersed repeated sequence;
KW eukaryote; restricted polymerase chain reaction fingerprinting;
KW identification; DNA specimen; discrimination; ss.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
PN JP2913035-B1.
XX
XX 28-JUN-1999.
XX
PD 10-JUL-1998; 98JP-00195692.
XX
PF 10-JUL-1998; 98JP-00195692.
XX
PR 10-JUL-1998; 98JP-00195692.
XX
XX (NORQ) NORINSUISANSHO SUIANCHO YOSHOKU KENKYUSHOCHO.
XX
PA WPI, 1999-583348/50.
XX
DR Restriction primer for distinguishing individuals with short interspersed
XX repeated sequence of eukaryotes by restricted polymerase chain reaction
XX fingerprinting.
XX
XX Claim 6; Page 3; 17pp; Japanese.
XX
XX The present invention describes a restriction primer for eukaryotic short
XX interspersed repeated sequences (SINE), which has one or more additional
XX bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
XX the SINE. The annealing temperature of the primer to the DNA sequence is
XX kept higher than the fusion temperature of the primer during polymerase
XX chain reaction (PCR). The PCR fragments obtained are subjected to
XX electrophoresis to obtain a fingerprint. By comparing the polymorphs from
XX the electrophoresis band pattern, eukaryotic individuals are
XX distinguished. The primer is used for amplifying a eukaryotic
XX deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
XX polymerase chain reaction (PCR) fingerprinting. In particular it may be
XX used for individual identification of humans for medical and legal
XX applications and ecological studies. DNA specimens in traces
XX (approximately 10 ng in mass) can be used for individual discrimination
XX of eukaryotes using the primer in a polymerase chain reaction (PCR).
XX AAZ25143 to AAZ25191 represent specifically claimed examples of primers
XX from the present invention
XX
SQ Sequence 22 BP; 6 A; 5 C; 7 G; 4 T; 0 U; 0 Other;
XX
XX
Query Match 2.1%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 868 GGATTACAGCGGTGACCA 889
DB 1 GGATTACAGCGGTGACCACTA 22
XX
XX
RESULT 438
AAZ25149
ID AAZ25149 standard; DNA, 22 BP.
XX
XX AAZ25149;
XX
XX 13-DEC-1999 (first entry)
XX
XX Human short interspersed repetitive element PCR primer #7.
XX
XX Human; short interspersed repetitive element; SINE; PCR; primer;
KW

KW OncoRhynchus; restriction primer; short interspersed repeated sequence;
KW eukaryote; restricted polymerase chain reaction fingerprinting;
KM identification; DNA specimen; discrimination; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX JP2913035-B1.
XX
XX 28-JUN-1999.
XX
XX 10-JUL-1998; 98JP-00195692.
XX
XX 10-JUL-1998; 98JP-00195692.
XX
XX (NORQ) NORINSUISANSHO SUIANCHO YOSHOKU KENKYUSHOCHO.
XX
XX WPI; 1999-583348/50.
XX
XX Restriction primer for distinguishing individuals with short interspersed
PT repeated sequence of eukaryotes by restricted polymerase chain reaction
PT fingerprinting.
XX
XX Claim 6; Page 3; 17pp; Japanese.
XX
XX The present invention describes a restriction primer for eukaryotic short
CC interspersed repeated sequences (SINE), which has one or more additional
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
CC the SINE. The annealing temperature of the primer to the DNA sequence is
CC kept higher than the fusion temperature of the primer during polymerase
CC chain reaction (PCR). The PCR fragments obtained are subjected to
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from
CC the electrophoresis band pattern, eukaryotic individuals are
CC distinguished. The primer is used for amplifying a eukaryotic
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be
CC used individual identification of humans for medical and legal
CC applications and ecological studies. DNA specimens in traces
CC (approximately 10 ng in mass) can be used for individual discrimination
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).
CC AA225143 to AA225191 represent specifically claimed examples of primers
CC from the present invention
XX
XX Sequence 22 BP; 6 A; 5 C; 8 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 2.1%; Score 20.4; DB 1; Length 22;
XX Best Local Similarity 95.5%; Pred. No. 1.1e+03;
XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 868 GGATTACAGGCGGTGAGCCACCA 889
DB 1 GGATTACAGGCGGTGAGCCACCA 22
XX
XX RESULT 439
XX AA225146
XX AA225146 standard; DNA; 22 BP.
XX
XX AA225146;
XX
XX 13-DEC-1999 (first entry)
XX
XX Human short interspersed repetitive element PCR primer #4.
XX
XX Human; short interspersed repetitive element; SINE; PCR; primer;
KW OncoRhynchus; restriction primer; short interspersed repeated sequence;
KW eukaryote; restricted polymerase chain reaction fingerprinting;
XX identification; DNA specimen; discrimination; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX JP2913035-B1.
XX

XX
XX 28-JUN-1999.
XX
XX 10-JUL-1998; 98JP-00195692.
XX
XX 10-JUL-1998; 98JP-00195692.
XX
XX (NORQ) NORINSUISANSHO SUIANCHO YOSHOKU KENKYUSHOCHO.
XX
XX WPI; 1999-583348/50.
XX
XX Restriction primer for distinguishing individuals with short interspersed
PT repeated sequence of eukaryotes by restricted polymerase chain reaction
PT fingerprinting.
XX
XX Claim 6; Page 3; 17pp; Japanese.
XX
XX The present invention describes a restriction primer for eukaryotic short
CC interspersed repeated sequences (SINE), which has one or more additional
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
CC the SINE. The annealing temperature of the primer to the DNA sequence is
CC kept higher than the fusion temperature of the primer during polymerase
CC chain reaction (PCR). The PCR fragments obtained are subjected to
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from
CC the electrophoresis band pattern, eukaryotic individuals are
CC distinguished. The primer is used for amplifying a eukaryotic
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be
CC used individual identification of humans for medical and legal
CC applications and ecological studies. DNA specimens in traces
CC (approximately 10 ng in mass) can be used for individual discrimination
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).
CC AA225143 to AA225191 represent specifically claimed examples of primers
CC from the present invention
XX
XX Sequence 22 BP; 7 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 2.1%; Score 20.4; DB 1; Length 22;
XX Best Local Similarity 95.5%; Pred. No. 1.1e+03;
XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 868 GGATTACAGGCGGTGAGCCACCA 889
DB 1 GGATTACAGGCGGTGAGCCACCA 22
XX
XX RESULT 440
XX AAC69376/C
XX AAC69376 standard; DNA; 22 BP.
XX
XX AAC69376;
XX
XX 29-JAN-2001 (first entry)
XX
XX Human ABC1 BAC contig polymorphic site, SEQ ID NO:275.
XX
XX Human ABC1 cholesterol transporter; chromosome 9q31;
KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
KW Tangier disease; TD; familial HDL deficiency; FHL; polymorphism;
KW cardiovascular disease; coronary artery disease; coronary stenosis;
KW cerebrovascular disease; peripheral vascular disease;
KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
KW prognosis; prophylaxis; drug screening; transgenic animal; ds.
XX
XX Homo sapiens.
OS
XX WO20005318-A2.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-IB000532.
XX

PR 15-MAR-1999; 99US-0124702P.
 PR 08-JUN-1999; 99US-0138048P.
 PR 17-JUN-1999; 99US-0139600P.
 PR 01-SEP-1999; 99US-0151977P.
 XX (UYER-) UNIV BRITISH COLUMBIA.
 PA (XENO-) XENON BIORESEARCH INC.
 XX
 XX Hayden MR, Wilson AR, Pimstone SN,
 PI WPI; 2000-587528/55.
 DR
 XX
 XX New ABC1 polypeptide is useful for treating diseases associated with ABC1
 PT biological activity, e.g. Alzheimer's disease, Huntington's disease and
 PT cancer.
 XX
 XX Example; Fig 11; 229pp; English.
 PS
 XX
 XX The invention relates to the human ABC1 cholesterol transporter protein
 CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
 CC a member of the ATP-binding cassette (ABC transporter) superfamily of
 CC proteins, and plays a crucial role in cholesterol transport, particularly
 CC intracellular cholesterol trafficking in monocytes and fibroblasts, being
 CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is
 CC located on chromosome 9q31, and mutations in this gene are associated
 CC with two genetic HDL (high density lipoprotein) deficiency disorders,
 CC Tangier disease (TD) and familial HDL deficiency (FHD). These diseases
 CC are distinguishable in that TD is an autosomal recessive disorder, while
 CC FHD is inherited as an autosomal dominant trait. Low levels of HDL ('good
 CC cholesterol') in the blood correlate with a high risk of cardiovascular
 CC disease, particularly coronary artery disease, but also cerebrovascular
 CC disease, coronary restenosis, and peripheral vascular disease.
 CC Conversely, a high level of HDL has protective effects against
 CC cardiovascular disease. The invention provides genetic constructs and
 CC transgenic cells and non-human animals comprising human ABC1 nucleic
 CC acids, and methods of gene therapy for the treatment or prevention of
 CC cardiovascular disease comprising the administration of an expression
 CC vector encoding ABC1 or an active fragment thereof. The invention also
 CC encompasses compounds which mimic ABC1 activity, compounds which
 CC stimulate ABC1 expression and methods of screening for such compounds. It
 CC further relates to methods for determining whether a patient has an
 CC increased risk for cardiovascular disease due to polymorphisms in the
 CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or
 CC prevent cardiovascular disease, especially coronary artery disease,
 CC cerebrovascular disease, coronary restenosis or peripheral vascular
 CC disease. They may also be used in the treatment of diseases associated
 CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
 CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
 CC The invention specifically excludes proteins with the exact amino acid
 CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
 CC acid with the exact sequence as GenBank Accession No: AJ012376.1. The
 CC present sequence represents a polymorphic site of the human ABC1 gene
 XX
 XX Sequence 22 BP; 6 A; 2 C; 11 G; 3 T; 0 U; 0 Other;
 SQ
 XX Query Match 2.1%; Score 20.4; DB 1; Length 22;
 XX Best Local Similarity 95.5%; Pred. No. 1.1e+03;
 XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 533 TCCTCTGCTGCTGAGCTGCCAA 554
 DB 22 TTCTCTGCTGCTGAGCTGCCAA 1
 XX
 XX RESULT 441
 XX AAF74132
 XX ID AAF74132 standard; DNA; 22 BP.
 XX
 XX AAF74132;
 XX AC
 XX 30-APR-2001 (first entry)
 XX
 XX Primer #66.
 DE

XX
 XX Solute carrier family 6 neurotransmitter transporter; serotonin 4; SLC6A4;
 KW genotyping; allele specific oligonucleotide; ss.
 KW
 XX Homo sapiens.
 OS
 XX MO200109161-A1.
 EN
 XX
 XX 08-FEB-2001.
 PD
 XX
 XX 31-JUL-2000; 2000WO-US020638.
 PF
 XX
 XX 29-JUL-1999; 99US-0146290P.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 PA
 XX
 XX Denton RR, Duda A, Nandabalan K, Sanchis A, Stephens JC;
 PI WPI; 2001-123317/13.
 DR
 XX
 XX New isolated polynucleotide comprising a polymorphic variant for the
 PT solute carrier family 6 neurotransmitter transporter, serotonin member 4
 PT gene for identifying drugs for treating disorders related to expression
 PT of the protein.
 PS
 XX Example 1; Page 38; 152pp; English.
 PS
 XX The present invention relates to a polymorphic variant of a reference
 CC sequence for the solute carrier family 6 neurotransmitter transporter,
 CC serotonin member 4 (SLC6A4) gene or a fragment of it or a sequence
 CC complementary to the first sequence. The invention is used in producing a
 CC recombinant organism that can be used to express SLC6A4 for protein
 CC structure analysis and binding studies. A composition comprising a
 CC genotyping oligonucleotide is used to detect a polymorphism in the SLC6A4
 CC gene
 CC
 XX
 XX Sequence 22 BP; 6 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
 SQ
 XX Query Match 2.1%; Score 20.4; DB 1; Length 22;
 XX Best Local Similarity 95.5%; Pred. No. 1.1e+03;
 XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 870 ATTACGAGCTGTGAGCCACACG 891
 DB 1 ATTACGAGCTGTGAGCCACACG 22
 XX
 XX RESULT 442
 XX ADL66997 standard; DNA; 22 BP.
 XX ID ADL66997
 XX
 XX ADL66997;
 AC
 XX
 XX 03-JUN-2004 (first entry)
 DT
 XX
 XX Multiplex PCR primer #1.
 DE
 XX DNA polymerase; anti-DNAp antibody; reverse transcriptase;
 KW anti-RT antibody; single strand binding protein; SSB; ss; primer.
 XX
 XX Synthetic.
 OS
 XX
 XX MO2004022770-A2.
 EN
 XX
 XX 18-MAR-2004.
 PD
 XX
 XX 05-SEP-2003; 2003WO-US027705.
 PF
 XX
 XX 05-SEP-2002; 2002US-0408609P.
 PR
 XX 19-NOV-2002; 2002US-0427867P.
 PR
 XX (INVT-) INVITROGEN CORP.
 PA
 XX

PI Park K;
XX
XX WPI; 2004-248479/23.
XX
XX
XX New compositions comprising one or more anti-reverse transcriptase
PT antibodies, anti-DNA polymerases or single strand binding proteins,
XX useful for synthesizing nucleic acids.
XX
XX Example 4; Page 89; 201pp; English.
XX
XX The invention relates to a new composition which comprises at least one
CC anti-DNA polymerases (anti-DNA) antibody and/or at least one anti-
CC reverse transcriptase (anti-RT) antibody, and at least one single strand
CC binding protein (SSB) or at least two different SSBs. The compositions
CC are useful for nucleic acid synthesis reactions or are generated during
CC nucleic acid synthesis reactions. The methods are useful for synthesizing
CC one or more nucleic acid molecules. The compositions and methods are also
CC be used in amplifying nucleic acid molecules, in reverse transcription of
CC nucleic acid molecules and in coupled or uncoupled reverse
CC transcription/amplification. The present sequence is used in the
CC exemplification of the present invention.
XX
XX Sequence 22 BP; 4 A; 3 C; 10 G; 5 T; 0 U; 0 Other;
SQ
Query Match 2.1%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 647 GGCTGAGTGCAGTGGCGCAAT 668
DB 1 GGCTGAGTGCAGTGGCGCAAT 22
RESULT 443
AD030457
ID AD030457 standard; DNA; 22 BP.
XX
XX AD030457;
AC
XX
XX 29-JUL-2004 (first entry)
DT
XX
XX Human novel GPCR PGR4 RT-PCR primer, SEQ ID NO:1560.
DE
XX
XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; cardiovascular disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antianemic;
KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
KW CNS; central nervous system; respiratory; antidiabetic;
KW virucide; hepatotropic; antibacterial; antianemic; antidiabetic;
KW dermatological; anticancer; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotoxic; gene therapy; GPCR modulator; human;
KW PGR4; reverse transcription-PCR; RT-PCR; primer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO2004040000-A2.
PN
XX
XX 13-MAY-2004.
PD
XX
XX 09-SEP-2003; 2003WO-US028226.
PF
XX
XX 09-SEP-2002; 2002US-0409303P.
PR
XX 09-APR-2003; 2003US-0461329P.
XX
XX (PRIM-) PRIMAL INC.
PA
XX Galanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI

PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;
XX
XX WPI; 2004-390329/36.
XX
XX
XX Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
XX pectoris, Parkinson's disease.
XX
XX Disclosure; SEQ ID NO 1560; 542pp; English.
XX
XX The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders (e.g., autoimmune disorders or
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a PCR primer
CC used in the isolation of cDNA encoding the novel human GPCR PGR4. Note:
CC The full sequence data for this patent did not form part of the printed
CC specification; those sequences not shown were obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pcr_sequences.
XX
XX Sequence 22 BP; 3 A; 4 C; 8 G; 7 T; 0 U; 0 Other;
SQ
Query Match 2.1%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 201 GTTGCTCAGGCTGCTCGAAC 222
DB 1 GTTGCTCAGGCTGCTCGAAC 22
RESULT 444
AAF69748
ID AAF69748 standard; DNA; 23 BP.
XX
XX AAF69748;
AC
XX
XX 18-APR-2001 (first entry)
DT
XX
XX Human IL4Ralpha gene PCR primer #84.
DE
XX
XX Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;
KW allergic disease; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200104270-A1.
PN
XX
XX 18-JAN-2001.
PD
XX
XX

PF 13-JUL-2000; 2000WO-US019094.
XX
XX 13-JUL-1999; 99US-0143435P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
PI Windemuth AK;
XX
XX WPI; 2001-103078/11.
DR
XX
XX New isolated polynucleotide useful for the identification of therapeutics
PT in allergic diseases is new.
XX
XX Example 1; Page 64; 188pp; English.
PS
XX The present invention relates to polymorphisms of the human interleukin 4
CC receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference
CC sequence). Polynucleotides comprising polymorphic gene variants are
CC useful for therapeutic purposes. For example, where a patient may benefit
CC from expression of a particular IL4Ralpha protein isoform, an expression
CC vector encoding the isoform may be administered to the patient. It may
CC desirable to decrease or block expression of a particular IL4Ralpha
CC isogene, which may be done by turning off by transforming a targeted
CC organ, tissue or cell population with an expression vector that expresses
CC high levels of untranslatable mRNA for the isogene. Specific therapeutics
CC identified by these methods may be useful for allergic diseases. The
CC present sequence is a PCR primer for human IL4R-alpha
XX
XX Sequence 23 BP; 5 A; 8 C; 3 G; 7 T; 0 U; 0 Other;
SQ
Query Match 2.1%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 578 CCACCTACCTGCTAATTTT 599
DB 1 CCACACACCTGCTAATTTT 22
RESULT 445
AAH49787
ID AAH49787 standard; DNA; 24 BP.
XX
XX AAH49787;
AC
XX 25-SEP-2001 (first entry)
DT
XX
XX Human uncoiling enzyme 9 coding sequence PCR primer #2.
DE
XX
XX Human; uncoiling enzyme 9; cancer; haemopathy; HIV infection;
KM immunological disease; inflammation; gene therapy; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200149860-A1.
PN
XX
XX 12-JUL-2001.
PD
XX
XX 18-DEC-2000; 2000WO-CN000616.
PF
XX
XX 24-DEC-1999; 99CN-00125756.
PR
XX
XX (BIOW-) BIOWINDOW GENE DEV LTD SHANGHAI.
PA
XX
XX Mao Y, Xie Y;
PI
XX
XX WPI; 2001-432884/46.
DR
XX
XX Uncoiling enzyme 9 and encoded polynucleotide, applicable in diagnosis
PT and treatment of malignant tumor, hemopathy, HIV infection, immunological
PT diseases and various inflammation.
XX

PS Example 3; Page 11; 32pp; Chinese.
XX
XX The present invention provides the protein and coding sequences of human
CC uncoiling enzyme 9. The sequences can be used in the treatment of cancer,
CC haemopathy, HIV infection, immunological diseases and inflammation. The
CC present sequence is a PCR primer for the coding sequence of the invention
XX
XX Sequence 24 BP; 5 A; 4 C; 7 G; 8 T; 0 U; 0 Other;
SQ
Query Match 2.1%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 182 AGAGATGAGTTTCTCCATGTT 203
DB 1 AGAGATGAGTTTCTCCATGTT 22
RESULT 446
ABS56869
ID ABS56869 standard; DNA; 24 BP.
XX
XX ABS56869;
AC
XX
XX 30-JAN-2003 (first entry)
DT
XX
XX Human receptor related tyrosine kinase 10.01 cDNA RT-PCR primer #2.
DE
XX
XX Human; receptor related tyrosine kinase 10.01; primer; ss; peptic ulcer;
KM embryonic development deformity; tumour; diabetes; menstrual disorder;
KM cancer; anaemia; epilepsy; RT-PCR; reverse transcriptase.
XX
XX Homo sapiens.
OS
XX
XX CN1345961-A.
PN
XX
XX 24-APR-2002.
PD
XX
XX 29-SEP-2000; 2000CN-00125572.
PF
XX
XX 29-SEP-2000; 2000CN-00125572.
PR
XX
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
PA
XX
XX Mao Y, Xie Y;
PI
XX
XX WPI; 2002-539360/58.
DR
XX
XX New polypeptide-human receptor related tyrosine kinase 10.01 for treating
PT embryonic development deformity, tumor, diabetes, menstrual disorder,
PT peptic ulcer, anemia and epilepsy.
XX
XX Example 2; Page 18 (Disclosure); 34pp; Chinese.
PS
XX
XX The invention relates to the human receptor related tyrosine kinase
CC 10.01, a polynucleotide encoding the polypeptide and a method for
CC producing the polypeptide by DNA recombination technology. The
CC polypeptide is used for curing several diseases such as embryonic
CC development deformity, tumours, diabetes, menstrual disorder, peptic
CC ulcer, anaemia and epilepsy. This sequence represents a reverse
CC transcriptase PCR (RT-PCR) primer used in isolation of cDNA encoding
CC human receptor related tyrosine kinase 10.01
XX
XX Sequence 24 BP; 4 A; 7 C; 6 G; 7 T; 0 U; 0 Other;
SQ
Query Match 2.1%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 925 TGGATCTCACTCTGTACCA 946
DB 3 TGGATCTCACTCTGTACCA 24

```
RESULT 448
AAH40563/C
ID AAH40563 standard; DNA; 25 BP.
XX
XX AAH40563;
AC
XX
XX 14-AUG-2001 (first entry)
DT
XX
XX SNP specific SNPE primer SEQ ID 3359.
DE
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; primer; ss.
XX
XX Homo sapiens.
XX
XX OS
XX
XX PN WO200129262-A2.
XX
XX PD 26-APR-2001.
XX
XX PF 13-OCT-2000; 2000WO-US028436.
XX
XX PR 15-OCT-1999; 99US-0160096P.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX PI Picoult-Newburg L, Pohl M;
XX
XX DR MPI; 2001-290930/30.
XX
XX PT New genotyping oligonucleotide, useful for detecting the presence,
XX PT absence or identity of single polynucleotide polymorphism in a nucleic
XX PT acid sample.
XX
XX PS Claim 1; Page 67; 83pp; English.
XX
XX
XX Sequence AAH37205 - AAH40944 represent PCR primers, single nucleotide
XX primer extension (SNPE) primers, and the sequences of regions flanking
XX sites of single nucleotide polymorphisms SNPs. The present invention
XX includes kits for determining the presence or absence of a SNP, using the
XX oligonucleotides of the invention. The PCR primers are used to amplify a
XX SNP flanking sequence, the SNPE primer is used as a genotyping primer.
XX The oligonucleotides are useful for genotyping a nucleic acid sample by
XX performing a single-nucleotide primer extension reaction. The
XX oligonucleotides are useful for determining the presence, absence or
XX identity of a SNP and for genotyping nucleic acid samples, for e.g. to
XX assess by association analysis the genotype of an individual or group of
XX individuals, having a pathological phenotypic trait suspected of being
XX caused by one or more SNPs. Phenotypic traits include diseases e.g.
XX agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
XX dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
XX osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
XX traits also include symptoms of or susceptibility to multifactorial
XX disease of which a component is or may be genetic such as autoimmune
XX diseases, including, rheumatoid arthritis, multiple sclerosis,
XX inflammation, cancer, nervous system diseases and infection by pathogenic
XX microorganism. The method is also useful in forensic investigations and
XX paternity analysis. The present sequence represents a single nucleotide
XX primer extension (SNPE) primer specific for a human SNP containing DNA
XX sequence
SQ Sequence 25 BP; 7 A; 4 C; 11 G; 3 T; 0 U; 0 Other;
Query Match 2.1%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
DB 22 TCCTGCCTCAGCCTCCCAAGTA 1
RESULT 448
AAH38991/C
ID AAH38991 standard; DNA; 25 BP.
XX
XX AAH38991;
AC
XX
XX 14-AUG-2001 (first entry)
DT
XX
XX SNP specific SNPE primer SEQ ID 1787.
DE
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; primer; ss.
XX
XX Homo sapiens.
XX
XX OS
XX
XX PN WO200129262-A2.
XX
XX PD 26-APR-2001.
XX
XX PF 13-OCT-2000; 2000WO-US028436.
XX
XX PR 15-OCT-1999; 99US-0160096P.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX PI Picoult-Newburg L, Pohl M;
XX
XX DR MPI; 2001-290930/30.
XX
XX PT New genotyping oligonucleotide, useful for detecting the presence,
XX PT absence or identity of single polynucleotide polymorphism in a nucleic
XX PT acid sample.
XX
XX PS Claim 1; Page 59; 83pp; English.
XX
XX
XX Sequence AAH37205 - AAH40944 represent PCR primers, single nucleotide
XX primer extension (SNPE) primers, and the sequences of regions flanking
XX sites of single nucleotide polymorphisms SNPs. The present invention
XX includes kits for determining the presence or absence of a SNP, using the
XX oligonucleotides of the invention. The PCR primers are used to amplify a
XX SNP flanking sequence, the SNPE primer is used as a genotyping primer.
XX The oligonucleotides are useful for genotyping a nucleic acid sample by
XX performing a single-nucleotide primer extension reaction. The
XX oligonucleotides are useful for determining the presence, absence or
XX identity of a SNP and for genotyping nucleic acid samples, for e.g. to
XX assess by association analysis the genotype of an individual or group of
XX individuals, having a pathological phenotypic trait suspected of being
XX caused by one or more SNPs. Phenotypic traits include diseases e.g.
XX agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
XX dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
XX osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
XX traits also include symptoms of or susceptibility to multifactorial
XX disease of which a component is or may be genetic such as autoimmune
XX diseases, including, rheumatoid arthritis, multiple sclerosis,
XX inflammation, cancer, nervous system diseases and infection by pathogenic
XX microorganism. The method is also useful in forensic investigations and
XX paternity analysis. The present sequence represents a single nucleotide
XX primer extension (SNPE) primer specific for a human SNP containing DNA
XX sequence
SQ Sequence 25 BP; 5 A; 5 C; 11 G; 4 T; 0 U; 0 Other;
Query Match 2.0%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

Oy 843 CCTGCTGGGCTCCCAAGTCTG 867
 Db 25 CCGGCTTGACTCCCAAGTCTG 1

RESULT 449

AAH40899
 ID AAH40899 standard; DNA; 25 BP.

AC AAH40899;

DT 14-AUG-2001 (first entry)

DE SNP specific SNPE primer SEQ ID 3695.

XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
 XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
 XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
 XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
 XX inflammation; forensic investigation; paternity analysis; primer; ss.

OS Homo sapiens.

PN WO200129262-A2.

PD 26-APR-2001.

PF 13-OCT-2000; 2000WO-US028436.

PR 15-OCT-1999; 99US-0160096P.

PA (ORCH-) ORCHID BIOSCIENCES INC.

PI Picoult-Newburg L, Pohl M;

DR WPI; 2001-290930/30.

XX New genotyping oligonucleotide, useful for detecting the presence,
 PT absence or identity of single polynucleotide polymorphism in a nucleic
 PT acid sample.

PS Claim 1; Page 68; 83pp; English.

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC primer extension (SNPE) primers, and the sequences of regions flanking
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC includes kits for determining the presence or absence of a SNP, using the
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC performing a single-nucleotide primer extension reaction. The
 CC oligonucleotides are useful for determining the presence, absence or
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC assess by association analysis the genotype of an individual or group of
 CC individuals, having a pathological phenotypic trait suspected of being
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC traits also include symptoms of or susceptibility to multifactorial
 CC disease of which a component is or may be genetic such as autoimmune
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,
 CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC microorganism. The method is also useful in forensic investigations and
 CC paternity analysis. The present sequence represents a single nucleotide
 CC primer extension (SNPE) primer specific for a human SNP containing DNA
 CC sequence

SO Sequence 25 BP; 3 A; 9 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 2.0%; Score 20.2; DB 1; Length 25;
 Best Local Similarity 88.0%; Pred. No. 1.3e+03;

Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 990 CCTCCGGGCTCAGCGATTCTCT 1014
 Db 1 CCTCCGGGTTAGAGCATTCCT 25

RESULT 450

AAH37979/C

ID AAH37979 standard; DNA; 25 BP.

AC AAH37979;

DT 14-AUG-2001 (first entry)

DE SNP specific SNPE primer SEQ ID 775.

XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
 XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
 XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
 XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
 XX inflammation; forensic investigation; paternity analysis; primer; ss.

OS Homo sapiens.

PN WO200129262-A2.

PD 26-APR-2001.

PF 13-OCT-2000; 2000WO-US028436.

PR 15-OCT-1999; 99US-0160096P.

PA (ORCH-) ORCHID BIOSCIENCES INC.

PI Picoult-Newburg L, Pohl M;

DR WPI; 2001-290930/30.

XX New genotyping oligonucleotide, useful for detecting the presence,
 PT absence or identity of single polynucleotide polymorphism in a nucleic
 PT acid sample.

PS Claim 1; Page 53; 83pp; English.

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC primer extension (SNPE) primers, and the sequences of regions flanking
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC includes kits for determining the presence or absence of a SNP, using the
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC performing a single-nucleotide primer extension reaction. The
 CC oligonucleotides are useful for determining the presence, absence or
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC assess by association analysis the genotype of an individual or group of
 CC individuals, having a pathological phenotypic trait suspected of being
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC traits also include symptoms of or susceptibility to multifactorial
 CC disease of which a component is or may be genetic such as autoimmune
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,
 CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC microorganism. The method is also useful in forensic investigations and
 CC paternity analysis. The present sequence represents a single nucleotide
 CC primer extension (SNPE) primer specific for a human SNP containing DNA
 CC sequence

SO Sequence 25 BP; 3 A; 6 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 2.0%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 869 GATTACAGCGGTGACCCACACGCC 893
DB 25 GATTACAGAGTGCACACACGCC 1

RESULT 451

AAH37611/c
ID AAH37611 standard; DNA; 25 BP.
XX
XX AAH37611;
XX
XX 14-AUG-2001 (first entry)
XX
XX SNP specific SNPE primer SEQ ID 407.
XX
XX

Single nucleotide polymorphism; SNP; single nucleotide primer extension;
SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
Kw Leech-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
Kw polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
Kw acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
Kw inflammation; forensic investigation; paternity analysis; primer; ss.

Homo sapiens.

WO200129262-A2.

26-APR-2001.

13-OCT-2000; 2000WO-US028436.

15-OCT-1999; 99US-0160096P.

(ORCH-) ORCHID BIOSCIENCES INC.

Picoult-Newburg L, Pohl M;

WPI; 2001-290930/30.

New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polymorphic polymorphism in a nucleic
PT acid sample.

Claim 1; Page 52; 83pp; English.

Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinemia, diabetes insipidus, Leech-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a single nucleotide
CC primer extension (SNPE) primer specific for a human SNP containing DNA
XX sequence

Sequence 25 BP; 16 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 165 TTGTATTTTTTTTTTTAGAGATCG 189
DB 25 TTTTATTTTTTTTTTTAGAGATCG 1

RESULT 452

AAH39587
ID AAH39587 standard; DNA; 25 BP.
XX
XX AAH39587;
XX
XX 14-AUG-2001 (first entry)
XX
XX SNP specific SNPE primer SEQ ID 2383.
XX
XX

Single nucleotide polymorphism; SNP; single nucleotide primer extension;
SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
Kw Leech-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
Kw polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
Kw acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
Kw inflammation; forensic investigation; paternity analysis; primer; ss.

Homo sapiens.

WO200129262-A2.

26-APR-2001.

13-OCT-2000; 2000WO-US028436.

15-OCT-1999; 99US-0160096P.

(ORCH-) ORCHID BIOSCIENCES INC.

Picoult-Newburg L, Pohl M;

WPI; 2001-290930/30.

New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polymorphic polymorphism in a nucleic
PT acid sample.

Claim 1; Page 62; 83pp; English.

Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinemia, diabetes insipidus, Leech-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a single nucleotide
CC primer extension (SNPE) primer specific for a human SNP containing DNA
XX sequence

CC sequence
 XX SQ Sequence 25 BP; 4 A; 10 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 2.0%; Score 20.2; DB 1; Length 25;
 Best Local Similarity 88.0%; Pred. No. 1.3e+03;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 689 GCGTCCCGGGTCAAGTATTCCTCC 713
 DB 1 GCGTCCCGGGTCAAGTATTCCTCC 25
 RESULT 453
 AAH39123
 ID AAH39123 standard; DNA; 25 BP.
 AC AAH39123;
 XX
 XX 14-AUG-2001 (first entry)
 DT
 XX
 DE SNP specific SNPE primer SEQ ID 1919.
 XX
 XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
 XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
 XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
 XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
 XX inflammation; forensic investigation; paternity analysis; primer; ss.
 OS
 XX Homo sapiens.
 XX
 PN MO200129262-A2.
 XX
 PD 26-APR-2001.
 XX
 PF 13-OCT-2000; 2000MO-US028436.
 XX
 PR 15-OCT-1999; 99US-0160096P.
 XX
 PA (ORCH-) ORCHID BIOSCIENCES INC.
 XX
 PI Picoult-Newburg L, Pohl M;
 DR WPI; 2001-290930/30.
 XX
 PT New genotyping oligonucleotide, useful for detecting the presence,
 PT absence or identity of single polynucleotide polymorphism in a nucleic
 PT acid sample.
 PS
 XX Claim 1; Page 59; 83pp; English.
 XX
 CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC primer extension (SNPE) primers, and the sequences of regions flanking
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC includes kits for determining the presence or absence of a SNP, using the
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC performing a single-nucleotide primer extension reaction. The
 CC oligonucleotides are useful for determining the presence, absence or
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC assess by association analysis the genotype of an individual or group of
 CC individuals, having a pathological phenotypic trait suspected of being
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC traits also include symptoms of or susceptibility to multifactorial
 CC disease of which a component is or may be genetic such as autoimmune
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,
 CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC microorganism. The method is also useful in forensic investigations and

CC paternity analysis. The present sequence represents a single nucleotide
 CC primer extension (SNPE) primer specific for a human SNP containing DNA
 CC sequence
 XX SQ Sequence 25 BP; 4 A; 8 C; 5 G; 8 T; 0 U; 0 Other;
 Query Match 2.0%; Score 20.2; DB 1; Length 25;
 Best Local Similarity 88.0%; Pred. No. 1.3e+03;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 693 CCGGGTTCAGTATTCCTCTGCC 717
 DB 1 CCGGGTTCAGTATTCCTCTGCC 25
 RESULT 454
 AAH40067/c
 ID AAH40067 standard; DNA; 25 BP.
 AC AAH40067;
 XX
 XX 14-AUG-2001 (first entry)
 DT
 XX
 DE SNP specific SNPE primer SEQ ID 2863.
 XX
 XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
 XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
 XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
 XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
 XX inflammation; forensic investigation; paternity analysis; primer; ss.
 OS
 XX Homo sapiens.
 XX
 PN MO200129262-A2.
 XX
 PD 26-APR-2001.
 XX
 PF 13-OCT-2000; 2000MO-US028436.
 XX
 PR 15-OCT-1999; 99US-0160096P.
 XX
 PA (ORCH-) ORCHID BIOSCIENCES INC.
 XX
 PI Picoult-Newburg L, Pohl M;
 DR WPI; 2001-290930/30.
 XX
 PT New genotyping oligonucleotide, useful for detecting the presence,
 PT absence or identity of single polynucleotide polymorphism in a nucleic
 PT acid sample.
 PS
 XX Claim 1; Page 64; 83pp; English.
 XX
 CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC primer extension (SNPE) primers, and the sequences of regions flanking
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC includes kits for determining the presence or absence of a SNP, using the
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC performing a single-nucleotide primer extension reaction. The
 CC oligonucleotides are useful for determining the presence, absence or
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC assess by association analysis the genotype of an individual or group of
 CC individuals, having a pathological phenotypic trait suspected of being
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC traits also include symptoms of or susceptibility to multifactorial
 CC disease of which a component is or may be genetic such as autoimmune
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,

SQL Sequence 25 BP; 3 A; 9 C; 5 G; 8 T; 0 U; 0 Other;
Query Match 2.0%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
DB 1 TCCTGCTCAGTCTCCGAGTAGCT 25
536 TCCTGCTCAGCTCCGAGTAGCT 560
RESULT 457
ADB04614
ID ADB04614 standard; DNA; 25 BP.
AC ADB04614;
XX 20-NOV-2003 (first entry)
XX Human MD27 scanning oligonucleotide SEQ ID 5600.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX Homo sapiens.
XX
XX EP1281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-UTL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5600; 103bp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
SQL Sequence 25 BP; 4 A; 7 C; 10 G; 4 T; 0 U; 0 Other;
Query Match 2.0%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
DB 1 TCCTGCTCAGTCTCCGAGTAGCT 25
643 CCAGGCTGAGTGCAGTGGCGCAA 667
643 CCAGGCTGAGTGCAGTGGCGCAA 667
643 CCAGGCTGAGTGCAGTGGCGCAA 667

DB 1 CCTGGGCTGAGTGCAGTGGCCCA 25
RESULT 458
ADB04577
ID ADB04577 standard; DNA; 25 BP.
AC ADB04577;
XX 20-NOV-2003 (first entry)
XX
XX Human MD27 scanning oligonucleotide SEQ ID 5563.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX Homo sapiens.
XX
XX EP1281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-UTL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5563; 103bp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
SQL Sequence 25 BP; 4 A; 1 C; 4 G; 16 T; 0 U; 0 Other;
Query Match 2.0%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
DB 1 TTTTATTTTATTTTGGACAGAGT 25
605 TATTTTATTTTATTTTGGACAGAGT 629
RESULT 459
ADB04684
ID ADB04684 standard; DNA; 25 BP.
AC ADB04684;
AC ADB04684;

```

DT 20-NOV-2003 (first entry)
XX
XX Human MD27 scanning oligonucleotide SEQ ID 5670.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KV zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX EPI281758-A2.
PN
XX
XX 05-FEB-2003.
PD
XX
XX 30-JUL-2002; 2002EP-00016874.
PF
XX
XX 02-AUG-2001; 2001US-00922181.
PR
XX
XX (AEOM-) AEOMICA INC.
PA
XX
XX Shannon M, Gu Y, Nguyen C;
PI
XX
XX WPI; 2003-423107/40.
XX
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
XX
XX Example 8; SEQ ID NO 5670; 103bp; English.
XX
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1; MD24 is encoded at chromosome 6p21.3-22.2.
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX
XX Sequence 25 BP; 3 A; 8 C; 7 G; 7 T; 0 U; 0 Other;
SQ
XX
XX Query Match 2.0%; Score 20.2; DB 1; Length 25;
XX Best Local Similarity 88.0%; Pred. No. 1.3e+03;
XX Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0
XX
XX 538 CTGCTCAGCCCTCCCAAGTAGCTGG 562
QY ||||| ||||| ||||| ||||| |||||
XX 1 CTGCTCAGCTCCCGAGTAGCTGG 25
XX
XX
XX RESULT 460
XX ADB04683
XX ADB04683 standard; DNA; 25 BP.
XX
XX ADB04683;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MD27 scanning oligonucleotide SEQ ID 5669.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KV zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX

```

XX		developmental disorder; ss.
XX	OS	Homo sapiens.
XX	FN	EPI281758-A2.
XX	PD	05-FEB-2003.
XX	PF	30-JUL-2002; 2002EP-00016874.
XX	PR	02-AUG-2001; 2001US-00922181.
XX	PA	(AEOM-) AEOMICA INC.
XX	PI	Shannon M, Gu Y, Nguyen C;
XX	DR	WPI; 2003-423107/40.
XX	PT	New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MD23, MD24, MD27 or MD212, e.g. cancer.
XX	PS	Example 8; SEQ ID NO 5669; 103pp; English.
CC	CC	The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2, MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy, or in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MD23, MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic acids and proteins are also useful for diagnosing or monitoring a disease caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic acids can also be used as probes to detect and characterize gross alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as vaccines. The present sequence was used to illustrate the invention.
SO		Sequence 25 BP; 3 A; 9 C; 6 G; 7 T; 0 U; 0 Other;
		Query Match 2.0%; Score 20.2; DB 1; Length 25; Best Local Similarity 88.0%; Pred. No. 1.3e+03; Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY	537	CCTGCGTCAGCCTCCCAAGTGTGCTG 561 1 CCTGCTTCAGTCTCCCGAATGACTG 25
DB		
	RESULT 461	
	ADB04576	
ID	ADB04576 standard; DNA; 25 BP.	
AC	ADB04576;	
DT	20-NOV-2003 (first entry)	
DE	Human MD27 scanning oligonucleotide SEQ ID 5562.	
KX		Cytoskeletal; immunostimulant; gene therapy; vaccine; human;
KM		zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW		chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer; developmental disorder; ss.
OS		Homo sapiens.
PN		EPI281758-A2.
PD		05-FEB-2003.
XX		

CC or HLA-B62 constraint property of a cytotoxic T-cell (CTL) or a peptide
CC comprising a TRG2-41 sequence capable of recognising and inducing the HLA
CC -B53 of a CTL. The peptide of the invention demonstrates cytotoxic
CC activity and may be useful for inducing a cytotoxic T-cell in order to
CC treat cancer, preferably epithelial cancer, more preferably lung cancer,
CC stomach cancer, colon cancer, prostatic cancer and/or melanoma. The
CC treatment may comprise the use of a vaccine. The current sequence is that
CC of the probe of the invention which was used to analyse human testin-
CC related gene (TRG) expression.

XX Sequence 25 BP; 7 A; 9 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 20.2; DB 1; Length 25;

Best Local Similarity 88.0%; Pred. No. 1.3e+03;

Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 181 TTGAGATGAGTTTCTCCATGTTGG 205
DB 25 TAGAGACGGGTTTCACCATGTTGG 1

RESULT 464

AAT73704
ID AAT73704 standard; DNA; 20 BP.

AC AAT73704;

DT 27-FEB-1998 (first entry)

DE PCR primer used to prepare probes for diagnosing Alzheimer's disease.

XX PCR primer BK33; Alzheimer's disease; probe; diagnosis; fluorescence;

KW yeast artificial chromosome library; YAC; chromosome 14; present; ss.

XX Synthetic.

XX FR2742758-A1.

XX 27-JUN-1997.

XX 28-OCT-1994; 94FR-00012941.

XX 28-OCT-1994; 94FR-00012941.

PA (ASFR-) ASSOC FR CONTRA MYOPATHIES ASSOC LOI.

PI Weissenbach J, Heilig R;

DR WPI; 1997-353201/33.

XX Probes for diagnosing Alzheimer's disease - hybridising with chromosome
PT 14 segments cloned in yeast artificial chromosome library.

PS Example 1; Page 8; 21pp; French.

XX PCR primers AAT73703-4 were used to prepare probes (containing Alu
CC repeats) for detecting a mutation in the locus of chromosome 14
CC associated with a presenile form of Alzheimer's disease. Each of the
CC probes hybridises with one of the two human chromosomal DNA segments
CC cloned in the CEPH yeast artificial chromosome (YAC) library under the
CC accession numbers YAC 934A3 identifiable by genetic marker D14S251) and
CC YAC 854F5 (identifiable by genetic marker D14S76). The probes are useful
CC for diagnosis of the form of Alzheimer's disease associated with
CC chromosome 14 by a method comprising making a preparation of metaphase
CC chromosomes from the patient's lymphoblastoid cells on a microscope
CC slide, contacting the preparation under DNA hybridisation conditions with
CC the pair of probes or with one of the probes and another probe that
CC hybridises with YAC 905C2 from the same library, and detecting the
CC hybridised probes and their relative positions on a significant number of
CC pairs of chromosomes

XX Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 865 CTGGATTACAGGGCTGAGC 884
DB 1 CTGGATTACAGGGCTGAGC 20

RESULT 465

AAT73703/C
ID AAT73703 standard; DNA; 20 BP.

AC AAT73703;

DT 27-FEB-1998 (first entry)

DE PCR primer SRI used to prepare probes for diagnosing Alzheimer's.

XX PCR primer SRI; Alzheimer's disease; probe; diagnosis; fluorescence;

KW yeast artificial chromosome library; YAC; chromosome 14; present; ss.

XX Synthetic.

XX FR2742758-A1.

XX 27-JUN-1997.

XX 28-OCT-1994; 94FR-00012941.

XX 28-OCT-1994; 94FR-00012941.

PA (ASFR-) ASSOC FR CONTRA MYOPATHIES ASSOC LOI.

PI Weissenbach J, Heilig R;

DR WPI; 1997-353201/33.

XX Probes for diagnosing Alzheimer's disease - hybridising with chromosome
PT 14 segments cloned in yeast artificial chromosome library.

PS Example 1; Page 8; 21pp; French.

XX PCR primers AAT73703-4 were used to prepare probes (containing Alu
CC repeats) for detecting a mutation in the locus of chromosome 14
CC associated with a presenile form of Alzheimer's disease. Each of the
CC probes hybridises with one of the two human chromosomal DNA segments
CC cloned in the CEPH yeast artificial chromosome (YAC) library under the
CC accession numbers YAC 934A3 identifiable by genetic marker D14S251) and
CC YAC 854F5 (identifiable by genetic marker D14S76). The probes are useful
CC for diagnosis of the form of Alzheimer's disease associated with
CC chromosome 14 by a method comprising making a preparation of metaphase
CC chromosomes from the patient's lymphoblastoid cells on a microscope
CC slide, contacting the preparation under DNA hybridisation conditions with
CC the pair of probes or with one of the probes and another probe that
CC hybridises with YAC 905C2 from the same library, and detecting the
CC hybridised probes and their relative positions on a significant number of
CC pairs of chromosomes

XX Sequence 20 BP; 3 A; 9 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 643 CCCAGGCTGAGTGCAGTGG 662
DB 20 CCCAGGCTGAGTGCAGTGG 1

RESULT 466

AAV85582
ID AAV85582 standard; DNA; 20 BP.

```

XX AAV85582;
XX 10-FEB-1999 (first entry)
XX LRP5 PCR primer Gpi 1F.
XX LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis;
XX insulin dependent diabetes mellitus; autoimmune disease;
XX glomerulonephritis; inflammation; viral infection; osteoporosis;
XX hypercholesterolemia; Alzheimer's disease; low density lipoprotein;
XX PCR primer; ss.
XX Synthetic.
XX Homo sapiens.
XX MO9846743-A1.
XX 22-OCT-1998.
XX 15-APR-1998; 98WO-GB001102.
XX 15-APR-1997; 97US-0043553P.
XX 05-JUN-1997; 97US-0048740P.
XX (WELL) WELLCOME TRUST LTD.
XX (MERI) MERCK & CO INC.
XX Todd JA, Hess JM, Caskey CT, Cox RD, Gerhold D, Hammond H;
XX Hey P, Kawaguchi Y, Merriman TR, Metzker ML, Nakagawa Y;
XX Phillips MS, Twells RCJ;
XX WPI; 1998-594573/50.
XX New isolated LDL-receptor related protein - used to develop products for
XX treating, e.g. elevated triglyceride levels, diabetes, autoimmune
XX disorders, inflammation or Alzheimer's disease.
XX Claim 12; Page 98; 200Pp; English.
XX The present invention describes LRP5 (low density lipoprotein (LDL)
XX receptor related protein, previously designated LRP-3). AAV8552 to
XX CAAV85586 represent PCR primer used for obtaining LRP5 cDNA. Nucleic acid
XX molecules (NAs) encoding LRP5 can be used for determining if an
XX individual is susceptible to insulin dependent diabetes mellitus (IDDM).
XX The NAs or proteins can be used for reducing triglyceride levels in the
XX serum of an individual. Therapies that affect LRP5 may also be useful in
XX the treatment of autoimmune diseases such as glomerulonephritis, diseases
XX and disorders involving disruption of endocytosis and/or antigen
XX presentation, cytokine clearance and/or inflammation, viral infection,
XX pathogenic bacterial toxin contamination, elevation of free fatty acids
XX or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's
XX disease and cardiovascular disease. Products from the present invention
XX can also be used for detection, diagnosis and drug screening
XX
XX Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
SQ
XX
XX Query Match 2.0%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1112 AGGCTGATCTCAAACTCTG 1131
XX |||||
XX 1 AGGCTGATCTCAAACTCTG 20
XX
XX RESULT 467
XX AAV69963
XX AAV69963 standard; DNA; 20 BP.
XX
XX AAV69963;
XX
XX 04-FEB-1999 (first entry)

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```

XX Human c-fos protein antisense oligonucleotide #25.
XX Human; c-fos; c-jun; activating protein 1; AP-1; diagnosis; metastasis;
XX antisense oligonucleotide; phosphorothioate; regulation;
XX malignant tumour; cell cycle expression; hyperproliferative disease; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX Key Location/Qualifiers
XX modified_base 1..20
XX /note="phosphorothioate linkages"
XX
XX MO9846272-A1.
XX 22-OCT-1998.
XX 14-APR-1998; 98WO-US007386.
XX 14-APR-1997; 97US-00837201.
XX (ISIS-) ISIS PHARM INC.
XX Dean NM, McKay R, Miraglia L, Baker B;
XX WPI; 1998-609906/51.
XX Antisense oligonucleotides regulating Activating Protein 1 subunits -
XX hybridise with c-fos and c-jun mRNA, used for regulating metastasis, cell
XX cycle expression and hyperproliferative disease.
XX Claim 5; Page 76; 120Pp; English.
XX AAV69949 to AAV69977 represent antisense oligonucleotides which are
XX specifically hybridisable with a region of a nucleic acid encoding human
XX c-Fos protein. The antisense compound regulates the expression of the c-
XX Fos protein. The present invention also describes antisense
XX oligonucleotides which regulate the c-jun protein. The antisense
XX oligonucleotides are used for the diagnosis and treatment of diseases or
XX disorders associated with Activating Protein 1 expression, of which c-Fos
XX and c-jun are subunits. The antisense oligonucleotides are used in
XX compositions as c-Fos and/or c-jun together with a carrier and a
XX chemotherapeutic agent. They are used to regulate the expression of c-Fos
XX or c-jun in cells or tissues, preferably by inhibiting metastasis. They
XX also regulate cell cycle expression and can be used to treat an animal
XX with, or being prone to, a hyperproliferative disease
XX
XX Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 2.0%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 843 CCGCTCGAGCTCCCAAG 862
XX |||||
XX 1 CCGCTCGAGCTCCCAAG 20
XX
XX RESULT 468
XX AA237736/C
XX AA237736 standard; DNA; 20 BP.
XX
XX AA237736;
XX
XX 07-JUN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #266.
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisense; modulation; oligonucleotide; expression; inhibition;
XX hyperproliferation; blood cancer; brain cancer; breast cancer;

```

KW lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;
KM restenosis; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9949065-A1.
XX
XX 30-SEP-1999.
XX
XX 26-MAR-1999; 99WO-US006702.
XX
XX 26-MAR-1998; 98US-00048810.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowse LM;
XX WPI; 1999-610754/52.
XX
XX New antisense compounds used to treat eg. hyperproliferative conditions.
XX
XX Example 9; Page 55; 157pp; English.
XX
XX AA237473-237738 represent human mdm2 phosphorothioate oligonucleotides.
XX
XX AA237471, AA237472, AA237739, AA237740 and AA237741 are used in the
XX exemplification of the present invention. The present invention describes
XX novel nucleotide antisense compounds, targeted to the 5' untranslated,
XX translation termination codon, or 3' untranslated region of a nucleic
XX acid encoding human mdm2, that modulates expression of human mdm2. The
XX oligonucleotides mediate their effect by antisense inhibition of
XX hyperproliferative gene expression. The antisense compound is used to
XX treat an animal having a disease or condition associated with mdm2,
XX particularly a hyperproliferative condition, more particularly cancer,
XX especially of the blood, brain, breast, lung or soft tissue, or
XX psoriasis, fibrosis, atherosclerosis or restenosis
XX
SQ Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 851 GGCCTCCCAAGTCTGGGA 870
DB 20 GGCCTCCCAAGTCTGGGA 1

RESULT 469
AA237712/C
ID AA237712 standard; DNA; 20 BP.
XX
XX AA237712;
XX
XX 07-JAN-2000 (first entry)
XX
XX Human mdm2 phosphorothioate oligodeoxynucleotide #242.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisense; modulation; oligonucleotide; expression; inhibition;
XX hyperproliferation; blood cancer; brain cancer; breast cancer;
XX lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;
XX restenosis; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO9949065-A1.
XX
XX 30-SEP-1999.
XX
XX 26-MAR-1999; 99WO-US006702.
XX
XX

PR 26-MAR-1998; 98US-00048810.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowse LM;
XX WPI; 1999-610754/52.
XX
XX New antisense compounds used to treat eg. hyperproliferative conditions.
XX
XX Example 9; Page 54; 157pp; English.
XX
XX AA237473-237738 represent human mdm2 phosphorothioate oligonucleotides.
XX
XX AA237471, AA237472, AA237739, AA237740 and AA237741 are used in the
XX exemplification of the present invention. The present invention describes
XX novel nucleotide antisense compounds, targeted to the 5' untranslated,
XX translation termination codon, or 3' untranslated region of a nucleic
XX acid encoding human mdm2, that modulates expression of human mdm2. The
XX oligonucleotides mediate their effect by antisense inhibition of
XX hyperproliferative gene expression. The antisense compound is used to
XX treat an animal having a disease or condition associated with mdm2,
XX particularly a hyperproliferative condition, more particularly cancer,
XX especially of the blood, brain, breast, lung or soft tissue, or
XX psoriasis, fibrosis, atherosclerosis or restenosis
XX
SQ Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 937 CTGTTACCCAGGCTGAGTG 956
DB 20 CTGTTACCCAGGCTGAGTG 1

RESULT 470
AA237737/C
ID AA237737 standard; DNA; 20 BP.
XX
XX AA237737;
XX
XX 07-JAN-2000 (first entry)
XX
XX Human mdm2 phosphorothioate oligodeoxynucleotide #267.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisense; modulation; oligonucleotide; expression; inhibition;
XX hyperproliferation; blood cancer; brain cancer; breast cancer;
XX lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;
XX restenosis; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO9949065-A1.
XX
XX 30-SEP-1999.
XX
XX 26-MAR-1999; 99WO-US006702.
XX
XX 26-MAR-1998; 98US-00048810.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowse LM;
XX WPI; 1999-610754/52.
XX
XX New antisense compounds used to treat eg. hyperproliferative conditions.
XX
XX Example 9; Page 55; 157pp; English.
XX
XX

CC AA237473-237738 represent human mdm2 phosphorothioate oligonucleotides.
 CC AA237471, AA237472, AA237739, AA237740 and AA237741 are used in the
 CC exemplification of the present invention. The present invention describes
 CC novel nucleotide antisense compounds, targeted to the 5' untranslated,
 CC translation termination codon, or 3' untranslated region of a nucleic
 CC acid encoding human mdm2, that modulates expression of human mdm2. The
 CC oligonucleotides mediate their effect by antisense inhibition of
 CC hyperproliferative gene expression. The antisense compound is used to
 CC treat an animal having a disease or condition associated with mdm2,
 CC especially a hyperproliferative condition, more particularly cancer,
 CC psoriasis, fibrosis, atherosclerosis or restenosis
 CC
 SQ Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 388 CAAAGTGTGGATTACAG 407
 DB 20 CAAAGTGTGGATTACAG 1

RESULT 471
 ID AAA96410 standard; DNA; 20 BP.

AC AAA96410;
 XX
 DT 08-FEB-2001 (first entry)

DE Primer used to amplify a sara43/44 polymorphic microsatellite repeat.

XX Autoimmune disease; polymorphic microsatellite repeat; PMR; CD28 gene;
 XX ICOS gene; CTLA4 gene; costimulatory receptor gene locus; CGRI; lupus;
 XX insulin-dependent diabetes mellitus; IDDM; Addison's disease; leprosy;
 XX Graves disease; autoimmune hypochyroidism; myasthenia gravis; thymoma;
 XX chryoiditis; postpartum thyroiditis; rheumatoid arthritis;
 XX Hashimoto's disease; coeliac disease; PCR primer; ss.

OS Homo sapiens.
 XX
 PN WO200056856-A2.
 XX
 PD 28-SEP-2000.

PF 24-MAR-2000; 2000MO-US07938.

PR 25-MAR-1999; 99US-0126215P.

PA (GBMY) GENETICS INST INC.

PI Ling V, Wu P, Gray GS;

DR WPI; 2000-628257/60.

PT Determining predisposition of humans to develop autoimmune disease
 PT involves detecting polymorphic microsatellite repeat sequence within
 PT human costimulatory receptor gene locus.

PS Claim 16; Page 154; 160pp; English.

XX PCR primers AAA96409-10 were used to amplify polymorphic microsatellite
 CC repeat (PMR) sequences from the human costimulatory receptor gene locus
 CC (hCGRI). The primers are used in the method of the invention. The
 CC specification describes a method for determining the predisposition of a
 CC human subject to develop autoimmune disease. The method comprises
 CC detecting a PMR sequence in the CD28, ICOS gene or CTLA4 gene of the
 CC human costimulatory receptor gene locus (hCGRI). PMR sequences vary in
 CC length among individuals and can be amplified to generate products that
 CC differ in size. These products can then be detected by rapid and
 CC convenient high resolution processes. The method is useful for

CC determining the predisposition of insulin-dependent diabetes mellitus
 CC (IDDM), Addison's disease, Graves disease, autoimmune hypochyroidism,
 CC myasthenia gravis, thymoma, lupus, thyroiditis, postpartum thyroiditis,
 CC rheumatoid arthritis, Hashimoto's disease, coeliac disease and leprosy.
 CC PMR sequences within hCGRI are useful as markers in a variety of assays
 CC and in the field of forensic medicine, disease diagnosis and human genome
 CC mapping

SQ Sequence 20 BP; 3 A; 9 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 643 CCCAGGCTGGAGTGCAGTGG 662
 DB 20 CCCAGGCTGGAGTGCAGTGG 1

RESULT 472
 ID AA235378
 XX AA235378 standard; DNA; 20 BP.

AC AA235378;

XX 27-MAR-2000 (first entry)

DE Interspersed repeated sequence PCR primer ALU5.

XX Human; absorptive hypercalciuria; osteoporosis; nephrolithiasis;
 XX osteopathic; anticalciuric; chromosome 1q23.3-q24; therapy; diagnosis;
 XX PCR primer; ss.

OS Homo sapiens.

PN WO967426-A1.

PD 29-DEC-1999.

PF 23-JUN-1999; 99WO-US014347.

PR 23-JUN-1998; 98US-0090348P.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Reed-Glומר BY, Pak CYC;

DR WPI; 2000-116959/10.

PT Novel genomic region useful in screening for absorptive hypercalciuria or
 PT osteoporosis with hypercalciuria.

PS Example 3; Page 125; 153pp; English.

XX The present sequence is that of interspersed repeated sequence PCR (IRS-
 CC PCR) primer ALU5 used to identify human-specific sequences in yeast
 CC artificial chromosomes (YAC) derived from the human chromosome 1q23.3-q24
 CC region. The chromosomal region contains the locus associated with
 CC absorptive hypercalciuria (AH). IRS-PCR fingerprints were generated, and
 CC genes contained within YACs were identified by exon trapping. cDNA
 CC corresponding to the AH gene was isolated (see AA235376). Identification
 CC of the AH genomic region allows genetic screening for increased risk of
 CC developing AH or osteoporosis with hypercalciuria

SQ Sequence 20 BP; 5 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 868 GGATTACAGGCGTACGCAC 887
 DB 1 GGATTACAGGCGTACGCAC 20

KW	hyperproliferative disorder; developmental disorder; antisense;
KX	phosphorothioate backbone; ss.
OS	Homo sapiens.
OS	Synthetic.
XX	
PH	Key
FT	modified_base
FT	location/Qualifiers
FT	1..20
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "Phosphorothioate backbone"
FT	
FT	modified_base
FT	1..5
FT	/tag= b
FT	/mod_base= OTHER
FT	/note= "Methoxyethyl residues"
FT	2
FT	/tag= d
FT	/mod_base= m5c
FT	
FT	modified_base
FT	3
FT	/tag= e
FT	/mod_base= m5c
FT	4
FT	/tag= f
FT	/mod_base= m5c
FT	11
FT	/tag= g
FT	/mod_base= m5c
FT	16..20
FT	/tag= c
FT	/mod_base= OTHER
FT	/note= "Methoxyethyl residues"
FT	20
FT	/tag= h
FT	/mod_base= m5c
FT	
FT	modified_base
FT	y
PN	WO200152865-A1.
PD	26-JUN-2001.
XX	
PF	16-JAN-2001; 2001WO-US001411.
XX	
PR	21-JAN-2000; 2000US-00488856.
XX	
PA	(ISIS-) ISIS PHARM INC.
PI	Monia BP, McKay R, Butler MM, Wyatt JR;
XX	
DR	WPI; 2001-442247/47.
XX	
PT	Antisense compound 8 to 30 nucleobases in length comprising a compound
PT	that is targeted to a nucleic acid molecule encoding glycogen synthase
PT	kinase 3 alpha, useful for the treatment of e.g. diabetes and
PT	hyperproliferative disorders.
XX	
PS	Example 15; Page 83; 115pp; English.
CC	The invention relates to an antisense compound 8 to 30 nucleobases in
CC	length targeted to a nucleic acid encoding glycogen synthase kinase 3
CC	alpha. The antisense compound specifically hybridises with and inhibits
CC	the expression of glycogen synthase kinase 3 alpha. The antisense
CC	compound is useful for the treatment of a diseases associated with
CC	glycogen synthase kinase 3 alpha such as diabetes, a neurological
CC	disorder, a haematopoietic disorder, a hyperproliferative disorder or a
CC	developmental disorder. The antisense compounds may also be used
CC	prophylactically to prevent or delay infection, inflammation or tumour
CC	formation. The present sequence is a phosphorothioate antisense
CC	oligonucleotide targeted to human glycogen synthase kinase 3 alpha
CC	genomic DNA
XX	
SQ	Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
Query Match	2.0%; Score 20; DB 1; Length 20;
Best Local Similarity	100.0%; Pred. No. 1.le+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 385 TCCCAAGTCTGGATTAC 404
 DB 1 TCCCAAGTCTGGATTAC 20

RESULT 475
 AAK95176/c
 ID AAK95176 standard; DNA; 20 BP.

AC AAK95176;

DT 06-NOV-2001 (first entry)

DE Human cDNA clone-specific primer, SEQ ID NO: 4421.

KW Human; full length cDNA; cDNA synthesis; oligo-capping; PCR primer; ss.

OS Homo sapiens.

PN EP130094-A2.

PD 05-SEP-2001.

PF 07-JUL-2000; 2000EP-00114089.

PR 08-JUL-1999; 99JP-00194486.

PR 11-JAN-2000; 2000JP-00118774.

PR 02-MAY-2000; 2000JP-00183765.

(HELI-) HELIX RES INST.

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

DR WPI; 2001-524255/58.

PT 830 Primers useful for synthesizing full length cDNA clones and their use
 in genetic manipulation.

PS Example 18; Page 132; 1380pp + Sequence Listing; English.

CC The invention relates to primers for synthesizing full length cDNA
 clones. 830 cDNA molecules encoding a human protein have been isolated
 and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 been determined. Primers for synthesizing the full length cDNA are useful
 for clarifying the function of the protein encoded by the cDNA. The full
 length clones were obtained by construction of full length enriched cDNA
 libraries that were synthesized by the oligo-capping method. The primers
 enable the production of the full length cDNA easily without any special
 methods. The present sequence is a primer used to amplify a human cDNA
 clone provided in the invention

CC Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03; Mismatches 0; Indels 0; Gaps 0;

QY 388 CAAAGTCTGGATTACAGG 407
 DB 20 CAAAGTCTGGATTACAGG 1

RESULT 476
 AAF80866/c
 ID AAF80866 standard; DNA; 20 BP.

AC AAF80866;

DT 02-MAY-2001 (first entry)

DE Human mdm2 phosphorothioate oligonucleotide #240.

KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

OS Homo sapiens.

PN US6184212-B1.

PD 06-FEB-2001.

PF 26-MAR-1999; 99US-00280805.

PR 26-MAR-1998; 98US-00048810.

PA (ISIS-) ISIS PHARM INC.

PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowseart LM;

DR WPI; 2001-190948/19.

PT Novel antisense compound 8-30 nucleobases in length targeted to a nucleic
 acid molecule encoding human mdm-2 useful for modulating the expression
 of human mdm-2 and reducing hyperproliferation of human cells.

PS Example 9; Col 31; 77pp; English.

CC The present invention relates to an antisense compound 8-30 nucleobases
 in length targeted to nucleobases 1-308 of the 5' untranslated region,
 CC 1776-1806 of the translation termination codon region or 1818-2370 of the
 CC 3' untranslated region of a nucleic acid molecule encoding human mdm-2.
 CC The invention is useful for reducing hyperproliferation of human cells,
 CC modulating the expression of mdm2 in human cells or tissues or in vitro.
 CC The hyperproliferative disorder includes cancer or psoriasis

CC Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03; Mismatches 0; Indels 0; Gaps 0;

QY 937 CTGTACCCAGGCTGGATG 956
 DB 20 CTGTACCCAGGCTGGATG 1

RESULT 477

AAAF80891/c
 ID AAF80891 standard; DNA; 20 BP.

AC AAF80891;

DT 02-MAY-2001 (first entry)

DE Human mdm2 phosphorothioate oligonucleotide #265.

KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

OS Homo sapiens.

PN US6184212-B1.

PD 06-FEB-2001.

PF 26-MAR-1999; 99US-00280805.

PR 26-MAR-1998; 98US-00048810.

PA (ISIS-) ISIS PHARM INC.

PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowseart LM;

DR WPI; 2001-190948/19.

PT Novel antisense compound 8-30 nucleobases in length targeted to a nucleic
PT acid molecule encoding human mdm-2 useful for modulating the expression
PT of human mdm-2 and reducing hyperproliferation of human cells.
XX
PS Example 9; Col 33; 77bp; English.
XX
CC The present invention relates to an antisense compound 8-30 nucleobases
CC in length targeted to nucleobases 1-308 of the 5' untranslated region,
CC 1776-1806 of the translation termination codon region or 1818-2370 of the
CC 3' untranslated region of a nucleic acid molecule encoding human mdm-2.
CC The invention is useful for reducing hyperproliferation of human cells,
CC modulating the expression of mdm2 in human cells or tissues or in vitro.
CC The hyperproliferative disorder includes cancer or psoriasis
CC
XX Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 20 CAAAGTCTGGGATTACAG 1
OY 388 CAAAGTCTGGGATTACAG 407
DB 20 CAAAGTCTGGGATTACAG 1
RESULT 478
AAF08090/C
ID AAF08090 standard; DNA; 20 BP.
AC AAF08090;
DT 02-MAY-2001 (first entry)
XX
XX Human mdm2 phosphorothioate oligonucleotide #264.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
XX Homo sapiens.
XX
XX US6184212-B1.
XX
XX 06-FEB-2001.
XX
XX 26-MAR-1999; 99US-00280805.
XX
XX 26-MAR-1998; 98US-00048810.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Miragila LJ, Nero P, Graham MJ, Monia BP, Cowseart LM;
XX
XX MPI; 2001-190948/19.
XX
XX Novel antisense compound 8-30 nucleobases in length targeted to a nucleic
PT acid molecule encoding human mdm-2 useful for modulating the expression
PT of human mdm-2 and reducing hyperproliferation of human cells.
XX
PS Example 9; Col 33; 77bp; English.
XX
CC The present invention relates to an antisense compound 8-30 nucleobases
CC in length targeted to nucleobases 1-308 of the 5' untranslated region,
CC 1776-1806 of the translation termination codon region or 1818-2370 of the
CC 3' untranslated region of a nucleic acid molecule encoding human mdm-2.
CC The invention is useful for reducing hyperproliferation of human cells,
CC modulating the expression of mdm2 in human cells or tissues or in vitro.
CC The hyperproliferative disorder includes cancer or psoriasis
CC
XX Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
SQ

OY 851 GGCTCCCAAGTCTGGGA 870
DB 20 GGCTCCCAAGTCTGGGA 1
RESULT 479
AAH38246
ID AAH38246 standard; DNA; 20 BP.
XX
AC AAH38246;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific lower PCR primer SEQ ID 1042.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200129262-A2.
XX
XX 26-APR-2001.
XX
XX 13-OCT-2000; 2000WO-US028436.
XX
XX 15-OCT-1999; 99US-0160096P.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX Picoule-Newburg L, Pohl M;
XX
XX MPI; 2001-290930/30.
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
XX Claim 1; Page 55; 83bp; English.
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the phenotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
XX for a human SNP containing DNA sequence
XX
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```

QY      385 TCCCAAAGTGTGGATTAC 404
          |||||
Db      1 TCCCAAAGTGTGGATTAC 20

```

RESULT 480
AAS29506/c
ID AAS29506 standard; DNA; 20 BP.

DT 21-NOV-2001 (first entry)

Human mdm2 antisense oligonucleotide 31791.

Human; *mdm2*; hyperproliferative disorder; cancer; psoriasis; atherosclerosis; tumour; cystostatic; anti psoriatic; anti arteriosclerotic; vasotropic; antisense; phosphorothioate; ss

	Key	Location/Qualifiers
FH	modified_base	1. .20
FT		

US2001016575-A1
PN

PD 23-AUG-2001.

02-JAN-2001; 2001US-00752983.

26-MAR-1998; 98US-00048810.

PR 26-MAR-1999; 99US-00280805.

PA (MIRA/) MIRAGLIA L J
PA (NERO/) NERO P.
PA (GRAH/) GRAHAM M J.
PA (MONI/) MONIA B P.
PA (COWS/) COWSERT L M.

PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsert LM;

DR WPI; 2001-535565/59.

PT An antisense compound, useful for treating e.g. cancer, comprises PT nucleobases targeted a region (e.g. translation termination codon region) PT of a nucleic acid encoding human mdm2.

PS Example 9; Page 18; 81pp; English.

The present invention relates to antisense compounds, 8-30 nucleobases in length targeted to the 5' untranslated region, translation termination codon region, 3' untranslated region, coding region or translation start site of a nucleic acid encoding human mdm2, where the antisense compound modulates the expression of human mdm2. The antisense oligonucleotides of the invention are useful for encoding human mdm2 and for inhibiting the expression of human mdm2. They may be used for treating an animal having a disease or condition associated with amplification of mdm2 gene or overexpression of mdm2 e.g. a hyperproliferative disorder such as cancer (blood, brain, breast, lung, or a soft tissue cancer) and psoriasis, fibrosis, atherosclerosis or restenosis, tumours, colorectal carcinoma and chronic myelogenous leukemia. The antisense compound may be administered with a chemotherapeutic agent to overcome drug resistance. The antisense compound reduces hyperproliferation of human cells. The method, which involves the use of the antisense compound, is also useful for detecting the role of mdm2 expression in various cell functions and physiological processes and useful in both clinical research and diagnostic tools. AAS29242-AAS29507 represent the human mdm2 antisense

oligonucleotides of the present invention

```

QY      388 CAAAGTCTGGATTACAGG 407
          |||||
Db      20 CAAAGTCTGGATTACAGG 1

```

RESULT 481
AAS29505/c
ID AAS29505 standard; DNA; 20 BP.

DT 21-NOV-2001 (first entry)

Human mdm2 antisense oligonucleotide 31630.

Human; mcm2; hyperproliferative disorder; cancer; psoriasis;
 atherosclerosis; tumour; cystostatic; anti psoriatic;
 anti arteriosclerotic; vasotropic; antisenese; phosphorothioate; ss

PH	Key	Location/Qualifiers
FT	modified_base	1..20
FT		/"cag= a
FT		/mod_base= OTHER
FT		/note= "OTHER= All phosphorothioate linkages, additionally bases 1-6 and bases 15-20 are 2'-O-methoxyethyl bases, and bases 7-14 are deoxynucleotides"
FT		

PN US2001016575-A1.

23-AUG-2001. PD

02-JAN-2001; 2001US-00752983.

26-MAR-1998; 98US-00048810.

'26-MAR-1999; 99US-00280805.
PR

PA	(MIRA/)	MIRAGLIA L. J.
PA	(NERO/)	NERO P.
PA	(GRAH/)	GRAHAM M. J.
PA	(MONI/)	MONIA B. P.
PA	(COWS/)	COMSERT L. M.

Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowbert LM;

DR WPI; 2001-535565/59.

PT An antisense compound, useful for treating e.g. cancer, comprises PT nucleobases targeted a region (e.g. translation termination codon region) PT of a nucleic acid encoding human mdm2.

PS Example 9; Page 18; 81pp; English.

AA The present invention relates to antisense compounds, 8-30 nucleobases in length targeted to the 5' untranslated region, translation termination codon region, 3' untranslated region, coding region or translation start site of a nucleic acid encoding human mdm2, where the antisense compound modulates the expression of human mdm2. The antisense oligonucleotides of the invention are useful for encoding human mdm2 and for inhibiting the expression of human mdm2. They may be used for treating an animal having a disease or condition associated with amplification of mdm2 gene or overexpression of mdm2 e.g. a hyperproliferative disorder such as cancer (blood, brain, breast, lung, or a soft tissue cancer) and psoriasis, fibrosis, atherosclerosis or restenosis, tumours, colorectal carcinoma

XX	CC	and chronic myelogenous leukemia. The antisense compound may be
XX	CC	administered with a chemotherapeutic agent to overcome drug resistance.
XX	CC	The antisense compound reduces hyperproliferation of human cells. The
XX	CC	method, which involves the use of the antisense compound, is also useful
XX	CC	for detecting the role of mdm2 expression in various cell functions and
XX	CC	physiological processes and useful in both clinical research and
XX	CC	diagnostic tools. AAS29242-AAS29507 represent the human mdm2 antisense
XX	CC	oligonucleotides of the present invention
XX	CC	
XX	CC	Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
XX	CC	
XX	CC	Query Match 2.0%; Score 20; DB 1; Length 20;
XX	CC	Best Local Similarity 100.0%; Pred. No. 1.1e+03;
XX	CC	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX	CC	
XX	CC	851 GGCTCCCAAGTCTGCGA 870
XX	CC	
XX	CC	20 GGCTCCCAAGTCTGCGA 1
XX	CC	
XX	CC	RESULT 482
XX	CC	AAS29481/c
XX	CC	ID AAS29481 standard; DNA; 20 BP.
XX	CC	AAS29481;
XX	CC	
XX	CC	21-NOV-2001 (first entry)
XX	CC	
XX	CC	Human mdm2 antisense oligonucleotide 31781.
XX	CC	
XX	CC	Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
XX	CC	atherosclerosis; tumour; cytostatic; anti psoriatic;
XX	CC	anti atherosclerotic; vasotropic; antisense; phosphorothioate; ss.
XX	CC	
XX	CC	Homo sapiens.
XX	CC	
XX	CC	
XX	CC	Key Location/Qualifiers
XX	CC	FT modified_base 1..20
XX	CC	FT /*tag= a
XX	CC	FT /mod_base= OTHER
XX	CC	FT /note= "OTHER= All phosphorothioate linkages,
XX	CC	additionally bases 1-6 and bases 15-20 are 2'-O-
XX	CC	methoxyethyl bases, and bases 7-14 are deoxynucleotides"
XX	CC	
XX	CC	US2001016575-A1.
XX	CC	
XX	CC	23-AUG-2001.
XX	CC	
XX	CC	02-JAN-2001; 2001US-00752983.
XX	CC	
XX	CC	26-MAR-1998; 98US-00048810.
XX	CC	PR 26-MAR-1999; 99US-00280805.
XX	CC	
XX	CC	(MIRA/) MIRAGLIA L J.
XX	CC	PA (NERO/) NERO P.
XX	CC	PA (GRAH/) GRAHAM M J.
XX	CC	PA (MONI/) MONIA B P.
XX	CC	PA (COMS/) COMSERT L M.
XX	CC	
XX	CC	Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowseert LM;
XX	CC	
XX	CC	WPI; 2001-535565/59.
XX	CC	
XX	CC	An antisense compound, useful for treating e.g. cancer, comprises
XX	CC	PT nucleobases targeted a region (e.g. translation termination codon region)
XX	CC	PT of a nucleic acid encoding human mdm2.
XX	CC	
XX	CC	Example 9; Page 18; 81pp; English.
XX	CC	
XX	CC	The present invention relates to antisense compounds, 8-30 nucleobases in
XX	CC	length targeted to the 5' untranslated region, translation termination
XX	CC	codon region, 3' untranslated region, coding region or translation start
XX	CC	site of a nucleic acid encoding human mdm2, where the antisense compound

CC	modulate the expression of human mdm2. The antisense oligonucleotides of
CC	the invention are useful for encoding human mdm2 and for inhibiting the
CC	expression of human mdm2. They may be used for treating an animal having
CC	a disease or condition associated with amplification of mdm2 gene or
CC	overexpression of mdm2 e.g. a hyperproliferative disorder such as cancer
CC	(blood, brain, breast, lung, or a soft tissue cancer) and psoriasis,
CC	fibrosis, atherosclerosis or restenosis, tumours, colorectal carcinoma
CC	and chronic myelogenous leukemia. The antisense compound may be
CC	administered with a chemotherapeutic agent to overcome drug resistance.
CC	The antisense compound reduces hyperproliferation of human cells. The
CC	method, which involves the use of the antisense compound, is also useful
CC	for detecting the role of mdm2 expression in various cell functions and
CC	physiological processes and useful in both clinical research and
CC	diagnostic tools. AA529242-AA529507 represent the human mdm2 antisense
CC	oligonucleotides of the present invention
CC	
XX	
XX	Sequence 20 BP, 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
XX	
XX	Query Match 2.0%; Score 20; DB 1; Length 20;
XX	Best Local Similarity 100.0%; Pred. NO. 1.1e+03;
XX	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	937 CTGTTACCCAGGCTGAGTG 956
Db	20 CTGTTACCCAGGCTGAGTG 1
XX	
XX	RESULT 483
ID	AAK98932 standard; DNA; 20 BP.
AC	AAK98932;
XX	
DT	24-MAY-2002 (first entry)
XX	
DE	Human Beta-globin 5' MAR antisense primer BMRI.
XX	
XX	Expression vector; beta-globin nuclear matrix attachment region; MAR;
KW	SV40 virus; gastrin; tumour growth factor beta soluble receptor II;
XX	TGF-beta SR11; TGF-beta-overexpressed disease; human; PCR; primer; ss.
OS	Homo sapiens.
XX	
XX	WO200214525-A2.
XX	
PD	21-FEB-2002.
XX	
XX	27-JUL-2001; 2001WO-KR001285.
XX	
XX	29-JUL-2000; 2000KR-00043996.
PR	
XX	
XX	(MOGA-) MOGAM BIOTECHNOLOGY RES INST.
PA	(PANG-) PAN-GEN BIOTECH LAB INC.
XX	
XX	Kim J, Kim J, Oh S, Yoon J, Baek K, Chung S, Park D, Yoon Y;
XX	WPI; 2002-269202/31.
DR	
XX	
XX	New expression vectors for use in animal cells (e.g. pMS, pSG and pMSG
PT	vectors), useful for producing recombinant proteins in various animal
PT	cells and recombinant protein having a unique structure and function.
XX	
XX	Example 1; Page 77; 85pp; English.
XX	
XX	The invention relates to new expression vectors for animal cells
CC	comprising a beta-globin nuclear matrix attachment region (MAR) sequence
CC	or its complementary sequence at 5'-terminal end of a promoter and/or a
CC	SV40 virus poly-A signal and transcription termination site of gastrin
CC	gene. The expression vectors are useful for producing recombinant
CC	proteins in various animals cells and recombinant protein having a unique
CC	structure and function. The vectors, which have increased expression
CC	efficiency and levels for foreign genes, are useful for expressing
CC	foreign proteins used in an animal cell system, e.g. tumour growth factor

CC beta soluble receptor II (TGF-beta SRII), which can be used for treatment
CC of TGF-beta-overexpressed disease. This polynucleotide sequence
CC represents a PCR primer of human Beta-globin 5' MAR of the invention
XX
SQ Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 722 CCTCTGACTGACTGACT 741
DB 1 CCTCTGACTGACTGACT 20

RESULT 484
ABS59253/c
ID ABS59253 standard; DNA; 20 BP.

XX ABS59253;

AC 05-NOV-2002 (first entry)

XX Human CAS gene antisense oligonucleotide, ISIS 128206.

XX Human; ss; antisense; cellular apoptosis susceptibility gene;
XX antiinflammatory; antitumour; cytostatic; CAS; CSE1; CSP;
XX chromosome 20q13; mitosis; apoptosis; proliferation; cancer;
XX Importin-alpha; nuclear localisation; cell cycle;
XX hyperproliferative disorder; degenerative disorder; Alzheimer's disease;
XX Parkinson's disease; amyotrophic lateral sclerosis; ALS;
XX retinitis pigmentosa; blood cell disorder; gene therapy; infection;
XX inflammation; tumour.

XX Homo sapiens.
OS Synthetic.

XX Location/Qualifiers
FH Key 1..20

FT /tag= a
FT /mod_base= OTHER
FT /note= "OTHER = phosphorothioate backbone, all cytidine
FT residues are 5-methylcytidines"

FT modified_base 1..5

FT /tag= b
FT /mod_base= OTHER

FT modified_base 16..20
FT /note= "OTHER = 2'-O-methoxyethyl nucleotides"

FT /tag= c
FT /mod_base= OTHER

FT /note= "OTHER = 2'-O-methoxyethyl nucleotides"

XX WO200246367-A2.

XX 13-JUN-2002.

XX 29-OCT-2001; 2001WO-US051048.

XX 01-NOV-2000; 2000US-00705299.

XX (ISIS-) ISIS PHARM INC.

XX Cowsett LM, Freier SM;

XX WPI; 2002-608254/65.

XX New antisense compound that hybridizes and inhibits nucleic acid encoding
PT cellular apoptosis susceptibility gene, useful for treating a
PT hyperproliferative disorder such as cancer.

XX Claim 3; Page 91; 135pp; English.

XX The invention discloses antisense compounds, of 8 - 50 nucleobases in

CC length, targeted to a nucleic acid molecule encoding a human cellular
CC apoptosis susceptibility gene (CAS or CSE1 or CSP), located on chromosome
CC 20q13. CAS has been implicated in the regulation of mitosis, apoptosis
CC and cellular proliferation and is highly expressed in some cancer cells.
CC CAS has also been shown to mediate export of importin-alpha from the
CC nucleus. Importin-alpha is a nuclear import receptor for nuclear
CC localisation signal-containing proteins and deregulation of importin
CC transport is involved in cell cycle defects. The antisense compounds
CC specifically hybridise with, and inhibit expression of, the gene or
CC specifically hybridise with an 8 nucleobase portion of its active site.
CC The antisense compounds are useful for inhibiting the expression of a
CC cellular apoptosis susceptibility gene in cells or tissues and for
CC treating an animal having a disease or condition associated with a
CC cellular apoptosis susceptibility gene, where the disease or condition is
CC a hyperproliferative disorder such as cancer, preferably breast or colon
CC cancer, degenerative disorders such as Alzheimer's disease, Parkinson's
CC disease, amyotrophic lateral sclerosis (ALS), retinitis pigmentosa and
CC blood cell disorders. The compounds are also useful for diagnostics,
CC therapeutics, prophylaxis, as research reagents and kits, for
CC distinguishing functions of various members of a biological pathway, in
CC antisense gene therapy and prophylactically (e.g. to prevent or delay
CC infection, inflammation or tumour formation). The antisense
CC oligonucleotides in ABS59252-ABS59322 are targeted to the human CAS gene

Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 381 AGCCTCCCAAAATGCTGCGA 400
DB 20 AGCCTCCCAAAATGCTGCGA 1

RESULT 485
ABS67840/c

ID ABS67840 standard; DNA; 20 BP.

XX ABS67840;

AC 29-NOV-2002 (first entry)

XX Human casein kinase 2-alpha prime antisense oligonucleotide #1.

XX Human; casein kinase 2-alpha prime; diabetes mellitus;

XX hyperproliferative disorder; breast cancer; prostate cancer;
XX liver cancer; infection; inflammation; tumour formation; cytostatic;
XX antidiabetic; antiinflammatory; antimicrobial; phosphorothioate;

XX antisense therapy; ss.

XX Homo sapiens.

XX WO200262951-A2.

XX 15-AUG-2002.

XX 01-FEB-2002; 2002WO-US002772.

XX 08-FEB-2001; 2001US-00780173.

XX (ISIS-) ISIS PHARM INC.

XX McKay R, Freier SM, Wyatt JR;

XX WPI; 2002-627539/67.

XX New antisense oligonucleotides targeted to nucleic acid encoding casein
PT kinase 2-alpha prime, useful for diagnosing and/or treating a disease or
PT condition associated with expression of casein kinase 2-alpha prime.

XX Claim 3; Page 94; 129pp; English.

XX

CC The present invention relates to antisense oligonucleotides and methods
CC for modulating the expression of human or mouse casein kinase 2- α
CC prime. The antisense oligonucleotides are useful for inhibiting the
CC expression of casein kinase 2- α prime, and for treating diseases or
CC conditions associated with aberrant expression of casein kinase 2- α
CC prime. Such diseases include diabetes mellitus, and hyperproliferative
CC disorders (particularly cancers e.g. breast cancer, prostate cancer, or
CC liver cancer). The antisense compounds are also useful for diagnostics,
CC therapeutics, prophylaxis, e.g. to prevent or delay infection,
CC inflammation or tumour formation, as research reagents and kits, and in
CC distinguishing between functions of various members of a biological
CC pathway. ABS67840-ABS67917 represent human or mouse casein kinase 2- α
CC prime antisense oligonucleotides which comprise a phosphorothioate
CC backbone
XX
SQ Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 645 CAGGCTGAGTGCAGTGGCG 664
DB 20 CAGGCTGAGTGCAGTGGCG 1

RESULT 486
AAL40355
ID AAL40355 standard; DNA; 20 BP.
XX
AC AAL40355;
XX
DT 19-SEP-2002 (first entry)
XX
DE Human caspase 6 antisense inhibition related oligo SEQ ID No 74.
XX
XX Muscular; cytosolic; neurotropic; neuroprotective; ophthalmological;
KW antiaplaemic; osteopathic; caspase 6; Rieger's syndrome; bone metabolism;
KW ataxia telangiectasia; hyperproliferative disorder; cholesterol disorder;
KW haematopoietic disorder; cancer; neurological; Alzheimer's disease;
KW apoptotic; human; ds.
XX
OS Homo sapiens.
XX
PN WO200229066-A1.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US030871.
XX
PR 04-OCT-2000; 2000US-00679299.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Brown-Driver VL, Zhang H, Watt AT;
XX
DR WPI: 2002-471315/50.
XX
PT An antisense oligonucleotide of 8 to 50 nucleotides in length that
XX inhibits caspase 6, is useful for treating Rieger's syndrome.
XX
PS Example 15; Page 89; 141pp; English.
XX
CC The invention relates to an antisense oligonucleotide compound of 8 to 50
CC nucleotides in length that is targeted to a nucleic acid molecule
CC encoding caspase 6, where the oligonucleotide specifically hybridises
CC with and inhibits the expression of caspase 6. The oligonucleotide of the
CC invention specifically hybridises to and inhibits expression of caspase 6
CC in cells or tissues. The oligonucleotides can be administered
CC therapeutically or prophylactically to treat an animal having a disease
CC or condition associated with caspase 6, such as Rieger's syndrome or
CC ataxia telangiectasia, hyperproliferative disorder, a haematopoietic
CC disorder, a bone metabolism or cholesterol disorder, various types of

CC cancer, neurological conditions such as Alzheimer's disease and other de-
CC regulated apoptotic pathological conditions. This polynucleotide sequence
CC represents a human caspase 6 oligonucleotide relating to the invention.
CC NOTE: This phosphorothioate oligonucleotide sequence has 2'-MOE wings and
CC a deoxy gap
XX
SQ Sequence 20 BP; 3 A; 4 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 TTGGTCAGGCTGCTCGAA 221
DB 1 TTGGTCAGGCTGCTCGAA 20

RESULT 487
AAL40351
ID AAL40351 standard; DNA; 20 BP.
XX
AC AAL40351;
XX
DT 19-SEP-2002 (first entry)
XX
DE Human caspase 6 antisense inhibition related oligo SEQ ID No 70.
XX
XX Muscular; cytosolic; neurotropic; neuroprotective; ophthalmological;
KW antiaplaemic; osteopathic; caspase 6; Rieger's syndrome; bone metabolism;
KW ataxia telangiectasia; hyperproliferative disorder; cholesterol disorder;
KW haematopoietic disorder; cancer; neurological; Alzheimer's disease;
KW apoptotic; human; ds.
XX
OS Homo sapiens.
XX
PN WO200229066-A1.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US030871.
XX
PR 04-OCT-2000; 2000US-00679299.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Brown-Driver VL, Zhang H, Watt AT;
XX
DR WPI: 2002-471315/50.
XX
PT An antisense oligonucleotide of 8 to 50 nucleotides in length that
XX inhibits caspase 6, is useful for treating Rieger's syndrome.
XX
PS Claim 3; Page 89; 141pp; English.
XX
CC The invention relates to an antisense oligonucleotide compound of 8 to 50
CC nucleotides in length that is targeted to a nucleic acid molecule
CC encoding caspase 6, where the oligonucleotide specifically hybridises
CC with and inhibits the expression of caspase 6. The oligonucleotide of the
CC invention specifically hybridises to and inhibits expression of caspase 6
CC in cells or tissues. The oligonucleotides can be administered
CC therapeutically or prophylactically to treat an animal having a disease
CC or condition associated with caspase 6, such as Rieger's syndrome or
CC ataxia telangiectasia, hyperproliferative disorder, a haematopoietic
CC disorder, a bone metabolism or cholesterol disorder, various types of
CC cancer, neurological conditions such as Alzheimer's disease and other de-
CC regulated apoptotic pathological conditions. This polynucleotide sequence
CC represents a human caspase 6 oligonucleotide relating to the invention.
CC NOTE: This phosphorothioate oligonucleotide sequence has 2'-MOE wings and
CC a deoxy gap
XX
SQ Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 387 CCAAGTCTGGGATTACAG 406
DB 1 CCAAGTCTGGGATTACAG 20

RESULT 488

ABL40354
ID ABL40354 standard; DNA; 20 BP.

AC AAL40354;

DT 19-SEP-2002 (first entry)

DE Human caspase 6 antisense inhibition related oligo SEQ ID No 73.

XX Muscular; cytosolic; neurotrophic; neuroprotective; ophthalmological;
XX anti-leukemic; osteopathic; caspase 6; Rieger's syndrome; bone metabolism;
XX ataxia telangiectasia; hyperproliferative disorder; cholesterol disorder;
XX haematopoietic disorder; cancer; neurological; Alzheimer's disease;
XX apoptotic; human; ds.

OS Homo sapiens.

PN WO200229066-A1.

PD 11-APR-2002.

PF 03-OCT-2001; 2001WO-US030871.

PR 04-OCT-2000; 2000US-00679299.

XX (ISIS-) ISIS PHARM INC.

PI Brown-Driver VL, Zhang H, Watt AT;

DR WPI; 2002-471315/50.

PT An antisense oligonucleotide of 8 to 50 nucleotides in length that
XX inhibits caspase 6, is useful for treating Rieger's syndrome.

PS Claim 3; Page 89; 141pp; English.

XX The invention relates to an antisense oligonucleotide compound of 8 to 50
XX nucleotides in length that is targeted to a nucleic acid molecule
XX encoding caspase 6, where the oligonucleotide specifically hybridises
XX with and inhibits the expression of caspase 6. The oligonucleotide of the
XX invention specifically hybridises to and inhibits expression of caspase 6
XX in cells or tissues. The oligonucleotides can be administered
XX therapeutically or prophylactically to treat an animal having a disease
XX or condition associated with caspase 6, such as Rieger's syndrome or
XX ataxia telangiectasia, hyperproliferative disorder, a haematopoietic
XX disorder, a bone metabolism or cholesterol disorder, various types of
XX cancer, neurological conditions such as Alzheimer's disease and other de-
XX regulated apoptotic pathological conditions. This polynucleotide sequence
XX represents a human caspase 6 oligonucleotide relating to the invention.
XX NOTE: This phosphorothioate oligonucleotide sequence has 2'-MOE wings and
XX a deoxy gap

SO Sequence 20 BP; 3 A; 9 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03; Indels 0; Gaps 0;

QY 211 CTGCTCTGGAAGTCCGACC 230
DB 1 CTGCTCTGGAAGTCCGACC 20

RESULT 489

ABL44512/C
ID ABL44512 standard; DNA; 20 BP.

AC ABL44512;

DT 11-APR-2002 (first entry)

DE Human chromosome 1p36-35 PCR primer SEQ ID NO:1556.

XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
XX PCR primer; ss.

OS Homo sapiens.

PN JP2001321190-A.

PD 20-NOV-2001.

PF 12-MAR-2001; 2001JP-00068285.

PR 10-MAR-2000; 2000JP-00066716.

XX (RIKA) RIKAGAKU KENKYUSHO.

PA (GENO-) GENOTEX YG.

DR WPI; 2002-144136/19.

PT Arraying genome clones.

PS Claim 4; Page 35; 528pp; Japanese.

XX The present invention describes a method of arraying genome clones. The
XX method comprises: (a) clones of the genomic libraries contained in
XX multiwell plates numbered for discrimination are mixed in each of the
XX multiwell plates; (b) a primer designed based on the chromosome marker
XX sequence is added to the mixture to carry out an amplification reaction;
XX (c) a signal corresponding to the marker is detected from the resultant
XX amplified product to specify the discrimination Nos. of the multiwell
XX plates containing the clones having said marker sequence; (d) the order
XX of the markers is changed so that the same discrimination Nos. succeed to
XX the maximum in the specified discrimination Nos. to array the multiwell
XX plates; (e) the clones in the multiwell plates of the specified
XX discrimination Nos. are mixed respectively in each wells of longitudinal
XX and lateral directions; (f) the mixed clones are cultured and the
XX resultant cultures are amplified by using the above primer; (g) signals
XX are detected from the amplified products; (h) the clones in the multiwell
XX plates are specified from the detected result; and (i) the clones are
XX reconstituted as the positions on the chromosome and arrayed. The
XX microarray is useful for gene analysis. ABL42957 to ABL45322 represent
XX PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
XX represent PCR primers for human chromosome 21q22.1, which are
XX specifically claimed for use in the present invention

SO Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03; Indels 0; Gaps 0;

QY 542 CTCAGCTCCCAAGTAGCTG 561
DB 20 CTCAGCTCCCAAGTAGCTG 1

RESULT 490

ABL44004
ID ABL44004 standard; DNA; 20 BP.

AC ABL44004;

DT 11-APR-2002 (first entry)

DE Human chromosome 1p36-35 PCR primer SEQ ID NO:1048.

XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX JP2001321190-A.
XX
XX 20-NOV-2001.
XX
XX 12-MAR-2001; 2001JP-00068285.
XX
XX 10-MAR-2000; 2000JP-00066716.
XX
XX (RIKA) RIKAGAKU KENKYUSHO.
XX (GENO-) GENOTEX YG.
XX
XX WPI; 2002-144136/19.
XX
XX Arraying genome clones.
XX
XX Claim 4; Page 25; 528pp; Japanese.
XX
XX The present invention describes a method of arraying genome clones. The
CC method comprises: (a) clones of the genomic libraries contained in
CC multiwell plates numbered for discrimination are mixed in each of the
CC multiwell plates; (b) a primer designed based on the chromosome marker
CC sequence is added to the mixture to carry out an amplification reaction;
CC (c) a signal corresponding to the marker is detected from the resultant
CC amplified product to specify the discrimination Nos. of the multiwell
CC plates containing the clones having said marker sequence; (d) the order
CC of the markers is changed so that the same discrimination Nos. succeed to
CC the maximum in the specified discrimination Nos. to array the multiwell
CC plates; (e) the clones in the multiwell plates of the specified
CC discrimination Nos. are mixed respectively in each well of longitudinal
CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals
CC are detected from the amplified products; (h) the clones in the multiwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstituted as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention
XX
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 384 CTCGCCAAGTCTGGGATTG 403
DB 1 CTCGCCAAGTCTGGGATTG 20
RESULT 491
ABA92187
ID ABA92187 standard; DNA; 20 BP.
XX
XX ABA92187;
XX
XX 06-JUN-2002 (first entry)
XX
XX Polymorphism 506B13CA1 reverse PCR primer.
XX
XX NALPN; nycetalopin; human; congenital stationary night blindness; CSNB;
KW glycosylphosphatidylinositol; GPI; proteoglycan; retina; polymorphism;
KW marker; PCR; primer; ss.
XX
XX Homo sapiens.
OS
XX
XX CA2306241-A1.
PN

XX
PD 12-NOV-2001.
XX
XX 12-MAY-2000; 2000CA-02306241.
XX
XX 12-MAY-2000; 2000CA-02306241.
XX
XX (BECH/) BECH-HANSEN N T.
XX
XX Bech-Hansen NT;
XX
XX WPI; 2002-242157/30.
XX
XX Novel purified mammalian retinal, kidney glycosylphosphatidylinositol-
PT anchored small leucine-rich proteoglycan and polymucopolysaccharides encoding
PT them used to diagnose complete X-linked congenital stationary night
PT blindness.
XX
XX Example 1; Page 28; 44pp; English.
XX
XX The present sequence is that of a reverse primer used, with the forward
CC primer given in ABA92186, in PCR analysis of polymorphism 506B13CA1
CC (DXS10042). This was 1 of 3 novel markers identified in a genotype
CC analysis of X-linked congenital stationary night blindness (CSNB)
CC families. The new, and some previously known, markers allowed an analysis
CC of selected recombinant X chromosomes to determine the CSNB1 minimal
CC region. To identify candidate genes for the CSNB1 locus, a robust
CC physical map of the CSNB1 minimal region in Xp11.4 was developed. This
CC identified the NALPN gene encoding nycetalopin (see AM51108). An extended
CC NALPN cDNA sequence (see ABA92185) was established by sequencing of PCR
CC and RAGE products obtained from retinal RNA. 11 different mutations were
CC identified in NALPN, none of which were observed in normal individuals.
CC These included missense mutations, insertions and deletions of the coding
CC region that are predicted to disrupt specific functions of nycetalopin.
CC and may be informative as to the structure-function relationship of the
CC protein. Such information may be useful for targeting therapy for retinal
CC disease. Identification of the NALPN gene will also provide a tool for
CC the diagnosis of complete X-linked CSNB in individuals suspected of
CC having this disorder
XX
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 385 TCCCAAGTCTGGGATTAC 404
DB 1 TCCCAAGTCTGGGATTAC 20
RESULT 492
ABA92208
ID ABA92208 standard; DNA; 20 BP.
XX
XX ABA92208;
XX
XX 06-JUN-2002 (first entry)
XX
XX Reverse PCR primer for polymorphism 506B13CA1.
XX
XX NYX; nycetalopin; human; congenital stationary night blindness; CSNB;
KW glycosylphosphatidylinositol; GPI; retina; SLP; SLP;
KW small leucine-rich proteoglycan; therapy; diagnosis; PCR; primer; ss.
XX
XX Homo sapiens.
OS
XX
XX CA2345915-A1.
XX
XX 12-NOV-2001.
PD
XX
XX 14-MAY-2001; 2001CA-02345915.
XX

PR 12-MAY-2000; 2000CA-02306241.
XX (BECH/) BECH-HANSEN N T.
PA
XX Bech-Hansen NT;
PI
XX WPI; 2002-242185/30.
DR
XX
XX Novel purified mammalian glycosyl-inositol phospholipid-anchored small
PT leucine-rich proteoglycan, and genes encoding proteoglycan which are
PT useful for diagnosing complete X-linked congenital stationary night
PT blindness.
PS
XX Example 1; Page 26; 65pp; English.
XX
XX The present sequence is that of a reverse primer used, with the forward
CC primer given in ABA92207, in PCR analysis of polymorphism 506B13CA1
CC (DXS10042). This was 1 of 3 novel markers identified in a genotype
CC analysis of X-linked congenital stationary night blindness (CSNB)
CC families. The new, and some previously known, markers allowed an analysis
CC of selected recombinant X chromosomes to determine the CSNB1 minimal
CC region. To identify candidate genes for the CSNB1 locus, a robust
CC physical map of the CSNB1 minimal region in Xp11.4 was developed. This
CC identified the NYX gene encoding nyctalopin (see AAMS1131). An extended
CC NYX cDNA sequence (see ABA92206) was established by sequencing of PCR and
CC RACE products obtained from retinal RNA. 14 different mutations were
CC identified in NYX genes from different CSNB families, none of which were
CC observed in normal individuals. These included missense, insertion, stop
CC and deletion mutations that are predicted to disrupt specific functions
CC of nyctalopin. The invention provides a method and kit for diagnosing
CC complete X-linked CSNB, which involves screening for alterations in the
CC gene nucleotide sequence. It also provides a method of screening drug
CC candidates that affect nyctalopin expression or production
SQ
XX Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 385 TCCCAAGTCTGGATTAC 404
DB 1 TCCCAAGTCTGGATTAC 20
RESULT 493
AAS96659
ID AAS96659 standard; DNA; 20 BP.
XX
AC AAS96659;
XX
DT 09-APR-2002 (first entry)
XX
DE Telomerase reverse transcriptase, antisense oligonucleotide #69.
XX
XX Telomerase reverse transcriptase; TERT; cytosolic; apoptosis;
KM cell growth inhibitor; antisense oligonucleotide; antisense technology;
KM ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200188198-A1.
PN
XX 22-NOV-2001.
PD
XX 15-MAY-2001; 2001WO-US015774.
PF
XX 16-MAY-2000; 2000US-00572423.
PR 07-DEC-2000; 2000US-00733294.
XX
XX (ISIS-) ISIS PHARM INC.
XX

PI Monia BP, Gaarde WA, Freier SM, Mancewicz E;
XX
XX WPI; 2002-075321/10.
DR
XX
XX New compound targeted to nucleic acid molecule encoding telomerase
PT transcriptase (TERT), which specifically hybridizes with and inhibits
PT expression of TERT, useful for modulating apoptosis and inhibiting cell
PT growth.
PS
XX Example 19; Page 91; 154pp; English.
XX
XX The invention describes a compound, 8-50 nucleobases in length targeted
CC to a nucleic acid molecule encoding human TERT (telomerase reverse
CC transcriptase), where the compound specifically hybridizes with and
CC inhibits the expression of TERT. A series of oligonucleotides were
CC designed to target different regions of the human TERT RNA. These were 20
CC nucleotides in length and composed of a central gap region consisting of
CC ten 2'-deoxynucleotides, flanked on both sides (5' and 3' directions) by
CC five-nucleotide wings. The wings were composed of 2'-methoxyethyl (2'-
CC MOE) nucleotides. The compounds were analysed for their effect on human
CC TERT mRNA levels by reverse transcriptase (RT)-polymerase chain reaction
CC (PCR). The compound is useful for inhibiting the expression of TERT in
CC cells or tissues, for treating a human having the expression of TERT
CC associated with TERT, for modulating apoptosis, for inhibiting cell
CC growth (preferably, cancer cell growth), in antisense therapy and for
CC diagnostics and therapeutics. This sequence is an antisense
CC oligonucleotide used to modulate the activity of nucleic acid molecules
CC encoding TERT, described in the method of the invention
SQ
XX Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 863 TGCTGGATTACAGCGCTA 882
DB 1 TGCTGGATTACAGCGCTA 20
RESULT 494
ABK91100/c
ID ABK91100 standard; DNA; 20 BP.
XX
AC ABK91100;
XX
DT 05-DEC-2002 (first entry)
XX
DE PCR primer Alu3, for human DNA derived from chromosome 21.
XX
XX Human; fluorescent labelling technique; fluorescent intercalating dye;
KM nucleic acid detection; electrophoresis; diagnostic assay;
KM cell labelling; PCR; primer; ss.
XX
XX Homo sapiens.
OS
XX US6428667-B1.
PN
XX 06-AUG-2002.
PD
XX 10-OCT-2000; 2000US-00686147.
PF
XX 14-MAR-1990; 90US-00493307.
PR 06-FEB-1992; 92US-00831823.
PR 02-DEC-1993; 93US-00161231.
PR 07-NOV-1997; 97US-00966398.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Glazer AN, Mathies RA, Peck K;
XX
XX WPI; 2002-722081/78.
XX

PT Detection of separated molecules involves use of a group comprising a
 PT double stranded DNA probe and fluorescent molecule.
 PS Disclosure; Col 8; 7pp; English.
 XX
 CC The present invention relates to novel fluorescent labelling techniques
 CC and fluorescent labels. The method and compositions of the invention are
 CC useful for detecting molecules using fluorescent labels where fluorescent
 CC intercalating dyes have strong non-covalently binding affinities for the
 CC DNA. The method is useful for detecting molecules e.g. nucleic acids,
 CC in electrophoresis methods. The method can also be applied to diagnostic
 CC assays and cell labelling. The fluorescent label is sensitive, stable and
 CC resistant to self-quenching. The present sequence represents a PCR primer
 CC used to amplify human DNA derived from chromosome 21
 SQ Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
 QY Query Match 2.0%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 388 CAAAGTGTGGGATTACAGG 407
 Db 20 CAAAGTGTGGGATTACAGG 1
 XX
 RESULT 495
 ACC40946
 ID ACC40946 standard; DNA; 20 BP.
 XX
 AC ACC40946;
 XX
 DT 23-MAY-2003 (first entry)
 XX
 DE Human superoxide dismutase 1 antisense inhibitor # ISIS 150500.
 XX
 KM Human; superoxide dismutase 1; antisense; neuroprotective; cyostatic;
 KM antiinflammatory; amyotrophic lateral sclerosis; apoptosis;
 KM hyperproliferative disorder; therapy; infection; inflammation; tumour;
 KM ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FT Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate linkages. All cytosines are 5-
 FT methylcytosine"
 FT modified_base 1..5
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 XX
 PN WO2003000707-A2.
 XX
 PD 03-JAN-2003.
 XX
 PF 19-JUN-2002; 2002WO-US019664.
 XX
 PR 21-JUN-2001; 2001US-00886360.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett FC, Doble K;
 XX
 DR WPI; 2003-184032/18.
 XX

PT Novel antisense compounds targeted to nucleic acids encoding human
 PT superoxide dismutase 1, for modulating expression of the dismutase and
 PT treating diseases or conditions, e.g. amyotrophic lateral sclerosis.
 PS Example 15; Page 77; 107pp; English.
 XX
 CC The invention relates to a compound of 8-50 nucleobases in length,
 CC targeted to a nucleic acid molecule encoding human superoxide dismutase
 CC 1. The compound specifically hybridises with and inhibits the expression
 CC of human superoxide dismutase 1 by hybridising with at least an 8-
 CC nucleobase portion of the nucleic acid molecule encoding the active site
 CC of the enzyme. The activity of compounds of the invention may be
 CC described as neuroprotective, cyostatic and antiinflammatory. The
 CC mechanism of action of compounds of the invention is antisense inhibition
 CC of human superoxide dismutase 1 expression by chimeric phosphorothioate
 CC oligonucleotides having 2'-methoxyethyl (2'-MOE) wings and a decoy gap.
 CC Compounds of the invention are useful for inhibiting the expression of
 CC human superoxide dismutase 1 in human cells or tissues, and for treating
 CC a disease or condition associated with this enzyme (antisense therapy),
 CC especially amyotrophic lateral sclerosis, a disease or condition arising
 CC from aberrant apoptosis and a hyperproliferative disorder. It may also be
 CC used in diagnostics, therapeutics and as a research reagent, e.g.
 CC prophylactically to prevent or delay infection, inflammation or tumour
 CC formation. Sequences given in records ACC40880-ACC40957 represent human
 CC superoxide dismutase 1 antisense inhibitor oligonucleotides
 SQ Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
 QY Query Match 2.0%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 729 AGTAGCTGGAGCTACAGGCG 748
 Db 1 AGTAGCTGGAGCTACAGGCG 20
 XX
 RESULT 496
 ABZ79385
 ID ABZ79385 standard; DNA; 20 BP.
 XX
 AC ABZ79385;
 XX
 DT 01-MAY-2003 (first entry)
 XX
 DE Acetyl-Coenzyme A-carboxylase-alpha gene PCR primer, SEQ ID 72.
 XX
 KM Human; enzyme; acetyl-Coenzyme A-carboxylase-alpha; ACC-alpha; cancer;
 KM breast; ovary; PCR; primer; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO2002100896-A2.
 XX
 PD 19-DEC-2002.
 XX
 PF 12-JUN-2002; 2002WO-FR002015.
 XX
 PR 13-JUN-2001; 2001FR-00007740.
 XX
 PR 05-MAR-2002; 2002FR-00002788.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 PA (UCLY-) UNIV LYON 1 BERNARD CLAUDE.
 XX
 PI Dalla Venezia NL, Magnard CM, Lenoir GM, Similnikova-Brard O;
 XX
 DR WPI; 2003-175165/17.
 XX
 PT In vitro diagnosis of cancer, particularly breast and ovarian cancer, or
 PT susceptibility, comprises detecting alterations in the acetyl coenzyme A-
 PT carboxylase alpha gene or protein expression.
 XX
 PS Example 1; Page 11; 56pp; French.


```

XX The present invention relates to human acetyl-Coenzyme A-carboxylase-
CC alpha (ACC-alpha; see AB279442), which can be used for in vitro diagnosis
CC of cancer (or of an increased risk of developing it), by detecting ACC-
CC alpha gene mutations or polymorphisms, or altered ACC-alpha protein
CC expression, relative to a control population. The method is particularly
CC used to diagnose cancer, especially of breast or ovary, or for assessing
CC the risk of developing such cancers. The present sequence is a PCR
CC primer, which was used in an example from the invention
XX
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
XX
Query Match      2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 385 TCCCAAGTCTGGGATTAC 404
DB 1 TCCCAAGTCTGGGATTAC 20
XX
RESULT 497
ID AAL60008/c
XX AAL60008 standard; DNA; 20 BP.
XX
AC AAL60008;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human GH-1 gene amplifying PCR primer, CRV156.lpl.
XX
KW Human; growth hormone 1; GH-1; single nucleotide polymorphism; SNP;
KW gene therapy; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO2003042226-A2.
XX
PD 22-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US035719.
XX
PR 09-NOV-2001; 2001US-0347448P.
XX
PA (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI Wood LS, Wagner S, Parodi LA;
XX
DR WPI; 2003-449555/42.
XX
PT New growth hormone 1 (GH-1) diagnostic polynucleotide, useful as markers
PT for the analysis of a disease, or of susceptibility to drug treatment for
PT GH-1 dysfunction or other diseases.
XX
PS Example 2; Page 30; 74pp; English.
XX
CC The invention relates to growth hormone 1 (GH-1) gene including single
CC nucleotide polymorphisms (SNP). The GH-1 diagnostic polynucleotide is
CC useful as markers for the analysis of a disease, of susceptibility to
CC drug treatment for GH-1 dysfunction or other diseases, or may be included
CC in any complete or partial genetic map of the human genome. GH-1 mutant
CC polypeptides are useful as antagonists of GH-1 hormone action.
CC Polynucleotides encoding these polypeptides are useful in gene therapy.
CC The present sequence is a PCR primer used for amplifying human GH-1 gene
XX
SQ Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match      2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 387 CCAAGTCTGGGATTACAG 406
DB 1 CCAAGTCTGGGATTACAG 20
XX

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DB 20 CCAAGTCTGGGATTACAG 1
XX
RESULT 498
ID ADD21702/c
XX ADD21702 standard; DNA; 20 BP.
XX
AC ADD21702;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #265.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW atherosclerosis; restenosis; apoptosis modulation; p21; ss;
KW 2'-methoxyethoxy-residue; phosphorothioate backbone.
XX
OS Homo sapiens.
XX
PN WO2003048315-A2.
XX
PD 12-JUN-2003.
XX
PF 02-DEC-2002; 2002WO-US038281.
XX
PR 04-DEC-2001; 2001US-00005344.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Miraglia LJ, Nero PS, Graham MJ, Monia BP, Koller E, Chiang MY;
PI Manoharan M;
XX
DR WPI; 2003-57263/54.
XX
PT Novel antisense compound targeted to 5' untranslated region, coding
PT region, or intron-exon junction of nucleic acid molecule encoding mdm2,
PT useful for treating e.g. cancer, psoriasis or restenosis by inhibiting
PT mdm2 expression.
XX
PS Example 9; SEQ ID NO 267; 289pp; English.
XX
CC The invention comprises antisense oligonucleotides which are targeted to
CC the human mdm2 gene. The antisense oligonucleotides of the invention are
CC useful for reducing hyperproliferation of human cells. The antisense
CC oligonucleotides are also useful for treating: hyperproliferative
CC disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or
CC restenosis. The antisense oligonucleotides are also useful for modulating
CC apoptosis, and for increasing expression of p21. The present DNA sequence
CC represents a human mdm2 gene antisense oligonucleotide of the invention.
CC The present sequence contains 2'-methoxyethoxy-residues and has a
CC phosphorothioate backbone.
XX
SQ Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
XX
Query Match      2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 388 CCAAGTCTGGGATTACAG 407
DB 20 CCAAGTCTGGGATTACAG 1
XX
RESULT 499
ID ADD21701/c
XX ADD21701 standard; DNA; 20 BP.
XX
AC ADD21701;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #264.
XX

```

XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KM hyperproliferative disorder; cancer; psoriasis; fibrosis;
KM atherosclerosis; restenosis; apoptosis modulation; p21; ss;
KM 2'-methoxyethoxy-residue; phosphorothioate backbone.
XX
OS Homo sapiens.
XX
XX WO2003048315-A2.
XX
XX 12-JUN-2003.
XX
XX 02-DEC-2002; 2002WO-US038281.
XX
XX 04-DEC-2001; 2001US-00005344.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Miraglia LJ, Nero PS, Graham MJ, Monia BP, Koller E, Chiang MY,
PI Manoharan M;
XX
XX WPI; 2003-577263/54.
XX
XX Novel antisense compound targeted to 5' untranslated region, coding
PT region, or intron:exon junction of nucleic acid molecule encoding mdm2,
PT useful for treating e.g. cancer, psoriasis or restenosis by inhibiting
PT mdm2 expression.
XX
XX Example 9; SEQ ID NO 266; 289pp; English.
XX
XX The invention comprises antisense oligonucleotides which are targeted to
CC the human mdm2 gene. The antisense oligonucleotides of the invention are
CC useful for reducing hyperproliferation of human cells. The antisense
CC oligonucleotides are also useful for treating: hyperproliferative
CC disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or
CC restenosis. The antisense oligonucleotides are also useful for modulating
CC apoptosis, and for increasing expression of p21. The present DNA sequence
CC represents a human mdm2 gene antisense oligonucleotide of the invention.
CC The present sequence contains 2'-methoxyethoxy-residues and has a
CC phosphorothioate backbone.
XX
XX Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 851 GGCTTCGCCAAAGTGCTGGGA 870
DB 20 GGCTTCGCCAAAGTGCTGGGA 1
RESULT 500
ADD21677/c
ID ADD21677 standard; DNA; 20 BP.
XX
XX ADD21677;
AC
XX
XX 15-JAN-2004 (first entry)
DT
XX
XX Human mdm2 antisense oligonucleotide #240.
DE
XX
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KM hyperproliferative disorder; cancer; psoriasis; fibrosis;
KM atherosclerosis; restenosis; apoptosis modulation; p21; ss;
KM 2'-methoxyethoxy-residue; phosphorothioate backbone.
XX
XX Homo sapiens.
OS
XX
XX WO2003048315-A2.
PN
XX
XX 12-JUN-2003.
PD
XX

PF 02-DEC-2002; 2002WO-US038281.
XX
XX 04-DEC-2001; 2001US-00005344.
PR
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Miraglia LJ, Nero PS, Graham MJ, Monia BP, Koller E, Chiang MY,
PI Manoharan M;
XX
XX WPI; 2003-577263/54.
XX
XX Novel antisense compound targeted to 5' untranslated region, coding
PT region, or intron:exon junction of nucleic acid molecule encoding mdm2,
PT useful for treating e.g. cancer, psoriasis or restenosis by inhibiting
PT mdm2 expression.
XX
XX Example 9; SEQ ID NO 242; 289pp; English.
XX
XX The invention comprises antisense oligonucleotides which are targeted to
CC the human mdm2 gene. The antisense oligonucleotides of the invention are
CC useful for reducing hyperproliferation of human cells. The antisense
CC oligonucleotides are also useful for treating: hyperproliferative
CC disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or
CC restenosis. The antisense oligonucleotides are also useful for modulating
CC apoptosis, and for increasing expression of p21. The present DNA sequence
CC represents a human mdm2 gene antisense oligonucleotide of the invention.
CC The present sequence contains 2'-methoxyethoxy-residues and has a
CC phosphorothioate backbone.
XX
XX Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 937 CTGTACCCAGGCTGGAGTG 956
DB 20 CTGTACCCAGGCTGGAGTG 1
RESULT 501
AB297911
ID AB297911 standard; DNA; 20 BP.
XX
XX AB297911;
AC
XX
XX 17-OCT-2003 (first entry)
DT
XX
XX Human RANTES oligonucleotide sequence.
DE
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KM antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KM antisense gene therapy; respiratory; lung; adenosine sensitivity;
KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KM lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200285308-A2.
FN
XX
XX 31-OCT-2002.
PD
XX
XX 23-APR-2002; 2002WO-US013135.
PF
XX
XX 24-APR-2001; 2001US-0286137P.
PR
XX
XX (EPIC-) EPIGENESIS PHARM INC.
PA
XX
XX Nyce JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
DR

XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ublquinone.
XX
PS Disclosure; SEQ ID NO 13153; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ublquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine or
CC receptor, producing bronchodilation, increasing levels of ublquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 732 AGCTGGACTACAGCGCCCC 751
DB 1 AGCTGGACTACAGCGCCCC 20
XX
RESULT 502
ABZ99076
ID ABZ99076 standard; DNA: 20 BP.
XX
AC ABZ99076;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human PDE4C oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ublquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ublquinone.
XX
PS Disclosure; SEQ ID NO 14318; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ublquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine or
CC receptor, producing bronchodilation, increasing levels of ublquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. NO. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 379 TCAGCTCCCAAGTGTGG 398
DB 1 TCAGCTCCCAAGTGTGG 20
XX
RESULT 503
ABZ98014
ID ABZ98014 standard; DNA: 20 BP.
XX
AC ABZ98014;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human RANTES oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ublquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Discloure; SEQ ID NO 13256; 872bp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 3 A; 4 C; 10 G; 3 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 646 AGGCTGAGTGCAGTGGCGC 665
DB 1 AGGCTGAGTGCAGTGGCGC 20
XX
RESULT 504
ABZ99055
ID ABZ99055 standard; DNA; 20 BP.
XX
AC ABZ99055;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human PDE4C oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
FN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI, 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Discloure; SEQ ID NO 14297; 872bp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 3 A; 5 C; 9 G; 3 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 643 CCCAGGCTGAGTGCAGTGG 662
DB 1 CCCAGGCTGAGTGCAGTGG 20
XX
RESULT 505
ABZ99075
ID ABZ99075 standard; DNA; 20 BP.
XX
AC ABZ99075;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human PDE4C oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
FN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI, 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

PS Disclosure; SEQ ID NO 14317; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 20 BP; 2 A; 12 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.le+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 TCCACCTGCTCAGCCTCCC 388
DB 1 TCCACCTGCTCAGCCTCCC 20

RESULT 506
ABZ92715
ID ABZ92715 standard; DNA; 20 BP.

XX ABZ92715;

XX 17-OCT-2003 (first entry)

XX Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

PS Disclosure; SEQ ID NO 7957; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 20 BP; 4 A; 9 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.le+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 540 GCCTCAGCTCCCAAGTAGC 559
DB 1 GCCTCAGCTCCCAAGTAGC 20

RESULT 507
ABZ92716
ID ABZ92716 standard; DNA; 20 BP.

XX ABZ92716;

XX 17-OCT-2003 (first entry)

XX Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 7958; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 4 A; 7 C; 6 G; 3 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 546 GCCTCCCAAGTAGCTGGAC 565
DB 1 GCCTCCCAAGTAGCTGGAC 20
XX
RESULT 508
ABZ99068
ID ABZ99068 standard; DNA; 20 BP.
XX
AC ABZ99068;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human PDE4C oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002MO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandraseagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shanabuddin S;
XX WPI; 2003-229219/22.
DR

XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 14310; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 5 A; 0 C; 5 G; 10 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 772 TTGTATTTTTRAGTAGAGATG 791
DB 1 TTGTATTTTTRAGTAGAGATG 20
XX
RESULT 509
ABX94882
ID ABX94882 standard; CDNA; 20 BP.
XX
AC ABX94882;
XX
DT 13-AUG-2003 (first entry)
XX
DE Human MBHBK receptor P2Y34 PCR primer #4.
XX
XX Human; receptor; MBHBK receptor; P2Y34 receptor; chromosome 1;
KW G protein-coupled receptor; immunomodulatory; gastrointestinal;
KW antiinflammatory; cardiovascular; gene therapy; intestinal function;
KW blood pressure; blood flow; blood coagulation; haematopoiesis;
KW interleukin; prostaglandin; inflammation; neuronal function; cell growth;
KW differentiation; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN DE10142478-A1.
XX
PD 20-MAR-2003.
XX
PF 31-AUG-2001; 2001DE-01042478.
XX
PR 31-AUG-2001; 2001DE-01042478.
XX
PA (BRUE/) BRUES M.
XX (BOEN/) BOENISCH H.
PA (VKUE/) VON KUEGELGEN I.
XX
PI Brues M, Boenisch H, Von Kuegelgen I;
XX

DR WPI; 2003-383212/37.
XX New human gene P2Y34 and encoded G protein-coupled receptor, useful for
PT treatment and diagnosis of receptor-associated diseases and for drug
PT screening.
PS Disclosure; Page 2; 6pp; German.
XX
XX This invention describes a novel human G protein-coupled receptor MBHBK
CC type, designated P2Y34 which is located on chromosome 1. The product of
CC the invention has immunomodulatory, gastrointestinal, anti-inflammatory
CC and cardiovascular activity, and can be used for gene therapy. The
CC receptor described in the disclosure may be implicated in regulation of
CC intestinal function, blood pressure, blood flow through organs and
CC regions of the body; blood coagulation, haematopoiesis and immune
CC reactions; release of interleukins and prostaglandins, i.e. in
CC inflammation; modulation of neuronal function and cell growth and
CC differentiation. The polynucleotide of the invention which encodes a G
CC protein-coupled receptor, and also its related cDNA, mRNA, protein,
CC antibodies and oligonucleotides, are useful in the diagnosis and
CC treatment of diseases associated with abnormal levels of P2Y34 expression
CC in screening assays for modulators, potential therapeutic agents; and
CC to produce transgenic animals, e.g. for identifying diseases associated
CC with abnormal expression of P2Y34. This sequence represents a PCR primer
CC used to amplify the gene encoding the human P2Y34 protein
XX
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 379 TCAGCTCCCAAGTGTGG 398
DB 1 TCAGCTCCCAAGTGTGG 20
RESULT 510
ADL25066/C
ID ADL25066 standard; DNA; 20 BP.
XX
XX ADL25066;
AC
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX Intestinal epithelium/peyer's patch M cell-associated PCR primer #211.
DE
XX Intestinal epithelium cell development; peyer's patch M cell development;
XX inflammatory bowel disease; glutenenteropathy; infectious disease;
KW autoimmune disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;
KW Grave's disease; multiple sclerosis; allergy; asthma; diabetic mellitus;
KW immune system disorder; hypersensitivity; anaphylaxis;
KW blood group incompatibility; ss; human; PCR; primer.
XX
XX Homo sapiens.
OS
XX
XX WO200280852-A2.
PN
XX
XX 17-OCT-2002.
PD
XX
XX 04-APR-2002; 2002WO-US010873.
PF
XX
XX 04-APR-2001; 2001US-0281416P.
PR
XX
XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
PA
XX
XX Brayden DJ, Byrne D, O'mahony DJ, Evans CF, Mah SP, Lo DD;
PI
XX
XX WPI; 2003-075470/07.
DR
XX
XX Novel isolated or purified polypeptide encoded by genes associated with
PT intestinal epithelium or M cell development, differentiation or function,
PT useful for treating autoimmune diseases and infectious diseases.

XX
PS Disclosure; SEQ ID NO 576; 152pp; English.
XX
XX The invention comprises DNA sequences which are associated with
CC intestinal epithelium and peyer's patch M cells. The DNA sequences of the
CC invention are useful for assessing, modifying, modulating or regulating
CC intestinal epithelium or M cell development. The DNA sequences of the
CC invention are also useful in the treatment of: inflammatory bowel
CC disease, glutenenteropathy, infectious diseases, autoimmune diseases
CC (e.g. haemolytic anaemia, rheumatoid arthritis, dermatitis, Grave's
CC disease, multiple sclerosis, allergy, asthma and diabetic mellitus),
CC diseases or disorders of the immune system, hypersensitivity,
CC anaphylaxis, and blood group incompatibility. The present DNA sequence
CC represents a PCR primer that was used to amplify an intestinal
CC epithelium/peyer's patch M cell-associated DNA sequence of the invention.
XX
SQ Sequence 20 BP; 4 A; 9 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 864 GCTGGATTACAGCGCTGAG 883
DB 20 GCTGGATTACAGCGCTGAG 1
RESULT 511
ADM65742
ID ADM65742 standard; DNA; 20 BP.
XX
XX ADM65742;
AC
XX
XX 03-JUN-2004 (first entry)
DT
XX
XX Human Y chromosome non-recombining region polymorphic fragment #301.
DE
XX ethnic origin determination; polymorphic site determination;
KW Y chromosome; paternity testing; forensic; diagnosis;
KW non-recombining region; human; NRY; polymorphic fragment; ds.
XX
XX Homo sapiens.
OS
XX
XX US2003134285-A1.
PN
XX
XX 17-JUL-2003.
PD
XX
XX 01-NOV-2001; 2001US-00002623.
PF
XX
XX 01-NOV-2000; 2000US-0245355P.
PR
XX
XX (OEFN/) OEFNER P J.
PA (UNDE/) UNDERHILL P A.
PI
XX
XX Oefner PJ, Underhill PA;
PI
XX
XX WPI; 2003-843259/78.
DR
XX
XX Determining the ethnic origin of a male by obtaining a nucleic acid
PT sample from the male and identifying at least two polymorphic markers in
PT the nucleic acid sample indicative of the ethnic origin of the male.
XX
XX Claim 24; Page 65; 74pp; English.
PS
XX
XX The invention describes a method of determining the ethnic origin of a
CC male comprising obtaining a nucleic acid sample from the male, and
CC identifying at least two polymorphic markers in the nucleic acid sample
CC indicative of the ethnic origin of the male, using at least one primer
CC pair from the primer pairs given in the specification. Also described is
CC a method of: identifying polymorphic sites in a nucleic acid; a kit for
CC determining the ethnic origin of an individual; determining the ethnic
CC origin of a human male individual; an isolated nucleic acid segment of a
CC human Y chromosome comprising at least 10 contiguous bases including at

CC least one of the polymorphic sites given in the specification; nucleic
CC acid primer pairs for amplifying polymorphic regions of the Y chromosome
CC given in the specification; and determining the paternity of a human male
CC individual. The method is useful for determining the ethnic origin of a
CC male, for paternity testing, for forensic studies or for diagnosis. This
CC sequence represents a fragment of the non-recombining region of the human
CC Y chromosome (NRY) comprising a polymorphism that can be used to
CC determine ethnic origin of a male.

XX Sequence 20 BP; 6 A; 3 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CAAAGTGTGGATTACAG 20

RESULT 512

ADM65739 standard; DNA; 20 BP.

ADM65739;

03-JUN-2004 (first entry)

Human Y chromosome non-recombining region polymorphic fragment #300.

ethnic origin determination; polymorphic site determination;

Y chromosome; paternity testing; forensic; diagnosis;

non-recombining region; human; NRY; polymorphic fragment; ds.

Homo sapiens.

US2003134285-A1.

17-JUL-2003.

01-NOV-2001; 2001US-00002623.

01-NOV-2000; 2000US-0245355P.

(OEFRN/) OEFRNER P J.

(UNDE/) UNDERHILL P A.

Oefner PJ, Underhill PA;

WPI; 2003-843259/78.

Determining the ethnic origin of a male by obtaining a nucleic acid

sample from the male and identifying at least two polymorphic markers in

the nucleic acid sample indicative of the ethnic origin of the male.

Claim 24; Page 64; 74pp; English.

The invention describes a method of determining the ethnic origin of a
male comprising obtaining a nucleic acid sample from the male, and
identifying at least two polymorphic markers in the nucleic acid sample
indicative of the ethnic origin of the male, using at least one primer
pair from the primer pairs given in the specification. Also described is
a method of: identifying polymorphic sites in a nucleic acid; a kit for
determining the ethnic origin of an individual; determining the ethnic
origin of a human male individual; an isolated nucleic acid segment of a
human Y chromosome comprising at least 10 contiguous bases including at
least one of the polymorphic sites given in the specification; nucleic
acid primer pairs for amplifying polymorphic regions of the Y chromosome
given in the specification; and determining the paternity of a human male
individual. The method is useful for determining the ethnic origin of a
male, for paternity testing, for forensic studies or for diagnosis. This
sequence represents a fragment of the non-recombining region of the human
Y chromosome (NRY) comprising a polymorphism that can be used to

CC determine ethnic origin of a male.

XX Sequence 20 BP; 6 A; 3 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CAAAGTGTGGATTACAG 20

RESULT 513

ADM65575 standard; DNA; 20 BP.

ADM65575;

03-JUN-2004 (first entry)

NRY polymorphism detection primer #489.

ethnic origin determination; polymorphic site determination;

Y chromosome; paternity testing; forensic; diagnosis;

non-recombining region; human; NRY; PCR; primer; ss.

Homo sapiens.

US2003134285-A1.

17-JUL-2003.

01-NOV-2001; 2001US-00002623.

01-NOV-2000; 2000US-0245355P.

(OEFRN/) OEFRNER P J.

(UNDE/) UNDERHILL P A.

Oefner PJ, Underhill PA;

WPI; 2003-843259/78.

Determining the ethnic origin of a male by obtaining a nucleic acid

sample from the male and identifying at least two polymorphic markers in

the nucleic acid sample indicative of the ethnic origin of the male.

Claim 24; Page 54; 74pp; English.

The invention describes a method of determining the ethnic origin of a
male comprising obtaining a nucleic acid sample from the male, and
identifying at least two polymorphic markers in the nucleic acid sample
indicative of the ethnic origin of the male, using at least one primer
pair from the primer pairs given in the specification. Also described is
a method of: identifying polymorphic sites in a nucleic acid; a kit for
determining the ethnic origin of an individual; determining the ethnic
origin of a human male individual; an isolated nucleic acid segment of a
human Y chromosome comprising at least 10 contiguous bases including at
least one of the polymorphic sites given in the specification; nucleic
acid primer pairs for amplifying polymorphic regions of the Y chromosome
given in the specification; and determining the paternity of a human male
individual. The method is useful for determining the ethnic origin of a
male, for paternity testing, for forensic studies or for diagnosis. This
sequence represents a primer used to detect polymorphisms in the non-
recombining region of the human Y chromosome (NRY).

Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 389 AAGTCTGGATTACAGC 408
 DB 20 AAGTCTGGATTACAGC 1

RESULT 514

ADM65745
 ID ADM65745 standard; DNA; 20 BP.

AC ADM65745;

DT 03-JUN-2004 (first entry)

DE Human Y chromosome non-recombining region polymorphic fragment #302.

KM ethnic origin determination; polymorphic site determination;

KW Y chromosome; paternity testing; forensic; diagnosis;

XX non-recombining region; human; NRY; polymorphic fragment; ds.

OS Homo sapiens.

PN US2003134285-A1.

PD 17-JUL-2003.

PF 01-NOV-2001; 2001US-00002623.

PR 01-NOV-2000; 2000US-0245355P.

PA (OEFN/) OEFNER P J.

PI (UNDE/) UNDERHILL P A.

PI Oefner PJ, Underhill PA;

DR WPI; 2003-843259/78.

PT Determining the ethnic origin of a male by obtaining a nucleic acid

PT sample from the male and identifying at least two polymorphic markers in

PT the nucleic acid sample indicative of the ethnic origin of the male.

XX Claim 24; Page 65; 74pp; English.

XX The invention describes a method of determining the ethnic origin of a

XX male comprising obtaining a nucleic acid sample from the male, and

XX identifying at least two polymorphic markers in the nucleic acid sample

XX indicative of the ethnic origin of the male, using at least one primer

XX pair from the primer pairs given in the specification. Also described is

XX a method of: identifying polymorphic sites in a nucleic acid; a kit for

XX determining the ethnic origin of an individual; determining the ethnic

XX origin of a human male individual; an isolated nucleic acid segment of a

XX human Y chromosome comprising at least 10 contiguous bases including at

XX least one of the polymorphic sites given in the specification; nucleic

XX acid primer pairs for amplifying polymorphic regions of the Y chromosome

XX given in the specification; and determining the paternity of a human male

XX individual. The method is useful for determining the ethnic origin of a

XX male, for paternity testing, for forensic studies or for diagnosis. This

XX sequence represents a fragment of the non-recombining region of the human

XX Y chromosome (NRY) comprising a polymorphism that can be used to

XX determine ethnic origin of a male.

XX Sequence 20 BP; 6 A; 3 C; 7 G; 4 T; 0 U; 0 Other;

XX Query Match 2.0%; Score 20; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 388 CAAAGTCTGGATTACAGG 407

DB 1 CAAAGTCTGGATTACAGG 20

RESULT 515

ADM65578/c

ID ADM65578 standard; DNA; 20 BP.

AC ADM65578;

DT 03-JUN-2004 (first entry)

DE NRY polymorphism detection primer #491.

KM ethnic origin determination; polymorphic site determination;

KW Y chromosome; paternity testing; forensic; diagnosis;

XX non-recombining region; human; NRY; PCR; primer; ss.

OS Homo sapiens.

PN US2003134285-A1.

PD 17-JUL-2003.

PF 01-NOV-2001; 2001US-00002623.

PR 01-NOV-2000; 2000US-0245355P.

PA (OEFN/) OEFNER P J.

PI (UNDE/) UNDERHILL P A.

PI Oefner PJ, Underhill PA;

DR WPI; 2003-843259/78.

PT Determining the ethnic origin of a male by obtaining a nucleic acid

PT sample from the male and identifying at least two polymorphic markers in

PT the nucleic acid sample indicative of the ethnic origin of the male.

XX Claim 24; Page 55; 74pp; English.

XX The invention describes a method of determining the ethnic origin of a

XX male comprising obtaining a nucleic acid sample from the male, and

XX identifying at least two polymorphic markers in the nucleic acid sample

XX indicative of the ethnic origin of the male, using at least one primer

XX pair from the primer pairs given in the specification. Also described is

XX a method of: identifying polymorphic sites in a nucleic acid; a kit for

XX determining the ethnic origin of an individual; determining the ethnic

XX origin of a human male individual; an isolated nucleic acid segment of a

XX human Y chromosome comprising at least 10 contiguous bases including at

XX least one of the polymorphic sites given in the specification; nucleic

XX acid primer pairs for amplifying polymorphic regions of the Y chromosome

XX given in the specification; and determining the paternity of a human male

XX individual. The method is useful for determining the ethnic origin of a

XX male, for paternity testing, for forensic studies or for diagnosis. This

XX sequence represents a primer used to detect polymorphisms in the non-

XX recombining region of the human Y chromosome (NRY).

XX Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

XX Query Match 2.0%; Score 20; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 389 AAGTCTGGATTACAGC 408

DB 20 AAGTCTGGATTACAGC 1

RESULT 516

ADM34330/c

ID ADM34330 standard; DNA; 20 BP.

AC ADM34330;

DT 03-JUN-2004 (first entry)

DE Human cytochrome cDNA sequence primer #2.

KW ss; primer; antiinflammatory; cryopyrin; inflammation;
 KW Familial cold urticaria; familial cold autoinflammatory syndrome;
 KW Muckle Wells Syndrome.
 OS Homo sapiens.
 XX WO2003031639-A2.
 XX
 XX 17-APR-2003.
 PD
 XX 04-OCT-2002; 2002WO-US031502.
 PF
 XX 05-OCT-2001; 2001US-0327728P.
 PR
 XX (LUDM-) LUDWIG INST CANCER RES.
 PA
 XX Hoffman H, Kolodner R;
 PI
 XX WPI; 2003-393448/37.
 DR
 XX
 XX New isolated cryopyrin protein and encoding nucleic acid, useful for
 PT diagnosing and treating inflammatory disorders, in particular familial
 PT cold urticaria, familial cold autoinflammatory syndrome and/or Muckle
 PT Wells Syndrome.
 PS
 XX Example 2; SEQ ID NO 2; 36pp; English.
 CC The invention relates to a novel isolated protein (I) comprises the amino
 CC acid sequence of wild type cryopyrin of 1034 amino acids, with the
 CC proviso that amino acid 198 is not Val, amino acid 352 is not Ala, amino
 CC acid 434 is not Ala, amino acid 627 is not Glu, or amino acid 703 is not
 CC Glu. The methods are useful for determining the presence of a disorder,
 CC treating inflammation, familial cold urticaria/familial cold
 CC autoinflammatory syndrome (FCU/FCAS) or Muckle Wells Syndrome (MWS), and
 CC identifying a substance useful in modulating binding of a cryopyrin
 CC protein to a second protein. The oligonucleotide is useful in diagnosing
 CC a disorder characterized by an aberrant CIAS1 gene. This sequence
 CC corresponds to a primer used to amplify the cryopyrin gene of the
 CC invention.
 CC
 XX SQ Sequence 20 BP; 6 A; 3 C; 7 G; 4 T; 0 U; 0 Other;
 Query Match 2.0%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 667 ATCTTGCTCACTGCACCT 686
 Db 20 ATCTTGCTCACTGCACCT 1
 RESULT 517
 ABB32099
 ID ABB32099 standard; DNA; 20 BP.
 XX
 AC ABB32099;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human PDE4C-derived oligonucleotide SEQ ID 14310.
 XX
 KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.
 XX
 XX Homo sapiens.
 OS
 XX WO200285309-A2.
 PN

XX 31-OCT-2002.
 PD
 XX 23-APR-2002; 2002WO-US031143.
 PF
 XX 24-APR-2001; 2001US-0286036P.
 PR
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX
 PA
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 DR WPI; 2003-093058/08.
 XX
 XX Pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.
 PS
 XX Claim 15; SEQ ID NO 14310; 763pp; English.
 CC This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating allergies and
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 CC
 XX SQ Sequence 20 BP; 5 A; 0 C; 5 G; 10 T; 0 U; 0 Other;
 Query Match 2.0%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 772 TTGATTTTGTAGTAGAGATG 791
 Db 1 TTGATTTTGTAGTAGAGATG 20
 RESULT 518
 ABB31045
 ID ABB31045 standard; DNA; 20 BP.
 XX
 AC ABB31045;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human RANTES-derived oligonucleotide SEQ ID 13256.
 XX
 XX Homo sapiens.
 OS
 XX WO200285309-A2.
 PN

Human; antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antiinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cyostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ss; primer.

OS Homo sapiens.

XX WO200285309-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D; PI Miller S, Tang L, Shahabuddin S; DR WPI; 2003-093058/08.

XX Claim 15; SEQ ID NO 13256; 763bp; English.

XX This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating allergies and bronchoconstriction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonucleotides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has antiallergic, antiinflammatory, antiasthmatic, analgesic, hypotensive, immunosuppressive and cyostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, CC inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. CC The reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonucleotides into products that free adenosine into the system e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to prevent any unwanted effects due to it

XX Sequence 20 BP; 3 A; 4 C; 10 G; 3 T; 0 U; 0 Other:

XX Query Match 2.0%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 646 AGGCTGAGTGCAGTGGCGC 665

XX 1 AGGCTGAGTGCAGTGGCGC 20

XX RESULT 519

XX ABE30942

XX ID ABE30942 standard; DNA; 20 BP.

XX AC ABE30942;

XX 29-JUL-2004 (first entry)

XX Human RANTES-derived oligonucleotide SEQ ID 13153.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antiinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cyostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.

XX WO200285309-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D; PI Miller S, Tang L, Shahabuddin S; DR WPI; 2003-093058/08.

XX Claim 15; SEQ ID NO 13153; 763bp; English.

XX This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating allergies and bronchoconstriction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonucleotides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has antiallergic, antiinflammatory, antiasthmatic, analgesic, hypotensive, immunosuppressive and cyostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, CC inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. CC The reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonucleotides into products that free adenosine into the system

CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 AGCTGGACTACAGCGCC 751
DB 1 AGCTGGACTACAGCGCC 20

RESULT 520

ABD32107
ID ABD32107 standard; DNA; 20 BP.

AC ABD32107;
XX

DT 29-JUL-2004 (first entry)

DE Human PDE4C-derived oligonucleotide SEQ ID 14318.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; antiasthmatic; antiinflammatory; antiasthmatic;
XX analgesic; hypotensive; immunosuppressive; cytoskeletal; cystic fibrosis;
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX pulmonary transplantation rejection; ss; primer.

OS Homo sapiens.

XX WO200285309-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPiG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shanabuddin S;

XX WPI; 2003-093058/08.

XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.

XX Claim 15; SEQ ID NO 14318; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,
XX comprising oligonucleotides, effective for alleviating
XX bronchoconstriction, respiratory tract inflammation, allergies and
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
XX surfactant depletion or hyposecretion, when administered to a mammal. The
XX oligonucleotides are derived from a gene encoding or regulating
XX expression of a target polypeptide associated with lung airway or lung
XX dysfunction or cancer and can be anti-sense to the corresponding mRNA.
XX The invention also describes a kit, that comprises: (a) a delivery
XX device, in separate containers, (b) the oligonucleotides, (c)
XX instructions for adding a carrier and for use of the kit. The composition
XX of the invention has antiasthmatic, antiinflammatory, antisthmatic,
XX analgesic, hypotensive, immunosuppressive and cytoskeletal activity, is a
XX beta-adrenergic agonist. The composition is useful for preventing or
XX treating a respiratory, lung or malignant disease. The administered
XX composition comprises oligo and is administered to reduce the production

CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated

CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it

SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 TCAGCTCCCAAGTCTGG 398

DB 1 TCAGCTCCCAAGTCTGG 20

RESULT 521

ABD28946
ID ABD28946 standard; DNA; 20 BP.

AC ABD28946;
XX

DT 29-JUL-2004 (first entry)

DE NS8473-derived oligonucleotide SEQ ID 7958.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; antiasthmatic; antiinflammatory; antiasthmatic;
XX analgesic; hypotensive; immunosuppressive; cytoskeletal; cystic fibrosis;
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX pulmonary transplantation rejection; ss; primer.

OS Homo sapiens.

XX WO200285309-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPiG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shanabuddin S;

XX WPI; 2003-093058/08.

XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.

XX Claim 15; SEQ ID NO 7958; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,
XX comprising oligonucleotides, effective for alleviating
XX bronchoconstriction, respiratory tract inflammation, allergies and
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,

CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 4 A; 7 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 546 GCCTCCCAAGTAGCTGGAC 565
1 GCCTCCCAAGTAGCTGGAC 20
Db 1 GCCTCCCAAGTAGCTGGAC 20
RESULT 522
ABD32106 standard; DNA; 20 BP.
ID ABD32106 standard; DNA; 20 BP.
AC ABD32106;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human PDB4C-derived oligonucleotide SEQ ID 14317.
XX
XX Human; anti-sense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX NYCE JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-093058/08.
DR

XX pharmaceutical composition for treating asthma, has anti-sense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 14317; 763pp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 2 A; 12 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 369 TCACCTGCCTCAGCTCCC 388
1 TCACCTGCCTCAGCTCCC 20
Db 1 TCACCTGCCTCAGCTCCC 20
RESULT 523
ABD32086 standard; DNA; 20 BP.
ID ABD32086 standard; DNA; 20 BP.
AC ABD32086;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human PDB4C-derived oligonucleotide SEQ ID 14297.
XX
XX Human; anti-sense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX

PD 31-OCT-2002.
XX 23-APR-2002; 2002WO-US013143.
XX 24-APR-2001; 2001US-0286036P.
XX (EPIG-) EPIGENESIS PHARM INC.
XX Nye JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
DR WPI; 2003-093058/08.
XX
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 14297; 763bp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antispasmodic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
XX Sequence 20 BP; 3 A; 5 C; 9 G; 3 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 643 CCCAGGCTGAGTCCAGTGG 662
DB 1 CCCAGGCTGAGTCCAGTGG 20
RESULT 524
ABD28945
ID ABD28945 standard; DNA; 20 BP.
XX
XX ABD28945;
AC
XX
XX 29-JUL-2004 (first entry)
DT
XX
XX N58473-derived oligonucleotide SEQ ID 7957.
DE
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;

KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antispasmodic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
XX Homo sapiens.
XX
XX WO200285309-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013143.
XX
XX 24-APR-2001; 2001US-0286036P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nye JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
DR WPI; 2003-093058/08.
XX
XX Claim 15; SEQ ID NO 7957; 763bp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antispasmodic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
XX Sequence 20 BP; 4 A; 9 C; 4 G; 3 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 540 GCTTCAGCTCCCAAGTGC 559
DB 1 GCTTCAGCTCCCAAGTGC 20

XX 22-APR-2004 (first entry)
XX
XX Human transforming growth factor-beta 2 antisense oligo, SEQ ID NO 88.
DE
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytosolic; nontropic; neuroprotective; immunosuppressive;
KM hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX immune; ss; human.
XX
OS Homo sapiens.
XX
XX US2004006030-A1.
XX
XX 08-JAN-2004.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM, Dobie KM;
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
XX Example 15; SEQ ID NO 88; 135bp; English.
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, nontropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition, and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
XX Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
SQ

Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 TGGGATTACAGCGGTGAGCC 885
DB 20 TGGGATTACAGCGGTGAGCC 1

RESULT 528
AD180221
ID AD180221 standard; DNA; 20 BP.
XX
XX AD180221;
AC
XX 22-APR-2004 (first entry)
DT
XX

DE Human transforming growth factor-beta 2 target DNA region, SEQ ID NO 222.
XX
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytosolic; nontropic; neuroprotective; immunosuppressive;
KM hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX immune; ss; human.
XX
OS Homo sapiens.
XX
XX US2004006030-A1.
XX
XX 08-JAN-2004.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM, Dobie KM;
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
XX Example 16; SEQ ID NO 222; 135bp; English.
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, nontropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition, and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
XX Sequence 20 BP; 3 A; 7 C; 7 G; 3 T; 0 U; 0 Other;
SQ

Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 850 CGGCTCCCAAGTGTGGG 869
DB 1 CGGCTCCCAAGTGTGGG 20

RESULT 529
ADJ53542
ID ADJ53542 standard; DNA; 20 BP.
XX
XX ADJ53542;
AC
XX 06-MAY-2004 (first entry)
DT
XX Human PPP3CB DNA antisense oligonucleotide #65.
DE
XX Human; PPP3CB; ss; antisense oligonucleotide; phosphorothioate linkage;
KM

KW 2'-O-methoxyethyl sugar moiety; 5-methylcytosine; autoimmune disorder;
KM Alzheimer's disease; immunosuppressive; nootropic; neuroprotective.
XX
XX Homo sapiens.
OS
XX US2004023382-A1.
PN
XX
XX 05-FEB-2004.
PD
XX 31-JUL-2002; 2002US-00210723.
PF
XX 31-JUL-2002; 2002US-00210723.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Dean NM, Bennett CF, Dobie KW;
PI WPI; 2004-142663/14.
DR
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding PPP3CB, useful for treating an autoimmune disorder,
PT or Alzheimer's disease.
CC
XX Example 15; SEQ ID NO 78; 91pp; English.
PS
XX The invention relates to an antisense oligonucleotide targeted to a
CC nucleic acid encoding the human PPP3CB polypeptide and inhibits
CC expression of the PPP3CB polypeptide. The antisense oligonucleotide
CC comprises at least one modified internucleoside linkage, i.e. a
CC phosphorothioate linkage, at least one modified sugar moiety, preferably
CC a 2'-O-methoxyethyl sugar moiety, or at least one modified nucleobase
CC comprising a 5-methylcytosine. The antisense oligonucleotides are useful
CC for inhibiting expression of the PPP3CB polypeptide and in preparation of
CC a composition for treating autoimmune disorders or Alzheimer's disease.
CC This sequence represents an antisense oligonucleotide of the invention.
SQ
XX Sequence 20 BP; 4 A; 9 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 541 CCTCAGCCTCCCAAGTAGCT 560
DB 1 CCTCAGCCTCCCAAGTAGCT 20
RESULT 530
ADJ53600/c
ID ADJ53600 standard; DNA; 20 BP.
XX
XX ADJ53600;
AC
XX 06-MAY-2004 (first entry)
DT
XX
XX Human PPP3CB DNA antisense oligonucleotide target region #51.
DE
XX
XX Human; PPP3CB; sg; antisense oligonucleotide; phosphorothioate linkage;
KM 2'-O-methoxyethyl sugar moiety; 5-methylcytosine; autoimmune disorder;
KM Alzheimer's disease; immunosuppressive; nootropic; neuroprotective.
XX
XX Homo sapiens.
OS
XX US2004023382-A1.
PN
XX
XX 05-FEB-2004.
PD
XX 31-JUL-2002; 2002US-00210723.
PF
XX 31-JUL-2002; 2002US-00210723.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX

PI Dean NM, Bennett CF, Dobie KW;
XX WPI; 2004-142663/14.
DR
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding PPP3CB, useful for treating an autoimmune disorder,
PT or Alzheimer's disease.
CC
XX Example 15; SEQ ID NO 136; 91pp; English.
PS
XX The invention relates to an antisense oligonucleotide targeted to a
CC nucleic acid encoding the human PPP3CB polypeptide and inhibits
CC expression of the PPP3CB polypeptide. The antisense oligonucleotide
CC comprises at least one modified internucleoside linkage, i.e. a
CC phosphorothioate linkage, at least one modified sugar moiety, preferably
CC a 2'-O-methoxyethyl sugar moiety, or at least one modified nucleobase
CC comprising a 5-methylcytosine. The antisense oligonucleotides are useful
CC for inhibiting expression of the PPP3CB polypeptide and in preparation of
CC a composition for treating autoimmune disorders or Alzheimer's disease.
CC This sequence represents an antisense oligonucleotide target region of
CC the invention.
SQ
XX Sequence 20 BP; 4 A; 3 C; 9 G; 4 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 541 CCTCAGCCTCCCAAGTAGCT 560
DB 20 CCTCAGCCTCCCAAGTAGCT 1
RESULT 531
ADJ60953
ID ADJ60953 standard; DNA; 20 BP.
XX
XX ADJ60953;
AC
XX 06-MAY-2004 (first entry)
DT
XX
XX Oligonucleotide associated to PDE4C #19.
DE
XX Interleukin; IL-4 receptor; IL-5 receptor; lung disease;
KM airway inflammation; allergy; asthma; impeded respiration;
KM cystic fibrosis; acute respiratory distress syndrome;
KM pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
KM sg.
XX
XX Homo sapiens.
OS
XX WO2004011613-A2.
PN
XX
XX 05-FEB-2004.
PD
XX
XX 25-JUL-2003; 2003WO-US023509.
PF
XX 29-JUL-2002; 2002US-0399076P.
PR
XX (EPIC-) EPIGENESIS PHARM INC.
PA
XX Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;
PI Shahbuddin S, Lu H, Cong H;
PI WPI; 2004-203534/19.
DR
XX
XX Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codons and introns of respiratory disease-relevant genes e.g.,
PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
PT disease e.g., asthma.
XX
XX Claim 2; SEQ ID NO 1809; 85pp; English.
XX

CC The present invention relates to an oligonucleotide anti-sense to e.g.,
CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
CC end of nucleic acid target comprising gene(s) chosen from e.g.
CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the
CC oligonucleotide and optionally surfactant operatively linked to the
CC oligonucleotide. The method is useful for preventing or treating a
CC respiratory or lung disease, which involves administering to the airways
CC of a subject an effective amount of an inhibitor. The oligonucleotide is
CC useful for production of a medicament for the prevention and/or treatment
CC of a respiratory or lung disease. The respiratory or lung disease is
CC chosen from airway inflammation, allergy(ies), asthma, impeded
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
CC obstruction. The present sequence represents an oligonucleotide of the
CC invention.

SQ Sequence 20 BP; 5 A; 0 C; 5 G; 10 T; 0 U; 0 Other;
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 772 TTGATTTTGTAGAGATG 791
|||||
1 TTGATTTTGTAGAGATG 20

DB

RESULT 532
ADJ60960
ID ADJ60960 standard; DNA; 20 BP.
XX
AC ADJ60960;
XX
DT 06-MAY-2004 (first entry)
XX
DE Oligonucleotide associated to PDEAC #26.
XX
KW interleukin; IL-4 receptor; IL-5 receptor; lung disease;
XX airway inflammation; allergy; asthma; impeded respiration;
XX cystic fibrosis; acute respiratory distress syndrome;
XX pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
XX ss.
XX
OS Homo sapiens.
XX
PN WO2004011613-A2.
XX
PD 05-FEB-2004.
XX
PF 25-JUL-2003; 2003WO-US023509.
XX
PR 29-JUL-2002; 2002US-0399076P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;
XX Shahabuddin S, Lu H, Cong H;
XX WPI, 2004-203534/19.
XX
DR WPI, 2004-203534/19.
XX
PT Novel single or multiple target oligonucleotide anti-sense to e.g.,
PT initiation codons and introns of respiratory disease-relevant genes e.g.,
PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
PT disease e.g., asthma.
XX
PS Claim 2; SEQ ID NO 1816; 85pp; English.
XX
CC The present invention relates to an oligonucleotide anti-sense to e.g.,
CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
CC end of nucleic acid target comprising gene(s) chosen from e.g.
CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the
CC oligonucleotide and optionally surfactant operatively linked to the
CC respiratory or lung disease, which involves administering to the airways
CC of a subject an effective amount of an inhibitor. The oligonucleotide is
CC useful for production of a medicament for the prevention and/or treatment
CC of a respiratory or lung disease. The respiratory or lung disease is

CC oligonucleotide. The method is useful for preventing or treating a
CC respiratory or lung disease, which involves administering to the airways
CC of a subject an effective amount of an inhibitor. The oligonucleotide is
CC useful for production of a medicament for the prevention and/or treatment
CC of a respiratory or lung disease. The respiratory or lung disease is
CC chosen from airway inflammation, allergy(ies), asthma, impeded
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
CC obstruction. The present sequence represents an oligonucleotide of the
CC invention.

SQ Sequence 20 BP; 2 A; 12 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 369 TCCACCTGCTCAGCTGCC 388
|||||
1 TCCACCTGCTCAGCTGCC 20

DB

RESULT 533
ADJ59879
ID ADJ59879 standard; DNA; 20 BP.
XX
AC ADJ59879;
XX
DT 06-MAY-2004 (first entry)
XX
DE Oligonucleotide associated to RANTES #128.
XX
KW interleukin; IL-4 receptor; IL-5 receptor; lung disease;
XX airway inflammation; allergy; asthma; impeded respiration;
XX cystic fibrosis; acute respiratory distress syndrome;
XX pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
XX ss.
XX
OS Homo sapiens.
XX
PN WO2004011613-A2.
XX
PD 05-FEB-2004.
XX
PF 25-JUL-2003; 2003WO-US023509.
XX
PR 29-JUL-2002; 2002US-0399076P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;
XX Shahabuddin S, Lu H, Cong H;
XX WPI, 2004-203534/19.
XX
DR WPI, 2004-203534/19.
XX
PT Novel single or multiple target oligonucleotide anti-sense to e.g.,
PT initiation codons and introns of respiratory disease-relevant genes e.g.,
PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
PT disease e.g., asthma.
XX
PS Claim 2; SEQ ID NO 735; 85pp; English.
XX
CC The present invention relates to an oligonucleotide anti-sense to e.g.,
CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
CC end of nucleic acid target comprising gene(s) chosen from e.g.
CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the
CC oligonucleotide and optionally surfactant operatively linked to the
CC respiratory or lung disease, which involves administering to the airways
CC of a subject an effective amount of an inhibitor. The oligonucleotide is
CC useful for production of a medicament for the prevention and/or treatment
CC of a respiratory or lung disease. The respiratory or lung disease is

CC chosen from airway inflammation, allergy(ies), asthma, impeded
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
CC obstruction. The present sequence represents an oligonucleotide of the
CC invention.
XX
SQ Sequence 20 BP; 3 A; 4 C; 10 G; 3 T; 0 U; 0 Other;
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 646 AGCGCTGAGTGCAGTGGCGC 665
Db 1 AGCGCTGAGTGCAGTGGCGC 20
RESULT 534
ADJ60940
ID ADJ60940 standard; DNA; 20 BP.
XX
AC ADJ60940;
XX
DT 06-MAY-2004 (first entry)
XX
DE Oligonucleotide associated to PDE4C #6.
XX
KM interleukin; IL-4 receptor; IL-5 receptor; lung disease;
XX airway inflammation; allergy; asthma; impeded respiration;
XX cystic fibrosis; acute respiratory distress syndrome;
XX pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
XX ss.
XX
OS Homo sapiens.
XX
PN WO2004011613-A2.
XX
PD 05-FEB-2004.
XX
PF 25-JUL-2003; 2003WO-US023509.
XX
PR 29-JUL-2002; 2002US-0399076P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;
PI Shahbuddin S, Lu H, Cong H;
XX
DR WPI; 2004-203534/19.
XX
PT Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codons and introns of respiratory disease-relevant genes e.g.,
PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
PT disease e.g., asthma.
XX
PS Claim 2; SEQ ID NO 1796; 85pp; English.
XX
CC The present invention relates to an oligonucleotide anti-sense to e.g.,
CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
CC end of nucleic acid target comprising gene(s) chosen from e.g.
CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the
CC oligonucleotide and optionally surfactant operatively linked to the
CC oligonucleotide. The method is useful for preventing or treating a
CC respiratory or lung disease, which involves administering to the airways
CC of a subject an effective amount of an inhibitor. The oligonucleotide is
CC useful for production of a medicament for the prevention and/or treatment
CC of a respiratory or lung disease. The respiratory or lung disease is
CC chosen from airway inflammation, allergy(ies), asthma, impeded
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
CC obstruction. The present sequence represents an oligonucleotide of the
CC invention.

CC invention.
XX
SQ Sequence 20 BP; 3 A; 5 C; 9 G; 3 T; 0 U; 0 Other;
QY 643 CCCAGGCTGAGTGCAGTGG 662
Db 1 CCCAGGCTGAGTGCAGTGG 20
RESULT 535
ADJ60961
ID ADJ60961 standard; DNA; 20 BP.
XX
AC ADJ60961;
XX
DT 06-MAY-2004 (first entry)
XX
DE Oligonucleotide associated to PDE4C #27.
XX
KM interleukin; IL-4 receptor; IL-5 receptor; lung disease;
XX airway inflammation; allergy; asthma; impeded respiration;
XX cystic fibrosis; acute respiratory distress syndrome;
XX pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
XX ss.
XX
OS Homo sapiens.
XX
PN WO2004011613-A2.
XX
PD 05-FEB-2004.
XX
PF 25-JUL-2003; 2003WO-US023509.
XX
PR 29-JUL-2002; 2002US-0399076P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;
PI Shahbuddin S, Lu H, Cong H;
XX
DR WPI; 2004-203534/19.
XX
PT Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codons and introns of respiratory disease-relevant genes e.g.,
PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
PT disease e.g., asthma.
XX
PS Claim 2; SEQ ID NO 1817; 85pp; English.
XX
CC The present invention relates to an oligonucleotide anti-sense to e.g.,
CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
CC end of nucleic acid target comprising gene(s) chosen from e.g.
CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the
CC oligonucleotide and optionally surfactant operatively linked to the
CC oligonucleotide. The method is useful for preventing or treating a
CC respiratory or lung disease, which involves administering to the airways
CC of a subject an effective amount of an inhibitor. The oligonucleotide is
CC useful for production of a medicament for the prevention and/or treatment
CC of a respiratory or lung disease. The respiratory or lung disease is
CC chosen from airway inflammation, allergy(ies), asthma, impeded
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
CC obstruction. The present sequence represents an oligonucleotide of the
CC invention.
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 TCAGCTCCCAAGCTCG 398
DB 1 TCAGCTCCCAAGCTCG 20

RESULT 536

ADJ59776
ID ADJ59776 standard; DNA; 20 BP.

AC ADJ59776;

DT 06-MAY-2004 (first entry)

DE Oligonucleotide associated to RANTES #25.

XX interleukin; IL-4 receptor; IL-5 receptor; lung disease;

KW airway inflammation; allergy; asthma; impeded respiration;

KW cystic fibrosis; acute respiratory distress syndrome;

KW pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;

KW ss.

OS Homo sapiens.

XX MO2004011613-A2.

PN 05-FEB-2004.

XX 25-JUL-2003; 2003WO-US023509.

XX 29-JUL-2002; 2002US-0399076P.

XX (EPG-) EPGENESIS PHARM INC.

PI Myce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;

PI Shahabuddin S, Lu H, Cong H;

XX WPI; 2004-203534/19.

PT Novel single or multiple target oligonucleotide anti-sense to e.g.

PT initiation codons and introns of respiratory disease-relevant genes e.g.,

PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory

PT disease e.g., asthma.

PS Claim 2; SEQ ID NO 632; 85bp; English.

XX The present invention relates to an oligonucleotide anti-sense to e.g.,

XX initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-

XX end of nucleic acid target comprising gene(s) chosen from e.g.

XX interleukin (IL)-4 receptor, IL-5 receptor or salts of the

XX oligonucleotide. The method is useful for preventing or treating a

XX respiratory or lung disease, which involves administering to the always

XX of a subject an effective amount of an inhibitor. The oligonucleotide is

XX useful for production of a medicament for the prevention and/or treatment

XX of a respiratory or lung disease. The respiratory or lung disease is

XX chosen from airway inflammation, allergy(ies), asthma, impeded

XX respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases

XX (COPD), allergic rhinitis (AR), acute respiratory distress syndrome

XX (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway

XX obstruction. The present sequence represents an oligonucleotide of the

XX invention.

XX Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;

QY Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 AGCTGGACTACAGCGCCC 751

DB 1 AGCTGGACTACAGCGCCC 20

RESULT 537

ADL23339

ID ADL23339 standard; DNA; 20 BP.

AC ADL23339;

DT 20-MAY-2004 (first entry)

DE Primer #1 for amplification of D6S105.

XX ss; primer; diagnosis; cervical intraepithelial neoplasia; CIN;

KW allelic deletion; FHIT; fragile histidine triad gene; PR;

KW progesterone receptor; DLEC1; deleted in lung and oesophageal cancer 1;

KW TRIM29; tripartite motif-containing 29; microsatellite; D3S1300; D3S1260;

KW D1S35; D1S528.

OS Homo sapiens.

OS Synthetic.

XX MO2004018711-A2.

XX 04-MAR-2004.

XX 20-AUG-2003; 2003WO-GB003637.

XX 24-AUG-2002; 2002GB-00019890.

XX 26-AUG-2002; 2002US-0405717P.

XX (UNLO) UNIV COLLEGE LONDON.

XX Ming-Qing D;

XX WPI; 2004-226867/21.

PT Diagnosing cervical intraepithelial neoplasia comprising detecting an

PT allelic deletion in genes selected from FHIT, PR, DLEC1- or TRIM 29 by

PT comparing the FHIT, PR, DLEC1 and/or TRIM 29 polynucleotides or proteins

PT present in the samples.

PS Disclosure; SEQ ID NO 21; 56bp; English.

XX This sequence represents a primer which was used in the method of the

XX invention for diagnosing susceptibility to persistence or progression of

XX cervical intraepithelial neoplasia (CIN) in an individual suffering from

XX the disease. The method comprises detecting an allelic deletion in one or

XX more genes selected from FHIT (fragile histidine triad gene), PR

XX (progesterone receptor), DLEC1 (deleted in lung and oesophageal cancer 1)

XX or TRIM29 (tripartite motif-containing 29) by comparing the FHIT, PR,

XX DLEC1 and/or TRIM29 polynucleotides or proteins present in the samples

XX derived from non-dyskaryotic and dyskaryotic samples, respectively. The

XX method is carried out using a kit comprising a panel of two or more pairs

XX of primers, where each pair of primers is suitable for amplifying a

XX microsatellite DNA marker selected from D3S1300, D3S1260, D1S35 or

XX D1S528, or a panel of two or more specific binding agents, where each

XX binding agent is capable of distinguishing between the normal and allelic

XX deletion forms of a polynucleotide or protein selected from FHIT, PR,

XX TRIM29 or DLEC1. The method is useful for diagnosing susceptibility to

XX persistence or progression of cervical intraepithelial neoplasia in an

XX individual suffering from the disease.

XX Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

QY Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 387 CCAAGTCTGGATTACAG 406

DB 1 CCAAGTCTGGATTACAG 20

```

RESULT 538
ADL3388/C
ID ADL32388 standard; DNA; 20 BP.
XX
XX ADL32388;
AC
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX Clone specific PCR primer to amplify human full length cDNA SeqID 4421.
DE
XX human; medicine; signal transduction; glycoprotein; transcription;
XX oligo-capping method; ss; PCR; primer.
XX
XX Homo sapiens.
OS
XX EP1396543-A2.
PN
XX 10-MAR-2004.
PD
XX
XX 07-JUL-2000; 2003EP-00025638.
PF
XX
XX 08-JUL-1999; 99JP-00194486.
PR
XX 11-JAN-2000; 2000JP-00118774.
PR
XX 02-MAY-2000; 2000JP-00183865.
PR
XX 07-JUL-2000; 2000EP-00114089.
XX
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H,
PI WPI; 2004-204755/20.
XX
XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full
PT length human cDNAs.
PT
XX
XX Example 18; SEQ ID NO 4421; 1340bp; English.
PS
XX
XX This invention relates to a novel primers useful for synthesizing full
XX length cDNA molecules that encode human proteins. Specifically, it refers
XX to secretory or membrane proteins that are potential therapeutic agents/
XX target molecules in the field of medicine, and in particular genes
XX encoding proteins that are associated with signal transduction,
XX glycoproteins and transcription. The present invention describes a method
XX for efficiently cloning a full length human cDNA from both the 5' and 3'
XX ends using the oligo-capping method. This oligonucleotide sequence is a
XX human clone specific PCR primer used in an exemplification of the
XX invention.
XX
XX Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
SQ

```

```

Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 388 CAAAGTCTGGGATTACAGG 407
DB 20 CAAAGTCTGGGATTACAGG 1

```

```

RESULT 539
ADL61592/C
ID ADL61592 standard; DNA; 20 BP.
XX
XX ADL61592;
AC
XX
XX 03-JUN-2004 (first entry)
DT
XX
XX Human protein tyrosine kinase biomarker-related RT-PCR primer SEQ ID 516.
XX
XX predictor set; protein tyrosine kinase biomarker; cytostatic;
XX antiangiogenic; vasotrophic; vulnerary; pharmacogenomic; drug sensitivity;
KW

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```

KW breast cancer; hypervascular disease; angiogenesis; wound healing scar;
KW human; ss; RT-PCR; PCR; primer.
XX
XX Homo sapiens.
XX
XX WO2004020583-A2.
XX
XX 11-MAR-2004.
XX
XX 26-AUG-2003; 2003WO-US026491.
XX
XX 27-AUG-2002; 2002US-0406385P.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Huang F, Han X, Reeves KA, Amler L, Fairchild CR, Lee FY,
PI Shaw P;
PI WPI; 2004-239171/22.
XX
XX New predictor sets with a plurality of polynucleotides and/or
PT polypeptides whose expression pattern predicts cell response to a
PT compound that modulates protein tyrosine kinase activity, useful in
PT treating breast cancer.
XX
XX disclosure; SEQ ID NO 516; 649pp; English.
XX
XX The invention relates to a novel predictor set comprising a plurality of
XX polynucleotides and/or polypeptides whose expression pattern is
XX predictive of the response of cells to treatment with a compound that
XX modulate protein tyrosine kinase activity or members of the protein
XX tyrosine kinase pathway. The molecules of the invention demonstrate
XX cytostatic, antiangiogenic, vasotrophic and vulnerary activities and may
XX be useful in the field of pharmacogenomics, in particular for determining
XX drug sensitivity and in treating breast cancer, hypervascular diseases,
XX angiogenesis and scars in wound healing. The current sequence is that of
XX a human protein tyrosine kinase biomarker-related RT-PCR primer of the
XX invention.
XX
XX Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 U; 0 Other;
SQ

```

```

Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 542 CTCAGCCTCCCAAGTAGCTG 561
DB 20 CTCAGCCTCCCAAGTAGCTG 1

```

```

RESULT 540
ADM14394/C
ID ADM14394 standard; DNA; 20 BP.
XX
XX ADM14394;
AC
XX
XX 01-JUN-2004 (first entry)
DT
XX
XX Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:581.
XX
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin H2 synthase; mPGEs-1 inhibitor;
KW microsomal prostaglandin H2 synthase inhibitor; cytostatic; antidiabetic;
KW immunomodulator; cardiatic; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotrophic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; jaehemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX

```


Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 382 GCCTCCCAAGTCTGGGAT 401
|||||
DB 20 GCCTCCCAAGTCTGGGAT 1

RESULT 542
ADM14277/c
ID ADM14277 standard; DNA; 20 BP.

AC ADM14277;
XX
XX
DT 01-JUL-2004 (first entry)

DE Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:464.

XX chimeric; antisense oligonucleotide; phosphorothioate; human;
KM microsome prostaglandin E2 synthase; mPGEs-1; mPGEs-1 inhibitor;
KM microsome prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KM immunomodulator; cardiant; neuroprotective; antiinflammatory;
KM neuroprotective; neurotropic; antiarthritic; vasotrophic; ophthalmological;
KM immunomodulatory; cardiovascular; gene therapy; inflammation;
KM Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KM reperfusion injury; ophthalmic disorder; immunological disorder;
KM cardiovascular disorder; neurological disorder; ss.

XX Homo sapiens.
OS Synthetic.

FT modified_base 1..20
FH Location/Qualifiers
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
FT 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"

XX WO2004028458-A2.
PN
XX
PD 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
PF
XX 25-SEP-2002; 2002US-0413549P.
PR
XX
XX (PHAA) PHARMACIA CORP.
PA
XX
XX Gierse JK;
PI
XX
XX WPI; 2004-305094/28.
DR
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGEs-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT lechemia.

XX
XX
PS Claim 4; SEQ ID NO 464; 132pp; English.

XX The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsome prostaglandin E2 synthase (mPGEs-1). The
CC human mPGEs-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding

CC mPGEs-1, which specifically hybridise with the nucleic acid mPGEs-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGEs-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGEs-1. mPGEs-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotrophic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGEs-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGEs-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.

XX
XX
SQ Sequence 20 BP; 3 A; 7 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 850 CGGCTCCCAAGTCTGGG 869
|||||
DB 20 CGGCTCCCAAGTCTGGG 1

RESULT 543
ADM14482/c
ID ADM14482 standard; DNA; 20 BP.

AC ADM14482;
XX
XX
DT 01-JUL-2004 (first entry)

DE Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:669.

XX chimeric; antisense oligonucleotide; phosphorothioate; human;
KM microsome prostaglandin E2 synthase; mPGEs-1; mPGEs-1 inhibitor;
KM microsome prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KM immunomodulator; cardiant; neuroprotective; antiinflammatory;
KM neuroprotective; neurotropic; antiarthritic; vasotrophic; ophthalmological;
KM immunomodulatory; cardiovascular; gene therapy; inflammation;
KM Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KM reperfusion injury; ophthalmic disorder; immunological disorder;
KM cardiovascular disorder; neurological disorder; ss.

XX Homo sapiens.
OS Synthetic.

FT modified_base 1..20
FH Location/Qualifiers
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
FT 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"

XX WO2004028458-A2.
PN
XX
PD 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
PF
XX 25-SEP-2002; 2002US-0413549P.
PR
XX
XX (PHAA) PHARMACIA CORP.
PA
XX

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PI Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 669; 132bp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 4 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 849 TCGGCTCCCAAGTCTGG 868
XX |||||
XX 20 TCGGCTCCCAAGTCTGG 1
XX
XX RESULT 544
XX ADM15309/C
XX ID ADM15309 standard; DNA; 20 BP.
XX
XX AC ADM15309;
XX
XX DT 01-JUL-2004 (first entry)
XX
XX DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1496.
XX
XX XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microosomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
XX microosomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
XX immunomodulator; cardiant; neuroprotective; antiinflammatory;
XX neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;
XX immunomodulatory; cardiovascular; gene therapy; inflammation;
XX Alzheimer's disease; arthritis; diabetes; cancer; ischemia;
XX reperfusion injury; ophthalmic disorder; immunological disorder;
XX cardiovascular disorder; neurological disorder; ss.
XX
XX OS Homo sapiens.
XX
XX XX Synthetic.
XX
XX PH Key location/Qualifiers
XX FT 1..20
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "phosphorothioate linkages and all cytidine
XX FT residues are 5-methylcytidines"
XX FT 1..5
XX FT /*tag= a
XX FT /mod_base= OTHER

```

```

FT FT /note= "2'-O-methoxyethyls"
FT FT 16..20
FT FT /*tag= c
FT FT /mod_base= OTHER
FT FT /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 1496; 132bp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 12 A; 4 C; 0 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 769 TTTTGTATTTTGTAGAG 788
XX |||||
XX 20 TTTTGTATTTTGTAGAG 1
XX
XX RESULT 545
XX ADM15160/C
XX ID ADM15160 standard; DNA; 20 BP.
XX
XX AC ADM15160;
XX
XX DT 01-JUL-2004 (first entry)
XX
XX DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1347.
XX
XX XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microosomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
XX microosomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
XX immunomodulator; cardiant; neuroprotective; antiinflammatory;
XX neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;
XX immunomodulatory; cardiovascular; gene therapy; inflammation;

```


KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
 KW reperfusion injury; ophthalmic disorder; immunological disorder;
 KW cardiovascular disorder; neurological disorder; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.

Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= b

FT /mod_base= OTHER
 FT /note= "phosphorothioate linkages and all cytidine
 FT residues are 5-methylcytidines"

FT modified_base 1..5
 FT /tag= a

FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyls"

FT modified_base 16..20
 FT /tag= c

FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyls"

PN WO2004028458-A2.

PD 08-APR-2004.

PF 25-SEP-2003; 2003WO-US030374.

PR 25-SEP-2003; 2002US-0413549P.

PA (PHAA) PHARMACIA CORP.

PI Gierse JK;

DR WPI; 2004-305094/28.

PT New antisense compound, having a sequence targeted to a nucleic acid
 PT encoding mPES-1, useful for preparing a composition for treating e.g.,
 PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
 PT ischemia.

PS Claim 4; SEQ ID NO 1347; 132pp; English.

XX The present sequence represents a chimeric antisense oligonucleotide
 CC targeted to human microsomal prostaglandin E2 synthase (mPES-1). The
 CC human mPES-1 gene is located on chromosome 9, more specifically to
 CC 9q34.3. The present invention also describes: (1) antisense compounds,
 CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
 CC mPES-1, which specifically hybridise with the nucleic acid mPES-1 and
 CC inhibits its expression; (2) a method of inhibiting the expression of
 CC mPES-1 in cells or tissues; and (3) a method of treating an animal
 CC having a disease or condition associated with mPES-1. mPES-1 chimeric
 CC antisense oligonucleotides and antisense compounds have cytoskeletal,
 CC anti-diabetic, immunomodulatory, cardiant, neuroprotective,
 CC anti-inflammatory, neuroprotective, nocrotropic, antiarthritic, vasotropic,
 CC ophthalmological, immunomodulatory and cardiovascular activities, and can
 CC be used as mPES-1 inhibitors and in gene therapy. The antisense compound
 CC can be used for preparing a composition for treating a disease or
 CC condition associated with mPES-1 e.g., inflammation, Alzheimer's
 CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
 CC ophthalmic, immunological, cardiovascular or neurological disorder.

XX Sequence 20 BP; 4 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 847 CCTGCGCTCCCAAGTCT 866
 DB 20 CCTGCGCTCCCAAGTCT 1

RESULT 546

ADMI4957/C

ID ADMI4957 standard; DNA; 20 BP.

AC ADMI4957;

DT 01-JUL-2004 (first entry)

XX Human mPES-1 chimeric antisense oligonucleotide SEQ ID NO:1144.

XX chimeric; antisense oligonucleotide; phosphorothioate; human;
 KW microsomal prostaglandin E2 synthase inhibitor; cytoskeletal; anti-diabetic;
 KW immunomodulatory; cardiant; neuroprotective; anti-inflammatory;
 KW neuroprotective; nocrotropic; antiarthritic; vasotropic; ophthalmological;
 KW immunomodulatory; cardiovascular; gene therapy; inflammation;
 KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
 KW reperfusion injury; ophthalmic disorder; immunological disorder;
 KW cardiovascular disorder; neurological disorder; ss.

OS Homo sapiens.
 OS Synthetic.

Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= b

FT /mod_base= OTHER
 FT /note= "phosphorothioate linkages and all cytidine
 FT residues are 5-methylcytidines"

FT modified_base 1..5
 FT /tag= a

FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyls"

FT modified_base 16..20
 FT /tag= c

FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyls"

PN WO2004028458-A2.

PD 08-APR-2004.

PF 25-SEP-2003; 2003WO-US030374.

PR 25-SEP-2003; 2002US-0413549P.

PA (PHAA) PHARMACIA CORP.

PI Gierse JK;

DR WPI; 2004-305094/28.

PT New antisense compound, having a sequence targeted to a nucleic acid
 PT encoding mPES-1, useful for preparing a composition for treating e.g.,
 PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
 PT ischemia.

PS Claim 4; SEQ ID NO 1144; 132pp; English.

XX The present sequence represents a chimeric antisense oligonucleotide
 CC targeted to human microsomal prostaglandin E2 synthase (mPES-1). The
 CC human mPES-1 gene is located on chromosome 9, more specifically to
 CC 9q34.3. The present invention also describes: (1) antisense compounds,
 CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
 CC mPES-1, which specifically hybridise with the nucleic acid mPES-1 and
 CC inhibits its expression; (2) a method of inhibiting the expression of
 CC mPES-1 in cells or tissues; and (3) a method of treating an animal
 CC having a disease or condition associated with mPES-1. mPES-1 chimeric
 CC antisense oligonucleotides and antisense compounds have cytoskeletal,
 CC anti-diabetic, immunomodulatory, cardiant, neuroprotective,
 CC anti-inflammatory, neuroprotective, nocrotropic, antiarthritic, vasotropic,
 CC ophthalmological, immunomodulatory and cardiovascular activities, and can
 CC be used as mPES-1 inhibitors and in gene therapy. The antisense compound

CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGEs-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.

XX Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 720 AGCCTCTGAGTAGCTGGGA 739

Db 20 AGCCTCTGAGTAGCTGGGA 1

RESULT 547
ADM1553/C
ID ADM1553 standard; DNA; 20 BP.

AC ADM1553;

DT 01-JUL-2004 (first entry)

DE Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:1740.

XX chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase inhibitor; mPGEs-1 inhibitor;
KW immunomodulator; cardiant; neuroprotective; antidiabetic;
KW neuroprotective; cardiant; neuroprotective; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antidiabetic;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.

OS Homo sapiens.
XX Synthetic.

Key Location/Qualifiers
modified_base 1..20

FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"

FT modified_base 1..5

FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"

FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"

FT WO2004028458-A2.

XX 08-APR-2004.

XX 25-SEP-2003; 2003WO-US030374.

XX 25-SEP-2002; 2002US-0413549P.

XX (PHAA) PHARMACIA CORP.

XX Gierse JK;

XX WPI; 2004-305094/28.

PT New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGEs-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischaemia.

PS Claim 4; SEQ ID NO 1740; 132pp; English.

XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGEs-1). The
CC human mPGEs-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGEs-1, which specifically hybridise with the nucleic acid mPGEs-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGEs-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGEs-1. mPGEs-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGEs-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGEs-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.

XX Sequence 20 BP; 11 A; 4 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 770 TTTTGATTTTATTAGTAGAGA 789

Db 20 TTTTGATTTTATTAGTAGAGA 1

RESULT 548

ADM15081/C
ID ADM15081 standard; DNA; 20 BP.

AC ADM15081;

DT 01-JUL-2004 (first entry)

DE Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:1268.

XX chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase inhibitor; mPGEs-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosaric; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antidiabetic;
KW neuroprotective; cardiant; neuroprotective; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antidiabetic;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.

OS Homo sapiens.
XX Synthetic.

Key Location/Qualifiers
modified_base 1..20

FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"

FT modified_base 1..5

FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"

FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"

FT WO2004028458-A2.

XX 08-APR-2004.

XX 25-SEP-2003; 2003WO-US030374.
PF
XX
XX 25-SEP-2002; 2002US-0413549P.
PR
XX
XX (PHAA) PHARMACIA CORP.
PA
XX
XX Gierse JK;
PI
XX
XX MPI; 2004-305094/28.
DR
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mpGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
XX
PS Claim 4; SEQ ID NO 1268; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mpGES-1). The
CC human mpGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mpGES-1, which specifically hybridize with the nucleic acid mpGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mpGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mpGES-1. MPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC anti-diabetic, immunomodulator, cardiant, neuroprotective,
CC anti-inflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mpGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mpGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 4 A; 7 C; 6 G; 3 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 719 CAGCCTCTGAGTAGCTGGG 738
Db 20 CAGCCTCTGAGTAGCTGGG 1
RESULT 549
ADM15268/c
ID ADM15268 standard; DNA; 20 BP.
XX
XX ADM15268;
AC
XX
XX 01-JUL-2004 (first entry)
DT
XX
XX Human mpGES-1 chimeric antisense oligonucleotide SEQ ID NO:1455.
DE
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mpGES-1; mpGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytostatic; anti-diabetic;
KW immunomodulator; cardiant; neuroprotective; anti-inflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; se.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT modified_base 1..20

FT
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX MPI; 2004-305094/28.
XX
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mpGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
XX Claim 4; SEQ ID NO 1455; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mpGES-1). The
CC human mpGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mpGES-1, which specifically hybridize with the nucleic acid mpGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mpGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mpGES-1. MPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC anti-diabetic, immunomodulator, cardiant, neuroprotective,
CC anti-inflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mpGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mpGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 3 A; 5 C; 9 G; 3 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 846 GCCTCGGCGCTCCCAAGTGC 865
Db 20 GCCTCGGCGCTCCCAAGTGC 1
RESULT 550
ADM14958/c
ID ADM14958 standard; DNA; 20 BP.
XX
XX ADM14958;
AC
XX
XX 01-JUL-2004 (first entry)
DT
XX
XX Human mpGES-1 chimeric antisense oligonucleotide SEQ ID NO:1455.
DE

XX	chimeric; antisense oligonucleotide; phosphorothioate; human;
KW	microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW	microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW	immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW	immunoprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW	immunomodulatory; cardiovascular; gene therapy; inflammation;
KW	Alzheimer's disease; arthritis; diabetes; cancer; ischemia;
KW	reperfusion injury; ophthalmic disorder; immunological disorder;
KW	cardiovascular disorder; neurological disorder; ss.
XX	
OS	Homo sapiens.
XX	Synthetic.
XX	
FT	Key
FT	Location/Qualifiers
FT	1..20
FT	/*tag= b
FT	/mod_base= OTHER
FT	/note= "phosphorothioate linkages and all cytidine
FT	residues are 5-methylcytidines"
FT	1..5
FT	/*tag= a
FT	/mod_base= OTHER
FT	/note= "2'-O-methoxyethyls"
FT	16..20
FT	/*tag= c
FT	/mod_base= OTHER
FT	/note= "2'-O-methoxyethyls"
XX	
PN	WO2004028458-A2.
XX	
PD	08-APR-2004.
XX	
XX	25-SEP-2003; 2003WO-US030374.
XX	
XX	25-SEP-2002; 2002US-0413549P.
PR	
XX	
PA	(PHMA) PHARMACIA CORP.
XX	
PI	Glaxo JK;
XX	
DR	WPI; 2004-305094/28.
XX	
PT	New antisense compound, having a sequence targeted to a nucleic acid
PT	encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT	inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT	ischemia.
XX	
PS	Claim 4; SEQ ID NO 1145; 132pp; English.
XX	
CC	The present sequence represents a chimeric antisense oligonucleotide
CC	targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC	human mPGES-1 gene is located on chromosome 9, more specifically to
CC	9q34.3. The present invention also describes: (1) antisense compounds,
CC	having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC	mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
CC	inhibit its expression; (2) a method of inhibiting the expression of
CC	mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC	having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC	antisense oligonucleotides and antisense compounds have cytostatic,
CC	antidiabetic, immunomodulatory, cardiant, neuroprotective,
CC	antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC	ophthalmological, immunomodulatory and cardiovascular activities, and can
CC	be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC	can be used for preparing a composition for treating a disease or
CC	condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC	disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
CC	ophthalmic, immunological, cardiovascular or neurological disorder.
XX	
SQ	Sequence 20 BP; 4 A; 5 C; 8 G; 3 T; 0 U; 0 Other;

Matches	20	Conservative	0	Mismatches	0	Indels	0	Gaps
Qy	848	CTCGGCTCCCAAGTCTG	867					
Db	20	CTCGGCTCCCAAGTCTG	1					
RESULT 551								
ID	AD045369	standard; DNA; 20 BP.						
XX	AD045369;							
XX	15-JUL-2004	(first entry)						
DE	Human oligonucleotide #735.							
XX	Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;							
KW	CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;							
KW	tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;							
KW	lung disease; hyper-responsiveness; adenosine; adenosine A receptor;							
KW	asthma; lung allergy; inflammation; inflammatory disease;							
KW	airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;							
KW	chronic obstructive pulmonary disease; COPD; allergic rhinitis;							
KW	acute respiratory distress syndrome; pulmonary hypertension;							
KW	lung inflammation; bronchitis; airway obstruction; bronchoconstriction.							
OS	Homo sapiens.							
XX	US2004049022-A1.							
XX	11-MAR-2004.							
XX	25-JUL-2003; 2003US-00627930.							
XX	23-APR-2002; 2002WO-US013135.							
PR	23-APR-2002; 2002WO-US013143.							
XX	(NYCE/) NYCE J W.							
XX	(SAND/) SANDRASAGRA A.							
PA	(TANG/) TANG L.							
PA	(AGUI/) AGUILAR D.							
PA	(MILL/) MILLER S.							
PA	(SHAH/) SHAHABUDDIN S.							
PA	(LUHH/) LU H.							
PA	(CONG/) CONG H.							
XX	Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;							
PI	Shahabuddin S, Lu H, Cong H;							
DR	WPI; 2004-293804/27.							
XX	Novel single or multiple target oligonucleotide anti-sense to e.g.							
PT	initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,							
PT	RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.							
PT	asthma.							
XX	Claim 2; SEQ ID NO 735; 174pp; English.							
PS	The invention relates to oligonucleotides anti-sense to an initiation							
CC	codon, coding region, 5' or 3' intron-exon junction, intron or region							
CC	with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target							
CC	chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)-							
CC	-5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,							
CC	tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention							
CC	also relates to a method of screening a candidate compound that binds to							
CC	one or more nucleic acid target(s) or expressed product(s), for the							
CC	prevention and/or treatment of a respiratory or lung disease. The							
CC	oligonucleotides are useful for reducing or inhibiting expression of a							
CC	gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,							
CC	CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,							
CC	tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are							
CC	useful for preventing or treating a respiratory or lung disease. The							

CC respiratory or lung disease is associated with hyper-responsiveness to
CC and/or increased levels of, adenosine and/or levels of adenosine A
CC receptor(s), and/or asthma and/or lung allergies associated with
CC inflammation or an inflammatory disease. The respiratory or lung disease
CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
CC hypertension, lung inflammation, bronchitis, airway obstruction or
CC bronchoconstriction. This sequence represents an oligonucleotide of the
CC invention.

XX SQ Sequence 20 BP; 3 A; 4 C; 10 G; 3 T; 0 U; 0 Other;

XX Query Match 2.0%; Score 20; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 646 AGGCTGAGTGCAGTGGCGC 665

Db 1 AGGCTGAGTGCAGTGGCGC 20

RESULT 552

AD046429 standard; DNA; 20 BP.

XX ADO46429;

XX 15-JUL-2004 (first entry)

XX Human oligonucleotide #1795.

XX Human; sg: interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
XX CCR1, CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
XX tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
XX lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
XX asthma; lung allergy; inflammation; inflammatory disease;
XX airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
XX chronic obstructive pulmonary disease; COPD; allergic rhinitis;
XX acute respiratory distress syndrome; pulmonary hypertension;
XX lung inflammation; bronchitis; airway obstruction; bronchoconstriction.

XX Homo sapiens.

XX US2004049022-A1.

XX 11-MAR-2004.

XX 25-JUL-2003; 2003US-00627930.

XX 23-APR-2002; 2002WO-US013135.

PR 23-APR-2002; 2002WO-US013143.

XX (NYCE/) NYCE J W.

PA (SAND/) SANDRASAGRA A.

PA (TANG/) TANG L.

PA (AGUI/) AGUIAR D.

PA (MTL/) MILLER S.

PA (SHAH/) SHAHABUDDIN S.

PA (LUH/) LU H.

PA (CONG/) CONG H.

PI NYCE JW, Sandrasagra A, Tang L, Aguiar D, Miller S;

PI Shahabuddin S, Lu H, Cong H;

XX WPI; 2004-293804/27.

XX Novel single or multiple target oligonucleotide anti-sense to e.g.

PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,

PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.

PT asthma.

PS Claim 2; SEQ ID NO 1796; 174pp; English.

XX The invention relates to oligonucleotides anti-sense to an initiation
CC codon, coding region, 5' or 3' intron-exon junction, intron or region
CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
CC -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
CC also relates to a method of screening a candidate compound that binds to
CC one or more nucleic acid target(s) or expressed product(s), for the
CC prevention and/or treatment of a respiratory or lung disease. The
CC oligonucleotides are useful for reducing or inhibiting expression of a
CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
CC useful for preventing or treating a respiratory or lung disease. The
CC respiratory or lung disease is associated with hyper-responsiveness to
CC and/or increased levels of, adenosine and/or levels of adenosine A
CC receptor(s), and/or asthma and/or lung allergies associated with
CC inflammation or an inflammatory disease. The respiratory or lung disease
CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
CC hypertension, lung inflammation, bronchitis, airway obstruction or
CC bronchoconstriction. This sequence represents an oligonucleotide of the
CC invention.

XX SQ Sequence 20 BP; 3 A; 5 C; 9 G; 3 T; 0 U; 0 Other;

XX Query Match 2.0%; Score 20; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 643 CCCAGGCTGAGTGCAGTGG 662

Db 1 CCCAGGCTGAGTGCAGTGG 20

RESULT 553

AD046442 standard; DNA; 20 BP.

XX ADO46442;

XX 15-JUL-2004 (first entry)

XX Human oligonucleotide #1808.

XX Human; sg: interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
XX CCR1, CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
XX tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
XX lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
XX asthma; lung allergy; inflammation; inflammatory disease;
XX airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
XX chronic obstructive pulmonary disease; COPD; allergic rhinitis;
XX acute respiratory distress syndrome; pulmonary hypertension;
XX lung inflammation; bronchitis; airway obstruction; bronchoconstriction.

XX Homo sapiens.

XX US2004049022-A1.

XX 11-MAR-2004.

XX 25-JUL-2003; 2003US-00627930.

XX 23-APR-2002; 2002WO-US013135.

PR 23-APR-2002; 2002WO-US013143.

XX (NYCE/) NYCE J W.

PA (SAND/) SANDRASAGRA A.

PA (TANG/) TANG L.

PA (AGUI/) AGUIAR D.

PA (MTL/) MILLER S.

PA (SHAH/) SHAHABUDDIN S.
 PA (LUHH/) LU H.
 PA (CONG/) CONG H.
 XX
 PI Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
 PI Shahabuddin S, Lu H, Cong H;
 XX
 DR WPI: 2004-293804/27.
 XX
 PT Novel single or multiple target oligonucleotide anti-sense to e.g.
 PT initiation codon, intron of respiratory disease-relevant gene e.g. CCRI,
 PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
 PT asthma.
 XX
 PS Claim 2; SEQ ID NO 1809; 174pp; English.
 XX
 CC The invention relates to oligonucleotides anti-sense to an initiation
 CC codon, coding region, 5' or 3' intron-exon junction, intron or region
 CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
 CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
 CC -5 receptor, CCRI, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
 CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
 CC also relates to a method of screening a candidate compound that binds to
 CC one or more nucleic acid target(s) or expressed product(s), for the
 CC prevention and/or treatment of a respiratory or lung disease. The
 CC oligonucleotides are useful for reducing or inhibiting expression of a
 CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
 CC CCRI, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
 CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
 CC useful for preventing or treating a respiratory or lung disease. The
 CC respiratory or lung disease is associated with hyper-responsiveness to
 CC and/or increased levels of, adenosine and/or levels of adenosine A
 CC receptor(s), and/or asthma and/or lung allergies associated with
 CC inflammation or an inflammatory disease. The respiratory or lung disease
 CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
 CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
 CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
 CC hypertension, lung inflammation, bronchitis, airway obstruction or
 CC bronchoconstriction. This sequence represents an oligonucleotide of the
 CC invention.
 XX
 SQ Sequence 20 BP; 5 A; 0 C; 5 G; 10 T; 0 U; 0 Other;
 XX
 Query Match 2.0%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 772 TTGATTTTCTAGTAGAGTG 791
 |||||
 1 TTGTATTTTCTAGTAGAGTG 20
 DB
 RESULT 554
 ADO45266
 ID ADO45266 standard; DNA; 20 BP.
 XX
 AC ADO45266;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Human oligonucleotide #632.
 XX
 KW Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
 KW CCR1; CCR3; Botaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
 KW tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
 KW lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
 KW asthma; lung allergy; inflammation; inflammatory disease;
 KW airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
 KW chronic obstructive pulmonary disease; COPD; allergic rhinitis;
 KW acute respiratory distress syndrome; pulmonary hypertension;
 KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
 XX
 OS Homo sapiens.

XX US2004049022-A1.
 PN
 XX
 PD 11-MAR-2004.
 XX
 PF 25-JUL-2003; 2003US-00627930.
 XX
 PR 23-APR-2002; 2002WO-US013135.
 PR 23-APR-2002; 2002WO-US013143.
 XX
 PA (NYCE/) NYCE J W.
 PA (SAND/) SANDRASAGRA A.
 PA (TANG/) TANG L.
 PA (AGUI/) AGUILAR D.
 PA (MILL/) MILLER S.
 PA (SHAH/) SHAHABUDDIN S.
 PA (LUHH/) LU H.
 PA (CONG/) CONG H.
 XX
 PI Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
 PI Shahabuddin S, Lu H, Cong H;
 XX
 DR WPI: 2004-293804/27.
 XX
 PT Novel single or multiple target oligonucleotide anti-sense to e.g.
 PT initiation codon, intron of respiratory disease-relevant gene e.g. CCRI,
 PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
 PT asthma.
 XX
 PS Claim 2; SEQ ID NO 632; 174pp; English.
 XX
 CC The invention relates to oligonucleotides anti-sense to an initiation
 CC codon, coding region, 5' or 3' intron-exon junction, intron or region
 CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
 CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
 CC -5 receptor, CCRI, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
 CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
 CC also relates to a method of screening a candidate compound that binds to
 CC one or more nucleic acid target(s) or expressed product(s), for the
 CC prevention and/or treatment of a respiratory or lung disease. The
 CC oligonucleotides are useful for reducing or inhibiting expression of a
 CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
 CC CCRI, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
 CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
 CC useful for preventing or treating a respiratory or lung disease. The
 CC respiratory or lung disease is associated with hyper-responsiveness to
 CC and/or increased levels of, adenosine and/or levels of adenosine A
 CC receptor(s), and/or asthma and/or lung allergies associated with
 CC inflammation or an inflammatory disease. The respiratory or lung disease
 CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
 CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
 CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
 CC hypertension, lung inflammation, bronchitis, airway obstruction or
 CC bronchoconstriction. This sequence represents an oligonucleotide of the
 CC invention.
 XX
 SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;
 XX
 Query Match 2.0%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 732 AGCTGGGACTACAGGCGCC 751
 |||||
 1 AGCTGGGACTACAGGCGCC 20
 DB
 RESULT 555
 ADO46449
 ID ADO46449 standard; DNA; 20 BP.
 XX
 AC ADO46449;
 XX

DT 15-JUL-2004 (first entry)
 XX
 DE Human oligonucleotide #1815.
 XX
 KM Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
 KM CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
 KM tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
 KM lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
 KM asthma; lung allergy; inflammation; inflammatory disease;
 KM airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
 KM chronic obstructive pulmonary disease; COPD; allergic rhinitis;
 KM acute respiratory distress syndrome; pulmonary hypertension;
 KM lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
 XX
 OS Homo sapiens.
 XX
 XX US2004049022-A1.
 XX
 PD 11-MAR-2004.
 XX
 PF 25-JUL-2003; 2003US-00627930.
 XX
 PR 23-APR-2002; 2002WO-US013135.
 PR 23-APR-2002; 2002WO-US013143.
 XX
 PA (NYCE/) NYCE J W.
 PA (SAND/) SANDRASAGRA A.
 PA (TANG/) TANG L.
 PA (AGUI/) AGUILAR D.
 PA (MILL/) MILLER S.
 PA (SHAH/) SHAHABUDDIN S.
 PA (LUHH/) LU H.
 PA (CONG/) CONG H.
 XX
 PI Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
 PI Shahabuddin S, Lu H, Cong H;
 XX
 DR WPI; 2004-293804/27.
 XX
 PT Novel single or multiple target oligonucleotide anti-sense to e.g.
 PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
 PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
 PT asthma.
 XX
 PS Claim 2; SEQ ID NO 1816; 174pp; English.
 XX
 CC The invention relates to oligonucleotides anti-sense to an initiation
 CC codon, coding region, 5' or 3' intron-exon junction, intron or region
 CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
 CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
 CC -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
 CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
 CC also relates to a method of screening a candidate compound that binds to
 CC one or more nucleic acid target(s) or expressed product(s), for the
 CC prevention and/or treatment of a respiratory or lung disease. The
 CC oligonucleotides are useful for reducing or inhibiting expression of a
 CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
 CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
 CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
 CC useful for preventing or treating a respiratory or lung disease. The
 CC respiratory or lung disease is associated with hyper-responsiveness to
 CC and/or increased levels of, adenosine and/or levels of adenosine A
 CC receptor(s), and/or asthma and/or lung allergies associated with
 CC inflammation or an inflammatory disease. The respiratory or lung disease
 CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
 CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
 CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
 CC hyperextension, lung inflammation, bronchitis, airway obstruction or
 CC bronchoconstriction. This sequence represents an oligonucleotide of the
 CC invention.
 XX
 SQ Sequence 20 BP; 2 A; 12 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 369 TCACCTGCTCAGCTCCC 388
 DB 1 TCACCTGCTCAGCTCCC 20
 RESULT 556
 ADO46450
 ID ADO46450 standard; DNA; 20 BP.
 AC ADO46450;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Human oligonucleotide #1816.
 XX
 KM Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
 KM CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
 KM tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
 KM lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
 KM asthma; lung allergy; inflammation; inflammatory disease;
 KM airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
 KM chronic obstructive pulmonary disease; COPD; allergic rhinitis;
 KM acute respiratory distress syndrome; pulmonary hypertension;
 KM lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
 XX
 OS Homo sapiens.
 XX
 XX US2004049022-A1.
 XX
 PD 11-MAR-2004.
 XX
 PF 25-JUL-2003; 2003US-00627930.
 XX
 PR 23-APR-2002; 2002WO-US013135.
 PR 23-APR-2002; 2002WO-US013143.
 XX
 PA (NYCE/) NYCE J W.
 PA (SAND/) SANDRASAGRA A.
 PA (TANG/) TANG L.
 PA (AGUI/) AGUILAR D.
 PA (MILL/) MILLER S.
 PA (SHAH/) SHAHABUDDIN S.
 PA (LUHH/) LU H.
 PA (CONG/) CONG H.
 XX
 PI Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
 PI Shahabuddin S, Lu H, Cong H;
 XX
 DR WPI; 2004-293804/27.
 XX
 PT Novel single or multiple target oligonucleotide anti-sense to e.g.
 PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
 PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
 PT asthma.
 XX
 PS Claim 2; SEQ ID NO 1817; 174pp; English.
 XX
 CC The invention relates to oligonucleotides anti-sense to an initiation
 CC codon, coding region, 5' or 3' intron-exon junction, intron or region
 CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
 CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
 CC -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
 CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
 CC also relates to a method of screening a candidate compound that binds to
 CC one or more nucleic acid target(s) or expressed product(s), for the
 CC prevention and/or treatment of a respiratory or lung disease. The
 CC oligonucleotides are useful for reducing or inhibiting expression of a
 CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
 CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,

CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
 CC useful for preventing or treating a respiratory or lung disease. The
 CC respiratory or lung disease is associated with hyper-responsiveness to
 CC and/or increased levels of, adenosine and/or levels of adenosine A
 CC receptor(s), and/or asthma and/or lung allergies associated with
 CC inflammation or an inflammatory disease. The respiratory or lung disease
 CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
 CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
 CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
 CC hypertension, lung inflammation, bronchitis, airway obstruction or
 CC bronchoconstriction. This sequence represents an oligonucleotide of the
 CC invention.

CC Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 379 TCAGCCTCCCAAGTGTGG 398
 |||||
 Db 1 TCAGCCTCCCAAGTGTGG 20

RESULT 557
 ADO81016/C
 ID ADO81016 standard; DNA; 20 BP.

AC ADO81016;

DT 29-JUL-2004 (first entry)

DE Human prion protein microsatellite locus primer #12.

KM gene typing; polymorphic microsatellite loci; PML;
 KM disease predisposition; microsatellite marker; prion disease;
 KM cystic fibrosis; malignant hyperthermia syndrome; metabolic disease;
 KM milk protein; hormone; transcription factor; p17-blue-vector; human;
 KM microsatellite; PCR; primer; ss.

OS Homo sapiens.

PN DE10236711-A1.

PD 26-FEB-2004.

PF 09-AUG-2002; 2002DE-01036711.

PR 09-AUG-2002; 2002DE-01036711.

PA (UVAH-) UNIV HOHENHEIM.

PI Geldermann H, Preuss S, Han Y;

DR WPI; 2004-215730/21.

PT Typing genes that contain polymorphic microsatellite loci, useful for
 PT identifying predisposition to disease, by amplification and determining
 PT length of amplicons.

PS Example 3; Page 34; 64pp; German.

CC The invention describes a method of typing (M1) a gene (I) that has one
 CC or more polymorphic microsatellite loci (PML). The method comprises: PCR
 CC amplification of at least one DNA region of (I) that includes PML, using
 CC as template a DNA sample containing at least one segment of (I); and
 CC determining the length of the resulting amplicon(s). Also described are:
 CC a method of determining (M2) microsatellite markers (MM) for
 CC predisposition to a disease, associated with a gene that includes one or
 CC more PML; and diagnosis (M3) of diseases associated with gene that
 CC include PML. The method is used to identify microsatellite markers, in a
 CC disease-related gene, that are associated with a predisposition to
 CC diseases and for diagnosis of such diseases, especially prion diseases

CC but also cystic fibrosis, malignant hyperthermia syndrome in pigs and
 CC metabolic diseases; also to type genes that encode milk proteins,
 CC hormones or transcription factors. The method is simpler, quicker and
 CC particularly less expensive than known methods based on sequencing. This
 CC sequence represents a primer used to genotype a region of the human prion
 CC protein (PrP) comprising a polymorphic microsatellite locus.

CC Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03; Mismatches 0; Indels 0; Gaps 0;

Qy 725 COTGAGTAGCTGGGACTACA 744
 |||||
 Db 20 COTGAGTAGCTGGGACTACA 1

RESULT 558
 ADO52209
 ID ADO52209 standard; DNA; 20 BP.

AC ADO52209;

DT 12-AUG-2004 (first entry)

DE Human inhibitor of apoptosis-like antisense oligonucleotide seqid 83.

KM cytosstatic; gene therapy; inhibitors of apoptosis-like; IAP-like;
 KM IAP-like modulator; IAP-like associated disorder;
 KM hyperproliferative disorder; human; antisense oligonucleotide;
 KM antisense technology; ss.

OS Homo sapiens.

PN modified_base

FT modified_base 1..20

FT /tag= b

FT /mod_base= OTHER

FT /note= "OTHER= Phosphorothioate backbone. All cytidines

FT are 5-methylcytidines"

FT modified_base 1..5

FT /tag= a

FT /mod_base= OTHER

FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"

FT modified_base 15..20

FT /tag= c

FT /mod_base= OTHER

FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"

PN US2004102395-A1.

PD 27-MAY-2004.

PF 22-NOV-2002; 2002US-00303325.

PR 22-NOV-2002; 2002US-00303325.

PA (ISIS-) ISIS PHARM INC.

PI Bennett CF, Dobie KW;

DR WPI; 2004-399725/37.

PT New compound targeted to a nucleic acid molecule encoding inhibitors of
 PT apoptosis (IAP)-like and inhibits expression of IAP-like, useful for
 PT modulating the expression of IAP-like or for treating, e.g.
 PT hyperproliferative disorder.

PS Example 14; SEQ ID NO 83; 58pp; English.

CC The invention describes a compound 8-80 nucleobases in length targeted to
 CC a nucleic acid molecule encoding inhibitors of apoptosis (IAP)-like,

CC where the compound specifically hybridises with the nucleic acid molecule
CC encoding IAP-like comprising 16000 bp (SEQ ID NO. 4) and inhibits the
CC expression of IAP-like. Also described are: inhibiting the expression of
CC IAP-like in cells or tissues; screening for a modulator of IAP-like; a
CC diagnostic method for identifying a disease state comprising identifying
CC the presence of IAP-like in a sample using at least one of the primers
CC selected from 2 sequences comprising SEQ ID NO. 5 or 6, or the probe
CC comprising SEQ ID NO. 7; a kit or assay device comprising the compound,
CC and treating an animal having a disease or condition associated with IAP-
CC like. The compound is useful for modulating the expression of IAP-like.
CC It is also useful for diagnosing or treating diseases associated with
CC expression of IAP-like, e.g. a hyperproliferative disorder. This sequence
CC represents a human inhibitor of apoptosis (IAP)-like antisense
CC oligonucleotide.
XX
SQ Sequence 20 BP; 3 A; 9 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 969 CTCGGCTCACTGCACTCT 988
DB 1 CTCGGCTCACTGCACTCT 20
RESULT 559
AD052273/C
ID AD052273 standard; DNA; 20 BP.
XX
XX AD052273;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human inhibitor of apoptosis-like antisense oligonucleotide seqid 149.
XX
XX cytosolic; gene therapy; inhibitors of apoptosis-like; IAP-like;
XX IAP-like modulator; IAP-like associated disorder;
XX hyperproliferative disorder; human; antisense oligonucleotide;
XX antisense technology; ss.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= Phosphorothioate backbone. All cytidines
FT are 5-methylcytidines"
FT 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
FT modified_base 15..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
XX
XX US2004102395-A1.
XX
XX 27-MAY-2004.
XX
XX 22-NOV-2002; 2002US-00303325.
XX
XX 22-NOV-2002; 2002US-00303325.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Dobie KW;
XX
XX WPI; 2004-399725/37.
XX
XX New compound targeted to a nucleic acid molecule encoding inhibitors of

PT apoptosis (IAP)-like and inhibits expression of IAP-like, useful for
PT modulating the expression of IAP-like or for treating, e.g.
PT hyperproliferative disorder.
XX
XX Example 14; SEQ ID NO 147; 58bp; English.
XX
CC The invention describes a compound 8-80 nucleobases in length targeted to
CC a nucleic acid molecule encoding inhibitors of apoptosis (IAP)-like,
CC where the compound specifically hybridises with the nucleic acid molecule
CC encoding IAP-like comprising 16000 bp (SEQ ID NO. 4) and inhibits the
CC expression of IAP-like. Also described are: inhibiting the expression of
CC IAP-like in cells or tissues; screening for a modulator of IAP-like; a
CC diagnostic method for identifying a disease state comprising identifying
CC the presence of IAP-like in a sample using at least one of the primers
CC selected from 2 sequences comprising SEQ ID NO. 5 or 6, or the probe
CC comprising SEQ ID NO. 7; a kit or assay device comprising the compound,
CC and treating an animal having a disease or condition associated with IAP-
CC like. The compound is useful for modulating the expression of IAP-like.
CC It is also useful for diagnosing or treating diseases associated with
CC expression of IAP-like, e.g. a hyperproliferative disorder. This sequence
CC represents a human inhibitor of apoptosis (IAP)-like antisense
CC oligonucleotide.
XX
SQ Sequence 20 BP; 5 A; 3 C; 9 G; 3 T; 0 U; 0 Other;
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 969 CTCGGCTCACTGCACTCT 988
DB 20 CTCGGCTCACTGCACTCT 1
RESULT 560
AAV27991/C
ID AAV27991 standard; DNA; 21 BP.
XX
XX AAV27991;
XX
DT 25-SEP-1998 (first entry)
XX
DE Ataxia telangiectasia exon 17 primer 2.
XX
XX ss; PCR; primer; amplification; ataxia telangiectasia; diagnosis; human;
XX radiation; breast cancer.
XX
XX Synthetic.
XX Homo sapiens.
XX WO9822621-A1.
XX
XX 28-MAY-1998.
XX
XX 17-NOV-1997; 97WO-US020953.
XX
XX 20-NOV-1996; 96US-00753147.
XX
XX (VIRG-) VIRGINIA MASON RES CENT.
XX
XX Concannon P;
XX
XX WPI; 1998-312503/27.
XX
XX Method of detecting ataxia telangiectasia - comprises use of primers
XX based on intron-exon boundaries, useful for diagnosing disease in
XX heterozygotes.
XX
XX Claim 6; Page 6; 47p; English.
XX
CC The primers AAV27964-V28066 are used to amplify ataxia telangiectasia
CC (ATM) exons and their adjacent splice junction sites. These can be used
CC as a method of detecting a mutation in the ATM gene by comparing the PCR

CC products of amplification from a sample from a patient suspected of
CC having an ATM mutation with a sample from a non-mutated ATM patient. This
CC method is especially useful for diagnosing ataxia telangiectasia in
CC heterozygotes and can be used to locate the positions of the mutation.
CC The diagnosis of ataxia telangiectasia in patients needing therapeutic
CC radiation will prevent fatal radiation burns and the development of
CC breast cancer which can occur

XX
SQ Sequence 21 BP; 3 A; 10 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 643 CCCAGGCTGAGTGCAGTGG 662
DB 21 CCCAGGCTGAGTGCAGTGG 2

RESULT 561
AAZ25145

ID AAZ25145 standard; DNA; 21 BP.

AC AAZ25145;

DT 13-DEC-1999 (first entry)

DE Human short interspersed repetitive element PCR primer #3.

XX Human; short interspersed repetitive element; SINE; PCR; primer;
XX Oncohychnus; restriction primer; short interspersed repeated sequence;
XX eukaryote; restricted polymerase chain reaction fingerprinting;
XX identification; DNA specimen; discrimination; ss.

XX Synthetic.

OS Homo sapiens.

XX JP2913035-B1.

XX 28-JUN-1999.

XX 10-JUL-1998; 98JP-00195692.

XX 10-JUL-1998; 98JP-00195692.

XX (NORQ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.

XX WPI; 1999-583348/50.

XX Restriction primer for distinguishing individuals with short interspersed
XX repeated sequence of eukaryotes by restricted polymerase chain reaction
XX fingerprinting.

XX Claim 6; Page 3; 17pp; Japanese.

XX The present invention describes a restriction primer for eukaryotic short
XX interspersed repeated sequences (SINE), which has one or more additional
XX bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
XX the SINE. The annealing temperature of the primer to the DNA sequence is
XX kept higher than the fusion temperature of the primer during polymerase
XX chain reaction (PCR). The PCR fragments obtained are subjected to
XX electrophoresis to obtain a fingerprint. By comparing the polymorphs from
XX the electrophoresis band pattern, eukaryotic individuals are
XX distinguished. The primer is used for amplifying a eukaryotic
XX deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
XX polymerase chain reaction (PCR) fingerprinting. In particular it may be
XX used individual identification of humans for medical and legal
XX applications and ecological studies. DNA specimens in traces
XX (approximately 10 ng in mass) can be used for individual discrimination
XX of eukaryotes using the primer in a polymerase chain reaction (PCR).
XX AAZ25143 to AAZ25191 represent specifically claimed examples of primers
XX from the present invention

SQ Sequence 21 BP; 5 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 868 GGATTACAGCGGTGAGCCAC 887
DB 1 GGATTACAGCGGTGAGCCAC 20

RESULT 562

AAZ25143

ID AAZ25143 standard; DNA; 21 BP.

AC AAZ25143;

DT 13-DEC-1999 (first entry)

DE Human short interspersed repetitive element PCR primer #1.

XX Human; short interspersed repetitive element; SINE; PCR; primer;
XX Oncohychnus; restriction primer; short interspersed repeated sequence;
XX eukaryote; restricted polymerase chain reaction fingerprinting;
XX identification; DNA specimen; discrimination; ss.

XX Synthetic.

OS Homo sapiens.

XX JP2913035-B1.

XX 28-JUN-1999.

XX 10-JUL-1998; 98JP-00195692.

XX 10-JUL-1998; 98JP-00195692.

XX (NORQ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.

XX WPI; 1999-583348/50.

XX Restriction primer for distinguishing individuals with short interspersed
XX repeated sequence of eukaryotes by restricted polymerase chain reaction
XX fingerprinting.

XX Claim 6; Page 3; 17pp; Japanese.

XX The present invention describes a restriction primer for eukaryotic short
XX interspersed repeated sequences (SINE), which has one or more additional
XX bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
XX the SINE. The annealing temperature of the primer to the DNA sequence is
XX kept higher than the fusion temperature of the primer during polymerase
XX chain reaction (PCR). The PCR fragments obtained are subjected to
XX electrophoresis to obtain a fingerprint. By comparing the polymorphs from
XX the electrophoresis band pattern, eukaryotic individuals are
XX distinguished. The primer is used for amplifying a eukaryotic
XX deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
XX polymerase chain reaction (PCR) fingerprinting. In particular it may be
XX used individual identification of humans for medical and legal
XX applications and ecological studies. DNA specimens in traces
XX (approximately 10 ng in mass) can be used for individual discrimination
XX of eukaryotes using the primer in a polymerase chain reaction (PCR).
XX AAZ25143 to AAZ25191 represent specifically claimed examples of primers
XX from the present invention

SQ Sequence 21 BP; 6 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 868 GGATTACAGCGGTGAGCCAC 887
|||||

DB 1 GGATTACAGCGGTAGCCAC 20

RESULT 563

AAZ25144
ID AAZ25144 standard; DNA; 21 BP.

AC AAZ25144;

DT 13-DEC-1999 (first entry)

DE Human short interspersed repetitive element PCR primer #2.

XX Human; short interspersed repetitive element; SINE; PCR; primer;

KW Oncohychnus; restriction primer; short interspersed repeated sequence;

KM eukaryote; restricted polymerase chain reaction fingerprinting;

XX identification; DNA specimen; discrimination; ss.

OS Synthetic.

OS Homo sapiens.

PN JP2913035-B1.

PD 28-JUN-1999.

PF 10-JUL-1998; 98JP-00195692.

PR 10-JUL-1998; 98JP-00195692.

XX (NORO) NORINSUISANSO SUISANCHO YOSHOKU KENKYUSHOCHO.

XX WPI; 1999-58348/50.

PT Restriction primer for distinguishing individuals with short interspersed

PT repeated sequence of eukaryotes by restricted polymerase chain reaction

PT fingerprinting.

XX Claim 6; Page 3; 17pp; Japanese.

CC The present invention describes a restriction primer for eukaryotic short

CC interspersed repeated sequences (SINE), which has one or more additional

CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of

CC the SINE. The annealing temperature of the primer to the DNA sequence is

CC kept higher than the fusion temperature of the primer during polymerase

CC chain reaction (PCR). The PCR fragments obtained are subjected to

CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from

CC the electrophoresis band pattern, eukaryotic individuals are

CC distinguished. The primer is used for amplifying a eukaryotic

CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by

CC polymerase chain reaction (PCR) fingerprinting. In particular it may be

CC used in individual identification of humans for medical and legal

CC applications and ecological studies. DNA specimens in traces

CC (approximately 10 ng in mass) can be used for individual discrimination

CC of eukaryotes using the primer in a polymerase chain reaction (PCR).

CC AAZ25143 to AAZ25191 represent specifically claimed examples of primers

CC from the present invention

XX Sequence 21 BP; 5 A; 5 C; 8 G; 3 T; 0 U; 0 Other;

XX Query Match 2.0%; Score 20; DB 1; Length 21;

XX Best Local Similarity 100.0%; Pred. No. 1.2e+03;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Db 868 GGATTACAGCGGTAGCCAC 887

XX 1 GGATTACAGCGGTAGCCAC 20

XX RESULT 564

XX ADG70428/c

XX ID ADG70428 standard; DNA; 21 BP.

XX AC ADG70428;

XX 11-MAR-2004 (first entry)

XX REN-34 SNP binding area oligo #2.

XX ANGE; CLLD8; CLLD7; ANGE-CLLD8; ANGE-CLLD7; CLLD7-CLLD8;

KW ANGE-CLLD8-CLLD7; antiallergic; antiallergic; dermatological;

KM antipyretic; antiinflammatory; gene therapy; IGE-mediated disease;

XX REN-34; ss.

XX Unidentified.

XX WO2003000727-A2.

XX 03-JAN-2003.

XX 21-JUN-2002; 2002WO-GB002859.

XX 21-JUN-2001; 2001GB-00015211.

XX 21-JUN-2001; 2001GB-00015212.

XX 21-JUN-2001; 2001GB-00015213.

XX (ISIS-) ISIS INNOVATIONS LTD.

XX Zhang Y, Moffatt M, Cookson W, Tinsley J;

XX WPI; 2003-201405/19.

XX New nucleic acid sequence comprising an ANGE, CLLD8 or CLLD7 mRNA, or

PT their hybrid, useful for screening agents for treating IGE-mediated

PT diseases, e.g. asthma, atopy, hay fever, eczema, atopic dermatitis, or

PT allergic rhinitis.

XX Disclosure; Page 429; 429pp; English.

XX The invention relates to a novel isolated or recombinant nucleic acid

XX sequence comprising an ANGE, CLLD8 or CLLD7 mRNA, or ANGE-CLLD8, ANGE-

XX CLLD7, CLLD7-CLLD8, or ANGE-CLLD8-CLLD7 hybrid mRNA sequence, its

XX complement, homologue or fragment. The novel nucleic acid sequences have

XX the following activities: antiallergic, antiallergic, dermatological,

XX antipyretic, and antiinflammatory. The nucleic acids of the invention may

XX be used in gene therapy to treat disorders. The nucleic acid sequences

XX are useful for screening agents that inhibit or enhance activity of an

XX ANGE, CLLD8 or CLLD7 gene. The agent or antibody is useful for treating

XX IGE-mediated diseases, such as asthma, atopy, hay fever, eczema, atopic

XX dermatitis, allergic rhinitis or non-atopic asthma. The antibody is

XX useful in an assay detecting or measuring the polypeptide in the sample.

XX The host cell is useful for producing, regulating and analyzing the

XX polypeptide. The splice variant of ANGE, CLLD8, or CLLD7 is useful for

XX diagnosing an IGE-mediated disease, atopy, a form of atopic disease or

XX non-atopic asthma, or predicting the severity, or predisposition to a

XX disease. This polynucleotide sequence represents an REN-34 SNP binding

XX oligo relating to the invention.

XX Sequence 21 BP; 5 A; 5 C; 9 G; 2 T; 0 U; 0 Other;

XX Query Match 2.0%; Score 20; DB 1; Length 21;

XX Best Local Similarity 100.0%; Pred. No. 1.2e+03;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Db 685 CTCTGCTCCCGGTTCAAG 704

XX 21 CTCTGCTCCCGGTTCAAG 2

XX RESULT 565

XX ADG70427

XX ID ADG70427 standard; DNA; 21 BP.

XX AC ADG70427;

XX DT 11-MAR-2004 (first entry)

DE REN-34 SNP binding area oligo #1.
XX
XX ANGE: CLD8; CLD7; ANGE-CLD8; ANGE-CLD7; CLD7-CLD8;
KM ANGE-CLD8-CLD7; antiallergic; antiasthmatic; dermatological;
KM antipyretic; antiinflammatory; gene therapy; IGE-mediated disease;
KM REN-34; ss.
XX
XX Unidentified.
OS
XX WO2003000727-A2.
PN
XX
XX 03-JAN-2003.
PD
XX
XX 21-JUN-2002; 2002WO-GB002859.
PF
XX
XX 21-JUN-2001; 2001GB-00015211.
PR 21-JUN-2001; 2001GB-00015212.
PR 21-JUN-2001; 2001GB-00015213.
XX
XX (ISIS-) ISIS INNOVATIONS LTD.
PA
XX Zhang Y, Moffatt M, Cookson W, Tinsley J;
PI WPI; 2003-201405/19.
DR
XX
XX New nucleic acid sequence comprising an ANGE, CLD8 or CLD7 mRNA, or
PT their hybrid, useful for screening agents for treating IGE-mediated
PT diseases, e.g. asthma, atopy, hay fever, eczema, atopic dermatitis, or
PT allergic rhinitis.
XX
XX
XX Disclosure; Page 429; 429pp; English.
PS
XX The invention relates to a novel isolated or recombinant nucleic acid
CC sequence comprising an ANGE, CLD8 or CLD7 mRNA, or ANGE-CLD8, ANGE-
CC CLD7, CLD7-CLD8, or ANGE-CLD8-CLD7 hybrid mRNA sequence, its
CC complement, homologue or fragment. The novel nucleic acid sequences have
CC the following activities: antiallergic, antiasthmatic, dermatological,
CC antipyretic, and antiinflammatory. The nucleic acids of the invention may,
CC be used in gene therapy to treat disorders. The nucleic acid sequences
CC are useful for screening agents that inhibit or enhance activity of an
CC ANGE, CLD8 or CLD7 gene. The agent or antibody is useful for treating
CC IGE-mediated diseases, such as asthma, atopy, hay fever, eczema, atopic
CC dermatitis, allergic rhinitis or non-atopic asthma. The antibody is
CC useful in an assay detecting or measuring the polypeptide in the sample.
CC The host cell is useful for producing, regulating and analyzing the
CC polypeptide. The splice variant of ANGE, CLD8, or CLD7 is useful for
CC diagnosing an IGE-mediated disease, atopy, a form of atopic disease or
CC non-atopic asthma, or predicting the severity, or predisposition to a
CC disease. This polynucleotide sequence represents an REN-34 SNP binding
CC oligo relating to the invention.
XX
XX
SQ Sequence 21 BP; 2 A; 9 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 2.0%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 685 CTCTGCTCCCGGTTCAAG 704
DB 1 CTCTGCTCCCGGTTCAAG 20
RESULT 566
AD011941/C
ID AD011941 standard; DNA; 21 BP.
XX
XX AD011941;
AC
XX
XX 15-JUL-2004 (first entry)
DT
XX
XX Single multiplex PCR primer #1313.
DE
XX
XX ss; primer; simultaneous amplification;
KM

KM single multiplex polymerase chain reaction; multifactorial disease;
KM genetic alteration; pharmacogenetic reaction; genotyping; polymorphism;
KM gene expression profiling.
XX
XX Synthetic.
OS
XX
XX WO2004033649-A2.
PN
XX
XX 22-APR-2004.
PD
XX
XX 07-OCT-2003; 2003WO-US031874.
PF
XX
XX 07-OCT-2002; 2002US-0417009P.
PR
XX
XX (UNNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
PA
XX
XX Li H, Li J;
PI
XX
XX WPI; 2004-340914/31.
DR
XX
XX Designing primers for simultaneous amplification of target DNA fragments
PT in a single multiplex polymerase chain reaction, for high throughput
PT multiplex DNA sequence amplification, comprises aligning two primers.
PT
XX
XX Disclosure; Page 39; 120pp; English.
PS
XX
XX The invention relates to a method of designing primers for simultaneous
CC amplification of target DNA fragments in a single multiplex polymerase
CC chain reaction by aligning a first primer and a second primer. The method
CC comprises: (a) aligning a first primer and a second primer; and (b)
CC selecting the first primer where the first primer at its 3' end does not
CC contain four or more bases that are perfectly matching to the 3' end
CC sequence of the first primer or a second primer, the first primer at its
CC 3' end does not contain seven or more bases that are perfectly matching
CC except one mismatch to the 3' end sequence of the first primer or the
CC second primer, the first primer at its 3' end does not contain six or
CC more bases that are perfectly matching to a sequence anywhere of the
CC first primer or the second primer, and the first primer at its 3' end
CC does not contain eleven or more bases that are perfectly matching except
CC one mismatch to a sequence anywhere of the first primer or the second
CC primer. The method is useful for designing primers for simultaneous
CC amplification of target DNA fragments in a single multiplex polymerase
CC chain reaction. It is also useful in the identification of multiple genes
CC related to multifactorial diseases, the genome-scale detection of genetic
CC alterations, the studies in pharmacogenetic reactions, the genotyping
CC genetic polymorphisms in a large population, the gene expression
CC profiling in various samples and high throughput genotyping technologies.
CC This sequence corresponds to an example of a primer of the invention.
XX
XX
SQ Sequence 21 BP; 4 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 2.0%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 545 AGCCTCCCAAGTAGCTGGGA 564
DB 20 AGCCTCCCAAGTAGCTGGGA 1
RESULT 567
AA225153
ID AA225153 standard; DNA; 22 BP.
XX
XX AA225153;
AC
XX
XX 13-DEC-1999 (first entry)
DT
XX
XX Human short interspersed repetitive element PCR primer #11.
DE
XX
XX Human, short interspersed repetitive element; SINE; PCR; primer;
KM Oncorhynchus; restriction primer; short interspersed repeated sequence;
KM eukaryote; restricted polymerase chain reaction fingerprinting;
KM

```

KW identification; DNA specimen; discrimination; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX JP2913035-B1.
XX
XX 28-JUN-1999.
XX
XX 10-JUL-1998; 98UP-00195692.
XX
XX 10-JUL-1998; 98UP-00195692.
XX
XX (NORQ ) NORINSUISANSHO SUIANCHO YOSHOKU KENKYUSHOCHO.
XX
XX WPI; 1999-583348/50.
XX
XX Restriction primer for distinguishing individuals with short interspersed
XX repeated sequence of eukaryotes by restricted polymerase chain reaction
XX fingerprinting.
XX
XX Claim 6; Page 3; 17pp; Japanese.
XX
XX The present invention describes a restriction primer for eukaryotic short
XX interspersed repeated sequences (SINE), which has one or more additional
XX bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
XX the SINE. The annealing temperature of the primer to the DNA sequence is
XX kept higher than the fusion temperature of the primer during polymerase
XX chain reaction (PCR). The PCR fragments obtained are subjected to
XX electrophoresis to obtain a fingerprint. By comparing the polymorphs from
XX the electrophoresis band pattern, eukaryotic individuals are
XX distinguished. The primer is used for amplifying a eukaryotic
XX deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
XX polymerase chain reaction (PCR) fingerprinting. In particular it may be
XX used individual identification of humans for medical and legal
XX applications and ecological studies. DNA specimens in traces
XX (approximately 10 ng in mass) can be used for individual discrimination
XX of eukaryotes using the primer in a polymerase chain reaction (PCR).
XX AA25143 to AA25191 represent specifically claimed examples of primers
XX from the present invention
XX
SQ Sequence 22 BP; 5 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
XX
XX
Query Match 2.0%; Score 20; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 868 GGATTACAGCGGTGAGCCAC 887
DB 1 GGATTACAGCGGTGAGCCAC 20
XX
RESULT 568
AA25148
ID AA25148 standard; DNA; 22 BP.
XX
XX AA25148;
XX
XX 13-DEC-1999 (first entry)
XX
XX Human short interspersed repetitive element PCR primer #6.
XX
XX Human short interspersed repetitive element; SINE; PCR; primer;
XX Oncothychnus; restriction primer; short interspersed repeated sequence;
XX eukaryote; restricted polymerase chain reaction fingerprinting;
XX identification; DNA specimen; discrimination; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX JP2913035-B1.
XX
XX 28-JUN-1999.
XX

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XX
XX 10-JUL-1998; 98UP-00195692.
XX
XX 10-JUL-1998; 98UP-00195692.
XX
XX (NORQ ) NORINSUISANSHO SUIANCHO YOSHOKU KENKYUSHOCHO.
XX
XX WPI; 1999-583348/50.
XX
XX Restriction primer for distinguishing individuals with short interspersed
XX repeated sequence of eukaryotes by restricted polymerase chain reaction
XX fingerprinting.
XX
XX Claim 6; Page 3; 17pp; Japanese.
XX
XX The present invention describes a restriction primer for eukaryotic short
XX interspersed repeated sequences (SINE), which has one or more additional
XX bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
XX the SINE. The annealing temperature of the primer to the DNA sequence is
XX kept higher than the fusion temperature of the primer during polymerase
XX chain reaction (PCR). The PCR fragments obtained are subjected to
XX electrophoresis to obtain a fingerprint. By comparing the polymorphs from
XX the electrophoresis band pattern, eukaryotic individuals are
XX distinguished. The primer is used for amplifying a eukaryotic
XX deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
XX polymerase chain reaction (PCR) fingerprinting. In particular it may be
XX used individual identification of humans for medical and legal
XX applications and ecological studies. DNA specimens in traces
XX (approximately 10 ng in mass) can be used for individual discrimination
XX of eukaryotes using the primer in a polymerase chain reaction (PCR).
XX AA25143 to AA25191 represent specifically claimed examples of primers
XX from the present invention
XX
SQ Sequence 22 BP; 6 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX
Query Match 2.0%; Score 20; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 868 GGATTACAGCGGTGAGCCAC 887
DB 1 GGATTACAGCGGTGAGCCAC 20
XX
RESULT 569
AA25154
ID AA25154 standard; DNA; 22 BP.
XX
XX AA25154;
XX
XX 13-DEC-1999 (first entry)
XX
XX Human short interspersed repetitive element PCR primer #12.
XX
XX Human short interspersed repetitive element; SINE; PCR; primer;
XX Oncothychnus; restriction primer; short interspersed repeated sequence;
XX eukaryote; restricted polymerase chain reaction fingerprinting;
XX identification; DNA specimen; discrimination; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX JP2913035-B1.
XX
XX 28-JUN-1999.
XX
XX 10-JUL-1998; 98UP-00195692.
XX
XX 10-JUL-1998; 98UP-00195692.
XX
XX (NORQ ) NORINSUISANSHO SUIANCHO YOSHOKU KENKYUSHOCHO.
XX
XX WPI; 1999-583348/50.
XX

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XX Restriction primer for distinguishing individuals with short interspersed
PT repeated sequence of eukaryotes by restricted polymerase chain reaction
PT fingerprinting.
XX
PS Claim 6, Page 3, 17pp; Japanese.
XX
CC The present invention describes a restriction primer for eukaryotic short
CC interspersed repeated sequences (SINE), which has one or more additional
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
CC the SINE. The annealing temperature of the primer to the DNA sequence is
CC kept higher than the fusion temperature of the primer during polymerase
CC chain reaction (PCR). The PCR fragments obtained are subjected to
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from
CC the electrophoresis band pattern, eukaryotic individuals are
CC distinguished. The primer is used for amplifying a eukaryotic
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be
CC used for individual identification of humans for medical and legal
CC applications and ecological studies. DNA specimens in traces
CC (approximately 10 ng in mass) can be used for individual discrimination
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).
CC AA25143 to AA25191 represent specifically claimed examples of primers
CC from the present invention
CC
XX
SQ Sequence 22 BP; 5 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 868 GGATTACAGCGCTAGCCAC 887
DB 1 GGATTACAGCGCTAGCCAC 20

RESULT 570
AA25150
ID AA25150 standard; DNA; 22 BP.
XX
AC AA25150;
XX
DT 13-DEC-1999 (first entry)
XX
DE Human short interspersed repetitive element PCR primer #8.
XX
KM Human; short interspersed repetitive element; SINE; PCR; primer;
KM Oncorhynchus; restriction primer; short interspersed repeated sequence;
KM eukaryote; restricted polymerase chain reaction fingerprinting;
KM identification; DNA specimen; discrimination; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN JP2913035-B1.
XX
PD 28-JUN-1999.
XX
PF 10-JUL-1998; 98JP-00195692.
XX
PR 10-JUL-1998; 98JP-00195692.
XX
PS (NORQ) NORINSUISANSO SUISANCHO YOSHOKU KENKYUSHOCHO.
XX
DR WPI; 1999-583348/50.
XX
PT Restriction primer for distinguishing individuals with short interspersed
PT repeated sequence of eukaryotes by restricted polymerase chain reaction
PT fingerprinting.
XX
PS Claim 6, Page 3, 17pp; Japanese.
XX
CC The present invention describes a restriction primer for eukaryotic short

CC interspersed repeated sequences (SINE), which has one or more additional
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
CC the SINE. The annealing temperature of the primer to the DNA sequence is
CC kept higher than the fusion temperature of the primer during polymerase
CC chain reaction (PCR). The PCR fragments obtained are subjected to
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from
CC the electrophoresis band pattern, eukaryotic individuals are
CC distinguished. The primer is used for amplifying a eukaryotic
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be
CC used for individual identification of humans for medical and legal
CC applications and ecological studies. DNA specimens in traces
CC (approximately 10 ng in mass) can be used for individual discrimination
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).
CC AA25143 to AA25191 represent specifically claimed examples of primers
CC from the present invention
CC
XX
SQ Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 868 GGATTACAGCGCTAGCCAC 887
DB 1 GGATTACAGCGCTAGCCAC 20

RESULT 571
AA25151
ID AA25151 standard; DNA; 22 BP.
XX
AC AA25151;
XX
DT 13-DEC-1999 (first entry)
XX
DE Human short interspersed repetitive element PCR primer #9.
XX
KM Human; short interspersed repetitive element; SINE; PCR; primer;
KM Oncorhynchus; restriction primer; short interspersed repeated sequence;
KM eukaryote; restricted polymerase chain reaction fingerprinting;
KM identification; DNA specimen; discrimination; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN JP2913035-B1.
XX
PD 28-JUN-1999.
XX
PF 10-JUL-1998; 98JP-00195692.
XX
PR 10-JUL-1998; 98JP-00195692.
XX
PS (NORQ) NORINSUISANSO SUISANCHO YOSHOKU KENKYUSHOCHO.
XX
DR WPI; 1999-583348/50.
XX
PT Restriction primer for distinguishing individuals with short interspersed
PT repeated sequence of eukaryotes by restricted polymerase chain reaction
PT fingerprinting.
XX
PS Claim 6, Page 3, 17pp; Japanese.
XX
CC The present invention describes a restriction primer for eukaryotic short
CC interspersed repeated sequences (SINE), which has one or more additional
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
CC the SINE. The annealing temperature of the primer to the DNA sequence is
CC kept higher than the fusion temperature of the primer during polymerase
CC chain reaction (PCR). The PCR fragments obtained are subjected to
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from
CC the electrophoresis band pattern, eukaryotic individuals are
CC distinguished. The primer is used for amplifying a eukaryotic

CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be
CC used individual identification of humans for medical and legal
CC applications and ecological studies. DNA specimens in traces
CC (approximately 10 ng in mass) can be used for individual discrimination
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).
CC AA25143 to AA25191 represent specifically claimed examples of primers
CC from the present invention
XX
SQ Sequence 22 BP; 5 A; 6 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 22;
Best local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 868 GGATTACAGCGCTGAGCCAC 887
DB 1 GGATTACAGCGCTGAGCCAC 20

RESULT 572
AA25147
ID AA25147 standard; DNA; 22 BP.
XX
AC AA25147;
XX
DT 13-DEC-1999 (first entry)
DE Human short interspersed repetitive element PCR primer #5.
XX
XX Human; short interspersed repetitive element; SINE; PCR; primer;
XX Oncohychnus; restriction primer; short interspersed repeated sequence;
KW eukaryote; restriction polymerase chain reaction fingerprinting;
KW identification; DNA specimen; discrimination; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN JP2913035-B1.
XX
PD 28-JUN-1999.
XX
PF 10-JUL-1998; 98JP-00195692.
XX
PR 10-JUL-1998; 98JP-00195692.
XX
PA (NORU) NORINSUISANSO SUISANCHO YOSHOKU KENKUSHOCHO.
XX
DR WPI; 1999-583348/50.
XX
PT Restriction primer for distinguishing individuals with short interspersed
PT repeated sequence of eukaryotes by restricted polymerase chain reaction
PT fingerprinting.
XX
PS Claim 6; Page 3; 17P; Japanese.
XX
CC The present invention describes a restriction primer for eukaryotic short
CC interspersed repeated sequences (SINE), which has one or more additional
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
CC the SINE. The annealing temperature of the primer to the DNA sequence is
CC kept higher than the fusion temperature of the primer during polymerase
CC chain reaction (PCR). The PCR fragments obtained are subjected to
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from
CC the electrophoresis band pattern, eukaryotic individuals are
CC distinguished. The primer is used for amplifying a eukaryotic
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be
CC used individual identification of humans for medical and legal
CC applications and ecological studies. DNA specimens in traces
CC (approximately 10 ng in mass) can be used for individual discrimination
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).
CC AA25143 to AA25191 represent specifically claimed examples of primers
CC from the present invention

XX
SQ Sequence 22 BP; 6 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 22;
Best local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 868 GGATTACAGCGCTGAGCCAC 887
DB 1 GGATTACAGCGCTGAGCCAC 20

RESULT 573
ABL55369
ID ABL55369 standard; DNA; 24 BP.
XX
AC ABL55369;
XX
DT 23-JUL-2002 (first entry)
DE Human leucine zipper protein 11.99 RT-PCR primer, SEQ ID NO:3.
XX
XX Human; leucine zipper protein 11.99; recombinant production; tumour;
KW cancer; embryonic development disorder; cytostatic; gene therapy;
KW reverse transcription-PCR; RT-PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN CN1331194-A.
XX
PD 16-JAN-2002.
XX
PF 30-JUN-2000; 2000CN-00116898.
XX
PR 30-JUN-2000; 2000CN-00116898.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-292862/34.
XX
PT Polypeptide-human leucine zipper protein 11.99 and polynucleotide for
PT coding it.
XX
PS Example 2; Page 19 (Disclosure); 35P; Chinese.
XX
CC The invention relates to human leucine zipper protein 11.99 (AA049285)
CC and to nucleic acids encoding it (ABL55368). The protein has a molecular
CC weight of 12 kD. The invention also relates to a method for the
CC recombinant production of the protein, an antagonist of the protein, and
CC the use of the protein, gene and antagonist in therapeutic applications.
CC Leucine zipper protein 11.99 can be used in the treatment of a variety of
CC diseases such as embryonic development disorders and tumours. Sequences
CC ABL55369-ABL55370 represent reverse transcription-PCR (RT-PCR) primers
CC used in an exemplification of the invention to isolate human leucine
CC zipper protein 11.99 cDNA
XX
SQ Sequence 24 BP; 4 A; 5 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 24;
Best local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 943 CCCAGGCTGAGTGCATAGG 962
DB 1 CCCAGGCTGAGTGCATAGG 20

RESULT 574
ADC56863/c
ID ADC56863 standard; DNA; 24 BP.
XX

AC ADC56863;
XX
DT 18-DEC-2003 (first entry)
XX
DE RT-PCR primer Seq IDs related to human protein 8-91.
XX
KW human; protein 8-91; diabetes; cancer; PCR; primer; RT-PCR;
XX reverse transcription PCR; ss.
OS Homo sapiens.
XX
XX CN1381492-A.
XX
XX 27-NOV-2002.
XX
XX 18-APR-2001; 2001CN-00112644.
XX
XX 18-APR-2001; 2001CN-00112644.
XX
XX (BIOM-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2003-249017/25.
XX
XX Polypeptide-human ribosomal protein -8.91 and polynucleotide for coding
XX it.
XX
XX Example 3; SEQ ID NO 3; 30pp; Chinese.
XX
XX This invention relates to a novel protein, human protein 8-91, and the
XX DNA sequence encoding it. The protein of the invention may be useful for
XX the treatment of diseases such as diabetes and cancer. The present
XX sequence is that of an RT-PCR primer which was used in the
XX exemplification of the invention.
XX
XX Sequence 24 BP; 4 A; 8 C; 6 G; 6 T; 0 U; 0 Other;
XX
XX
XX Query Match 2.0%; Score 20; DB 1; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 868 GGATTACAGCGCTGAGCCAC 887
XX 24 GGATTACAGCGCTGAGCCAC 5
XX
XX
XX RESULT 575
XX AAH77599
XX ID AAH77599 standard; DNA; 25 BP.
XX
XX AAH77599;
XX
XX 22-OCT-2001 (first entry)
XX
XX Human dihydropyrrrole-5-carboxylate reductase 30 PCR primer 2.
XX
XX Human; dihydropyrrrole-5-carboxylate reductase 30; cancer; cytosolic;
XX human immunodeficiency virus; HIV; infection; immunological disease;
XX inflammatory disease; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX CN1298002-A.
XX
XX 06-JUN-2001.
XX
XX 24-NOV-1999; 99CN-00124090.
XX
XX 24-NOV-1999; 99CN-00124090.
XX
XX (SHAN-) SHANGHAI BORONG GENE DEV CO LTD.
XX

PI Mao Y, Xie Y;
XX
XX WPI; 2001-483680/54.
XX
XX Human dihydropyrrrole-5-carboxylate reductase 30 as one new kind of
XX polypeptide and polynucleotides encoding this polypeptide.
XX
XX Example 3; Page 16 (disclosure); 26pp; Chinese.
XX
XX The invention relates to a novel polypeptide, human dihydropyrrrole-5-
XX carboxylate reductase 30, polynucleotides encoding this polypeptide and a
XX DNA recombination process to produce the polypeptide. The polypeptide is
XX useful for treating various diseases, such as malignant tumours,
XX nosohaemia, HIV infection, immunological diseases and inflammatory
XX diseases. The invention also provides an antibody against the
XX polypeptide. The present sequence is a primer used to amplify a
XX polynucleotide encoding the polypeptide of the invention
XX
XX Sequence 25 BP; 7 A; 1 C; 5 G; 12 T; 0 U; 0 Other;
XX
XX
XX Query Match 2.0%; Score 20; DB 1; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 770 TTTTGTATTTTGTAGTAGAGA 789
XX 6 TTTTGTATTTTGTAGTAGAGA 25
XX
XX
XX RESULT 576
XX AAF74080
XX ID AAF74080 standard; DNA; 23 BP.
XX
XX AAF74080;
XX
XX 30-APR-2001 (first entry)
XX
XX Primer #14.
XX
XX Solute carrier family 6 neurotransmitter transporter; serotonin 4; SLC6A4;
XX genotyping; allele specific oligonucleotide; ss.
XX
XX Homo sapiens.
XX
XX WO200109161-A1.
XX
XX 08-FEB-2001.
XX
XX 31-JUL-2000; 2000WO-US020638.
XX
XX 29-JUL-1999; 99US-0146290P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Denton RR, Duda A, Nandabalan K, Sanchis A, Stephens JC;
XX
XX WPI; 2001-123317/13.
XX
XX New isolated polynucleotide comprising a polymorphic variant for the
XX solute carrier family 6 neurotransmitter transporter, serotonin member 4
XX gene for identifying drugs for treating disorders related to expression
XX of the protein.
XX
XX Example 1; Page 33; 152pp; English.
XX
XX The present invention relates to a polymorphic variant of a reference
XX sequence for the solute carrier family 6 neurotransmitter transporter,
XX serotonin member 4 (SLC6A4) gene or a fragment of it or a sequence
XX complementary to the first sequence. The invention is used in producing a
XX recombinant organism that can be used to express SLC6A4 for protein
XX structure analysis and binding studies. A composition comprising a
XX genotyping oligonucleotide is used to detect a polymorphism in the SLC6A4
XX gene
XX

XX SQ Sequence 23 BP; 5 A; 3 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.8; DB 1; Length 23;

Best Local Similarity 91.3%; Pred. No. 1.2e+03; Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 862 GTGCTGGATTACAGCGGTGAGC 884
DB 1 GTGCTGGATTAGAGCGTGAAC 23

RESULT 577

ADCT9601
ID ADC79601 standard; DNA; 23 BP.

AC ADC79601;

DT 01-JAN-2004 (first entry)

DE Human p53 forward RT-PCR primer.

XX cytoplasmic; cancer; chemotherapy; carcinoma; tumour; RT-PCR; ss;
KW primer; primer.

OS Homo sapiens.

PN WO2003035894-A2.

PD 01-MAY-2003.

PF 28-OCT-2002; 2002WO-US034397.

PR 26-OCT-2001; 2001US-0330669P.

PR 04-APR-2002; 2002US-0369945P.

PA (IMMU-) IMMUNIVEST CORP.

PI O'hara SM, Zweitzig D, Foulk B;

DR WPI; 2003-482052/45.

XX Extracting intact cytoplasmic biomolecules e.g. proteins, nucleic acids
PT from cells, by treating sample comprising cells containing target cells
PT with permeabilizing agents to release biomolecules and recovering them.

XX Example 10; Page 59; 119pp; English.

XX The invention relates to a novel method for extracting intact cytoplasmic
CC biomolecules from cells. The method of the invention is useful for
CC extracting or acquiring cytoplasmic biomolecules such as proteins or
CC nucleic acids which include cytoplasmic RNA, nuclear and mitochondrial
CC RNA, nuclear and mitochondrial DNA, cytoplasmic mRNA, or their
CC combinations from cells. The method is useful in cancer screening,
CC selecting and monitoring for chemotherapy treatment or cancer recurrence.
CC This type of cell analysis is useful in cancer diagnostics. The method is
CC useful in profiling cells isolated from tissues or body fluids and serves
CC as an adjunct to clinical diagnosis of diverse carcinomas including early
CC stage detection and classification of circulating tumour cells. The
CC present sequence is used in the exemplification of the invention.

XX Sequence 23 BP; 3 A; 9 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.8; DB 1; Length 23;

Best Local Similarity 91.3%; Pred. No. 1.2e+03; Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 538 CTGCTCAGCTCCCAAGTAGCT 560
DB 1 CTGCTCAGCTCCGAGTAGCT 23

RESULT 578

ADE44542.
ID ADE44542 standard; DNA; 23 BP.

AC ADE44542;

DT 29-JAN-2004 (first entry)

DE Primer #1 to amplify the p53 gene for cancer-detection method.

XX ss; primer; diagnosis; cancer; epithelial cell; immunomagnetic particle;
KW prostate cancer; breast cancer; colon cancer; carcinoma; choristoma;
KW carcinoma; malignant carcinoma syndrome; carcinoma heart disease;
KW carcinoma.

OS Homo sapiens.

PN WO2003035895-A2.

PD 01-MAY-2003.

PF 28-OCT-2002; 2002WO-US034570.

PR 26-OCT-2001; 2001US-0330669P.

PR 04-APR-2002; 2002US-0369945P.

PA (IMMU-) IMMUNIVEST CORP.

PI O'hara SM, Zweitzig D, Foulk B;

DR WPI; 2003-421425/39.

XX Diagnosing severity of disease in a test subject, by mixing the sample
PT comprising cancer cells with immunomagnetic particles and separating cell
PT fraction to diagnose enriched fraction for the presence of cancer cells.
XX Example 10; Page 59; 105pp; English.

XX The invention relates to a method of diagnosing the severity of a disease
CC in a test subject, by obtaining a sample having a mixed cell population
CC suspected of containing cancer cells of epithelial origin, mixing the
CC sample with immunomagnetic particles which bind specifically to the
CC cancer cells, subjecting the mixture to produce a separated cell
CC fraction, and assaying the enriched fraction for the presence of a
CC cancer cells. The method is useful for diagnosing the severity of a
CC disease in a test subject. The test subject is for assessment of a
CC presence of circulating cancer cells. The test subject response to cancer
CC eradication procedures and is assessed by the presence of circulating
CC cancer cells. The test subject has been diagnosed with a cancer selected
CC from prostate cancer, breast cancer, colon cancer, carcinoma, choristoma,
CC carcinoma, malignant carcinoma syndrome, carcinoma heart disease, and
CC carcinoma e.g. Walker, basal cell, basaloid, mucinous, Brown-Pearce, ductal,
CC Ehrlich tumor, Krebs 2, Merkel cells, mucinous, and non-small cell lung.
CC This sequence represents a primer used to amplify a specific gene cDNA
CC sequence in the method of the invention.

XX Sequence 23 BP; 3 A; 9 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.8; DB 1; Length 23;

Best Local Similarity 91.3%; Pred. No. 1.2e+03; Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 538 CTGCTCAGCTCCCAAGTAGCT 560
DB 1 CTGCTCAGCTCCGAGTAGCT 23

RESULT 579

ADO47348
ID ADO47348 standard; DNA; 23 BP.

AC ADO47348;

DT 15-JUL-2004 (first entry)

XX Human SORBS1 gene sequencing primer #54.
DE
XX Single nucleotide polymorphism, SNP; human;
KM sorbin and SH3-domain-containing-1 gene; SORBS1; sequence determination;
KM insulin disorder; type 2 diabetes; obesity; hypertension;
KM atherosclerosis; metabolic syndrome; sequencing; primer; ss.
XX
OS Homo sapiens.
XX
XX US2004072230-A1.
XX
XX 15-APR-2004.
XX
XX 13-AUG-2003; 2003US-00639491.
XX
XX 14-AUG-2002; 2002US-0402911P.
XX
XX (HSIU/) HSIUNG C. A.
XX (CHUA/) CHUANG L.
XX (HSIA/) HSIAO C.
XX (TAIT/) TAI T.
XX
XX Hsiung CA, Chuang L, Hsiao C, Tai T;
XX
XX WPI, 2004-328567/30.
XX
XX Detecting at least one single nucleotide polymorphism in a human sorbin
PT and SH3-domain-containing-1 (SORBS1) gene, useful in diagnosing insulin
PT disorders like type 2 diabetes, obesity, hypertension and
PT atherosclerosis.
XX
XX Example 1; Page 8; 18pp; English.
XX
XX The present invention relates to a method of detecting at least one
CC single nucleotide polymorphism (SNP) in a human sorbin and SH3-domain-
CC containing-1 (SORBS1) gene. The method comprises determining the
CC nucleotide present at one or more positions chosen from 220; 249; -7 with
CC respect to exon 5; -25 with respect to exon 6; 682; +64 with respect to
CC exon 9; +61 with respect to exon 10; +69 with respect to exon 11; +33
CC with respect to exon 16; 1462; 1518; -6 with respect to exon 22; +79 with
CC respect to exon 24; and 2337. The invention also discloses primer
CC sequences that may be used for determining the SORBS1 gene sequence by
CC amplification and sequencing of the gene. The method is useful for
CC associating one or more SORBS1 SNPs with an insulin disorder e.g., type 2
CC diabetes, obesity, hypertension, atherosclerosis or metabolic syndrome.
CC The presence or absence of the SNP may be useful in determining whether
CC an individual is at increased or decreased risk for an insulin disorder.
CC The SNPs were identified by screening all of the exons, and 50-150 base
CC pairs of the flanking regions of the introns of the SNP in the human
CC SORBS1 gene. The present sequence represents a sequencing primer used to
CC screen the human SORBS1 gene.
XX
XX Sequence 23 BP; 8 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 2.0%; Score 19.8; DB 1; Length 23;
XX Best Local Similarity 91.3%; Pred. No. 1.2e+03;
XX Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 870 ATTACAGGCGTGAGCCACCACGC 892
DB 1 ATTACAGGCGATGAGCCACCACAC 23
XX
XX RESULT 580
XX AA227796/C
XX ID AA227796 standard; DNA; 24 BP.
XX AC AA227796;
XX
XX 23-DEC-1999 (first entry)
XX
XX PCR primer for human DNA marker clone G212.
DE

XX Tandem repeat sequence; DNA isolation; intermediate tandem repeat;
KM ITR sequence; pentanucleotide tandem repeat; stutter artifact;
KM DNA typing; DNA profiling; linkage analysis; criminal justice;
KM paternity testing; animal lineage analysis; microsatellite loci;
KM polymorphism detection; PCR primer; ss.
XX
OS Synthetic.
XX
XX Homo sapiens.
XX
XX WO9940194-A1.
XX
XX 12-AUG-1999.
XX
XX 04-FEB-1999; 99WO-US002345.
XX
XX 04-FEB-1998; 98US-00018584.
XX
XX (PROM-) PROMEGA CORP.
XX
XX Schumm JW, Bacher JW;
XX
XX WPI, 1999-590696/50.
XX
XX Isolating DNA containing intermediate tandem repeat sequences, useful in
PT DNA profiling.
XX
XX Claim 30; Page 21; 11pp; English.
XX
XX This sequence is a PCR primer for a human DNA marker clone used in the
CC method of the invention. The method is for isolating a fragment of DNA
CC containing an intermediate tandem repeat (ITR) sequence using
CC hybridization selection, and comprises: (a) providing several DNA
CC fragments, at least one of which contains an ITR sequence, a region of
CC the DNA fragment which contains at least one repeat unit consisting of a
CC sequence of five, six or seven bases repeated in tandem at least two
CC times; (b) providing a stationary support having at least one
CC oligonucleotide associated with it, where the oligonucleotide includes a
CC sequence of nucleotides which is complementary to a portion of the ITR
CC sequence; and (c) combining the DNA fragments with the support under
CC conditions where the DNA fragments including the DNA fragment containing
CC the ITR sequence hybridize to the support. The method is particularly
CC used to isolate DNA containing pentanucleotide tandem repeat sequences as
CC well as to detect target ITR DNA sequences having a low incidence of
CC stutter artifacts (no more than 2.4%). The method is useful in DNA
CC profiling for linkage analysis, criminal justice, paternity testing and
CC other forensic and medical uses. DNA typing is also useful for confirming
CC the lineage of horses, dogs and other prize animals. The invention
CC overcomes problems related to the use of microsatellite loci in DNA
CC profiling. The method can detect polymorphisms with a low incidence of
CC stutter artifacts, which has previously been a problem in interpreting
CC allelic content of loci. The development of markers based on larger
CC repeat units, enables easier separation of the fragments on larger
CC electrophoretic gels. This allows the simultaneous analysis of more loci
XX
XX Sequence 24 BP; 5 A; 7 C; 6 G; 6 T; 0 U; 0 Other;
SQ
XX
XX Query Match 2.0%; Score 19.8; DB 1; Length 24;
XX Best Local Similarity 91.3%; Pred. No. 1.3e+03;
XX Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 638 TGTCCACGAGCTGAGTGCACT 660
DB 23 TATCACCGAGCTGAGTGCAAT 1
XX
XX RESULT 581
XX AAA46454/C
XX ID AAA46454 standard; DNA; 24 BP.
XX AC AAA46454;
XX
XX 04-SEP-2000 (first entry)
XX
XX
DE

XX Oligonucleotide probe used to detect human cells.
 DE Transactivator; tetracycline-regulated system; promoter; nervous system;
 XX tyrosine hydroxylase; neurodegeneration; Parkinson's disease;
 KM nervous system injury; retinal degeneration; probe; ss.
 XX Synthetic.
 OS
 XX WO200028062-A1.
 PN
 XX 18-MAY-2000.
 PD
 XX 09-NOV-1999; 99WO-FR002752.
 PF
 XX 09-NOV-1998; 99FR-00014080.
 PR 03-MAR-1999; 99US-0122600P.
 XX (AVET) AVENTIS PHARMA SA.
 PA
 XX Mallet J, Corti O;
 PI
 XX WPI; 2000-387422/33.
 DR
 XX New nucleic acid for regulating gene expression, particularly expression
 PT of tyrosine hydroxylase for treatment of Parkinson's disease, includes
 PT the gene and tetracycline transactivator.
 XX
 PS Example; Page 24; 51pp; French.
 XX
 CC The specification describes a nucleic acid which comprises a region (R1)
 CC encoding the transactivator (tTA) of the tetracycline-regulated system,
 CC controlled by a moderate promoter; and a region (R2) comprising a nucleic
 CC acid of interest under control of a promoter sensitive to tTA. R1 and R2
 CC are arranged in the same transcriptional orientation. The nucleic acid is
 CC used to specifically express the nucleic acid of interest in vivo,
 CC particularly in the nervous system and especially expression of tyrosine
 CC hydroxylase for treatment of neurodegeneration (Parkinson's disease),
 CC nervous system injury and retinal degeneration. More generally, it can be
 CC used to express a very wide range of therapeutic products, e.g. enzymes,
 CC blood factors, cytokines, tumour suppressors, antibodies etc., for
 CC (immuno)therapy of infections, cancer, autoimmune diseases, restenosis,
 CC genetic diseases etc., also antigens for vaccination or antisense
 CC sequences and ribozymes. The present sequence represents a probe used to
 CC identify human cells, in the course of the invention
 XX
 SQ Sequence 24 BP; 4 A; 7 C; 8 G; 4 T; 0 U; 1 Other;
 XX
 Query Match 2.0%; Score 19.8; DB 1; Length 24;
 Best Local Similarity 91.3%; Pred. No. 1.3e+03;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 661 GGGCAATCTTGGCTCACTGCA 683
 DB 24 GGGCGATCTCGGCTCACTGCA 2
 XX
 RESULT 582
 AAH39521
 ID AAH39521 standard; DNA; 24 BP.
 XX
 AC AAH39521;
 XX
 DT 14-AUG-2001 (first entry)
 XX
 DE SNP specific upper PCR primer SEQ ID 2317.
 XX
 KM Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 KM SNP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
 KM Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
 KM polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
 KM acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
 KM inflammation; forensic investigation; paternity analysis; PCR primer; ss.

XX Homo sapiens.
 OS
 XX WO200129262-A2.
 PN
 XX 26-APR-2001.
 PD
 XX 13-OCT-2000; 2000WO-US028436.
 PF
 XX 15-OCT-1999; 99US-0160096P.
 PR (ORCH-) ORCHID BIOSCIENCES INC.
 PA
 XX Picoult-Newburg L, Pohl M;
 PI
 XX WPI; 2001-290930/30.
 DR
 XX New genotyping oligonucleotide, useful for detecting the presence,
 PT absence or identity of single polynucleotide polymorphism in a nucleic
 PT acid sample.
 XX
 PS Claim 1; Page 61; 83pp; English.
 XX
 CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC primer extension (SNPE) primers, and the sequences of regions flanking
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC includes kits for determining the presence or absence of a SNP, using the
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC performing a single-nucleotide primer extension reaction. The
 CC oligonucleotides are useful for determining the presence, absence or
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC assess by association analysis the genotype of an individual or group of
 CC individuals, having a pathological phenotypic trait suspected of being
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC traits also include symptoms of or susceptibility to multifactorial
 CC diseases of which a component is or may be genetic such as autoimmune
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,
 CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC microorganism. The method is also useful in forensic investigations and
 CC paternity analysis. The present sequence represents a PCR primer specific
 CC for a human SNP containing DNA sequence
 XX
 SQ Sequence 24 BP; 6 A; 7 C; 3 G; 8 T; 0 U; 0 Other;
 XX
 Query Match 2.0%; Score 19.8; DB 1; Length 24;
 Best Local Similarity 91.3%; Pred. No. 1.3e+03;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 577 ACCACTACACCTGGCTCAATTTT 599
 DB 1 ACCACTACGCGCTGACTCAATTTT 23
 XX
 RESULT 583
 AAH44468
 ID AAH44468 standard; DNA; 24 BP.
 XX
 AC AAH44468;
 XX
 DT 25-OCT-2001 (first entry)
 XX
 DE Enolpyruvate phosphate-dependent glycoposphotransferase 9 primer 1.
 XX
 KM Human; enolpyruvate phosphate-dependent glycoposphotransferase 9;
 KM cytosolic; antiinflammatory; haemostatic; immunomodulatory; anti-HIV;
 KM diagnostic; malignant neoplasm; haemopathy; HIV infection;
 KM immunological disease; inflammation; PCR primer; ss.

OS Homo sapiens.
XX WO200149836-A1.
XX 12-JUL-2001.
XX
XX 25-DEC-2000; 2000WO-CN000649.
XX 29-DEC-1999; 99CN-00127223.
XX
XX (UYFU-) UNIV FUDAN.
XX (SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD.
XX Mao Y, Xie Y;
XX WPI; 2001-432875/46.
XX
XX Enolpyruvate phosphate-dependent glycoposphotransferase 9 and encoded
PT polynucleotide, applicable in diagnosis and treatment of malignant
PT neoplasm, hemopathy, HIV infection, immunological diseases and various
PT inflammation.
XX
XX Example 3; Page 18; 35pp; Chinese.
XX
XX The present invention describes the human enolpyruvate phosphate-
CC dependent glycoposphotransferase 9 protein (I). (I) has cytosolic,
CC antiinflammatory, haemostatic, immunomodulatory and anti-HIV activities.
CC (I) and the polynucleotide encoding it are applicable in the diagnosis
CC and treatment of malignant neoplasm, haemopathy, HIV infection,
CC immunological diseases and various inflammations. The present sequence
CC represents a PCR primer for human enolpyruvate phosphate-dependent
CC glycoposphotransferase 9, which is used in an example from the present
CC invention
XX
SQ Sequence 24 BP; 4 A; 9 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 926 GGATCTCACTCTGTACCCAG 948
DB 2 GGAGTCTCACTCTGTACCCAG 24

RESULT 584
A164654/C
ID A164654 standard; DNA; 24 BP.
XX
XX A164654;
XX
XX 04-DEC-2001 (first entry)
XX
XX Human RNA helicase 10 PCR primer 2.
XX
XX Human; RNA helicase 10; cytosolic; virucidal; immunomodulatory;
KW antiinflammatory; haemostatic; malignant tumour; HIV; infection;
KW human immunodeficiency virus; immunological disease; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200172971-A1.
XX
XX 04-OCT-2001.
XX
XX 26-MAR-2001; 2001WO-CN000435.
XX
XX 27-MAR-2000; 2000CN-00115186.
XX
XX (SHAN-) SHANGHAI BIOWINOW GENE DEV INC.
XX Mao Y, Xie Y;
XX

DR WPI; 2001-597114/67.
XX
XX New human RNA helicase 10 and encoded polynucleotide, applicable in
PT diagnosis and treatment of malignant neoplasm, hemopathy, human
PT immunodeficiency virus infection, immunological diseases and
PT inflammation.
XX
XX Example 2; Page 17; 39pp; Chinese.
XX
XX The invention relates to human RNA helicase 10 with cytosolic,
CC virucidal, immunomodulatory, antiinflammatory and haemostatic activity.
CC The polypeptide and encoded polynucleotide are applicable in diagnosis
CC and treatment of malignant tumour, haemopathy, HIV infection,
CC immunological diseases and various inflammations. The present sequence is
CC that of a human RNA helicase 10 PCR primer, useful to the invention
XX
SQ Sequence 24 BP; 7 A; 6 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 993 CCCGCTCAAGCGATCTCTCTG 1015
DB 24 CTTGAGTCAAGCGATCTCTCTG 2

RESULT 585
ID ABL41338 standard; DNA; 24 BP.
XX
XX ABL41338;
XX
XX 22-MAY-2002 (first entry)
XX
XX Human TFIID subunit p30beta protein 12.54 PCR primer SEQ ID NO 3.
XX
XX Human; TFIID subunit p30beta protein 12.54; tumour; inflammation;
KW protein metabolism dysfunction; immunological disease; haemopathy; HIV;
KW infection; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX CN1326959-A.
XX
XX 19-DEC-2001.
XX
XX 05-JUN-2000; 2000CN-00116325.
XX
XX 05-JUN-2000; 2000CN-00116325.
XX
XX 05-JUN-2000; 2000CN-00116325.
XX
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-206968/27.
XX
XX New polypeptide-human TFIID subunit p 30 beta protein 12.54 and
PT polynucleotide encoding the polypeptide.
XX
XX Example 2; Page 19 (Disclosure); 35pp; Chinese.
XX
XX The invention relates to human TFIID subunit p30beta protein 12.54, the
CC polynucleotide encoding this polypeptide and DNA recombinant processes to
CC produce the polypeptide. The present invention also discloses the method
CC of applying the polypeptide in treating various diseases, such as protein
CC metabolism dysfunction, various tumours, inflammations and immunological
CC diseases, haemopathy and HIV infection. The present invention also
CC discloses the antagonist for resisting the polypeptide and its treatment
CC effect. The present invention also discloses the application of the
CC polynucleotide for encoding human TFIID subunit p30beta protein 12.54.
CC The present sequence is that of a PCR primer, useful in examples of the
CC invention

```

XX Sequence 24 BP; 1 A; 8 C; 7 G; 8 T; 0 U; 0 Other;
SQ
Query Match          2.0%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 930 TCTCACTCTGTATCCAGCGCTGG 952
DB ||||| ||||| ||||| |||||
2 TCTCTCTCTGTGGCCAGCGCTGG 24

RESULT 586
AA166361
ID AA166361 standard; DNA; 24 BP.
XX
AC AA166361;
XX
DT 23-JAN-2002 (first entry)
DE Human phosphatidylinositol-3 kinase 35 cDNA PCR primer #2.
XX
XX Human; phosphatidylinositol-3 kinase 35; PTDINS-3 kinase 35; cancer;
XX haemopathy; development disorder; HIV infection; immunological disease;
XX inflammation; gene therapy; PCR primer; 88.
XX Homo sapiens.
XX OS
XX PN WO200175014-A2.
XX
XX PD 11-OCT-2001.
XX
XX PF 16-MAR-2001; 2001WO-CN000328.
XX
XX PR 17-MAR-2000; 2000CN-00114973.
XX
XX PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
XX PI Mao Y, Xie Y;
XX
XX DR WPI; 2002-025836/03.
XX
XX PT New human phosphatidylinositol-3 (PTDINS3) kinase 35 for diagnosing and
XX treating malignant tumor, hemopathy, human immunodeficiency virus
XX infection, immunological diseases and various inflammations.
XX
XX PS Example 2; Page 12; 34pp; Chinese.
XX
XX CC The present invention provides the protein and coding sequences of human
XX phosphatidylinositol-3 (PTDINS-3) kinase 35. The sequences can be used in
XX the treatment of cancer, haemopathy, HIV infection, development
XX disorders, immunological diseases and inflammation. The present sequence
XX is a PCR primer for the coding sequence of the invention
XX
XX Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 U; 0 Other;
SQ
Query Match          2.0%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 427 TTTTATTTTATTTTATTTTAAAG 449
DB ||||| ||||| ||||| |||||
2 TTTTATTTTATTTTATTTTAAAG 24

RESULT 587
AAD38977
ID AAD38977 standard; DNA; 24 BP.
XX
AC AAD38977;
XX
DT 23-SEP-2002 (first entry)
XX

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```
DE Human GDD DNA amplifying reverse RT-PCR primer, GDDPr-4r.
KW Human; dipeptidyl peptidase; DPP; neoplasia; type II diabetes; cirrhosis;
KM autoimmunity; human immuno deficiency virus; HIV infection; cytostatic;
KW graft rejection; antidiabetic; antiinflammatory; immunosuppressive;
KM antiviral; enzyme; reverse transcription; RT-PCR; primer; ss.
OS Homo sapiens.
XX
XX MO200234900-A1.
XX
XX 02-MAY-2002.
XX
XX 29-OCT-2001; 2001MO-AU001388.
XX
XX 27-OCT-2000; 2000AU-00001078.
XX
XX (UNSY ) UNIV SYDNEY.
XX
XX Abbott CA, Gorrell MD;
XX
XX WPI; 2002-454646/48.
XX
XX New dipeptidyl peptidase (DPP) peptides, useful for screening inhibitors
XX of DPP catalytic activity, which may be employed to treat e.g. neoplasia,
XX type II diabetes, cirrhosis, autoimmunity, graft rejection and HIV
XX infection.
XX
XX Example; Page 33; 91pp; English.
XX
XX The present invention relates to dipeptidyl peptidase (DPP) proteins and
XX polypeptides encoding such proteins. The DPP peptides are useful for
XX screening inhibitors of DPP catalytic activity. The inhibitors are useful
XX for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
XX rejection and HIV (human immuno deficiency virus) infection. The present
XX DNA sequence is a reverse transcription (Rt)-PCR primer which is used for
XX amplifying human GDD DNA. This sequence is used in the exemplification of
XX the invention
XX
XX Sequence 24 BP; 2 A; 7 C; 8 G; 7 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred No.1.3e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0
QY 197 CCATGTTGGTCAGCGTGTCTTG 219
Db ||||||| ||||||||| |
2 CCATGTTGGCCAGCGTGTCTTG 24
RESULT 588
ABLA1577
ID ABL41577 standard; DNA; 24 BP.
XX
XX ABL41577;
AC
XX
XX 01-JUL-2002 (first entry)
DT
XX
XX primer #2 relating to human zinc finger protein 27.
DE
XX
XX Zinc finger, zinc finger protein 27; human; cancer; HIV; PCR; primer; ss
KM
XX
XX Homo sapiens.
OS
XX
XX CN1325869-A.
PN
XX
XX 12-DEC-2001.
PD
XX
XX 31-MAY-2000; 2000CN-00116276.
PF
XX
XX 31-MAY-2000; 2000CN-00116276.
PR
XX
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
PA
```

```
XX Mao Y, Xie Y;
XX
XX WPI; 2002-217538/28.
XX
XX Polypeptide-zinc finger protein 27 and polynucleotide for coding it.
XX
XX Example 2; Page 16 (disclosure); 33pp; Chinese.
XX
XX This invention relates to a novel polypeptide-zinc finger protein 27 and
XX the application of the polypeptide in treating diseases such as cancer
XX and HIV infection. The present sequence represents a primer relating to
XX the zinc finger protein 27 encoding sequence
XX
XX Sequence 24 BP; 4 A; 7 C; 5 G; 8 T; 0 U; 0 Other;
SQ
Query Match          2.0%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 752 ACCACGCGCTAGCTATTTTGG 774
DB 1 ACCACGCGCTAGCTATTTTGG 23
RESULT 589
AB270110
ID AB270110 standard; DNA; 24 BP.
XX
XX AB270110;
AC
XX
XX 24-APR-2003 (first entry)
XX
XX Human RNA polymerase I-40 kDa subunit 9.68 PCR primer #1.
XX
XX Human, RNA polymerase I-40 kDa subunit 9.68; cancer; cytostatic;
XX HIV infection; anti-HIV; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX CN1363655-A.
XX
XX 14-AUG-2002.
XX
XX 05-JAN-2001; 2001CN-00105029.
XX
XX 05-JAN-2001; 2001CN-00105029.
XX
XX 05-JAN-2001; 2001CN-00105029.
XX
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-742064/81.
XX
XX Polypeptide-human RNA polymerase I-40 kDa subunit 9.68 and polynucleotide
XX for coding it.
XX
XX Example 2; Page 17 (disclosure); 32pp; Chinese.
XX
XX The present invention relates to human RNA polymerase I-40 kDa subunit
XX 9.68 (see ABP59130). The protein can be used for treating diseases such
XX as cancer and HIV infection. The present sequence is a PCR primer, which
XX was used in an example from the invention
XX
XX Sequence 24 BP; 6 A; 8 C; 5 G; 5 T; 0 U; 0 Other;
SQ
Query Match          2.0%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 219 GAATCCCGACCTCAGATGATCC 241
DB 1 GAATCCCGACCTCAGATGATCC 23
```

```
RESULT 590
AD011357
ID AD011357 standard; DNA; 24 BP.
XX
XX AD011357;
AC
XX
XX 06-MAY-2004 (first entry)
XX
XX Human protein phosphatase 2A alpha subunit 22.66; RT-PCR primer #1.
XX
XX ss; human; protein phosphatase 2A alpha subunit 22.66; osteoma;
XX leukaemia; RT-PCR; reverse transcriptase; primer.
XX
XX Homo sapiens.
XX
XX CN1355310-A.
XX
XX 26-JUN-2002.
XX
XX 01-DEC-2000; 2000CN-00127647.
XX
XX 01-DEC-2000; 2000CN-00127647.
XX
XX (UYFU-) UNIV FUDAN.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2003-403873/39.
XX
XX Polypeptide-human protein phosphatase 2A alpha subunit 22.66 and
XX polynucleotide for coding it.
XX
XX Example 2; Page 18; 32pp; Chinese.
XX
XX The invention relates to a new human protein phosphatase 2A alpha subunit
XX 22.66 polypeptide, the polynucleotide encoding it, and the process for
XX preparing this polypeptide by DNA recombination technique. Also described
XX is the application of the said polypeptide in treating diseases such as
XX osteoma and leukaemia; the antagonist against this polypeptide and its
XX therapeutic action; and the application of the said polynucleotide
XX encoding this novel polypeptide. The present sequence represents a
XX reverse transcriptase (RT)-PCR primer used to isolate cDNA encoding human
XX protein phosphatase 2A alpha subunit 22.66.
XX
XX Sequence 24 BP; 4 A; 8 C; 5 G; 7 T; 0 U; 0 Other;
SQ
Query Match          2.0%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 997 GGCTCAAGCGATTCTCCTGCTC 1019
DB 2 GGCTCAAGCGATTCTCCTGCTC 24
RESULT 591
AD011357
ID AD011357 standard; DNA; 24 BP.
XX
XX AD011357;
AC
XX
XX 15-JUN-2004 (first entry)
XX
XX Single multiplex PCR primer #729.
XX
XX ss; primer; simultaneous amplification;
XX single multiplex polymerase chain reaction; multifactorial disease;
XX genetic alteration; pharmacogenetic reaction; genotyping; polymorphism;
XX gene expression profiling.
XX
XX Synthetic.
```


PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX Picoult-Newburg L., Pohl M;
XX
XX WPI; 2001-290930/30.
DR
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
XX
PS Claim 1; Page 57; 83pp; English.
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence
XX
SQ Sequence 21 BP; 7 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 696 GGGTTCAGTATTCCTCTGC 716
DB 21 GGGTTCAGTATTCCTCTGC 1
XX
RESULT 594
AAH38522
ID AAH38522 standard; DNA; 21 BP.
XX
AC AAH38522;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific lower PCR primer SEQ ID 1318.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KM SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
KM Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KM polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KM acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KM inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
OS Homo sapiens.
XX
XX WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028436.
XX
PR 15-OCT-1999; 99US-0160096P.

XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX Picoult-Newburg L., Pohl M;
XX
XX WPI; 2001-290930/30.
DR
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
XX
PS Claim 1; Page 56; 83pp; English.
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence
XX
SQ Sequence 21 BP; 6 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 388 CAAAGTCTGGGATTACAGGC 408
DB 1 CAAAGTCTGGGATTACAGGC 21
XX
RESULT 595
AAH39585
ID AAH39585 standard; DNA; 21 BP.
XX
AC AAH39585;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific upper PCR primer SEQ ID 2381.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KM SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
KM Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KM polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KM acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KM inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
OS Homo sapiens.
XX
XX WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028436.
XX

PR 15-OCT-1999; 99US-0160096P.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX Picoult-Newburg L, Pohl M;
PI WPI; 2001-290930/30.
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
XX Claim 1; Page 62; 83pp; English.
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNP) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNP primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence
XX
SQ Sequence 21 BP; 5 A; 9 C; 2 G; 5 T; 0 U; 0 Other;
Query Match 2.0%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 967 ATCTCGGCTCAGTGCACCTC 987
DB 1 ATCTCAGCTCAGTGCACCTC 21
RESULT 596
AAH8861/c
ID AAH8861 standard; DNA; 21 BP.
XX
XX AAH8861;
AC
XX
DT 09-SEP-2004 (revised)
DT 27-FEB-2002 (first entry)
XX
XX Human polymorphic oligonucleotide U39064 fragment #1.
XX
XX Human; single nucleotide polymorphic; SNP; forensic science;
KM paternity testing; phenotypic trait; genetic mapping; animal breeding;
KM plant breeding; ds.
XX
XX Homo sapiens.
OS Unidentified.
XX
XX Key Location/Qualifiers
FH 11
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO200134840-A2.

XX
ED 17-MAY-2001.
XX
XX 10-NOV-2000; 2000WO-US030766.
XX
XX 10-NOV-1999; 99US-0164596P.
PR
XX (GLAX) GLAXO GROUP LTD.
PA (AFFY-) AFFYMETRIX INC.
XX
PI Au K, Chen J, Patil N, Thomas D;
XX
XX WPI; 2001-335945/35.
XX
XX New polymorphic sites derived from the human genome are useful to
PT determine sites correlating with phenotypic traits, particularly disease,
PT and also in forensics and paternity testing.
XX
XX Claim 33; Page 8; 43pp; English.
XX
XX The present invention relates to human oligonucleotides comprising a
CC single nucleotide polymorphic site (SNP: AAH8797-AAH89219). The present
CC sequence is one such oligonucleotide. The oligonucleotides can be used in
CC forensics, paternity testing, correlation of polymorphisms with
CC phenotypic traits, genetic mapping of phenotypic traits and marker
CC assisted breeding of animals and crop plants
CC
CC Revised record issued on 09-SEP-2004 : Correction to Feature Table Key
XX
SQ Sequence 21 BP; 4 A; 5 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 2.0%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 870 ATTACAGGCTGTGAGCCACAC 890
DB 21 ATTACAGGCTGTGAGCCACAC 1
RESULT 597
AAH89111
ID AAH89111 standard; DNA; 21 BP.
XX
XX AAH89111;
AC
XX
DT 09-SEP-2004 (revised)
DT 27-FEB-2002 (first entry)
XX
XX Human polymorphic oligonucleotide U29874 fragment #4.
XX
XX Human; single nucleotide polymorphic; SNP; forensic science;
KM paternity testing; phenotypic trait; genetic mapping; animal breeding;
KM plant breeding; ds.
XX
XX Homo sapiens.
OS Unidentified.
XX
XX Key Location/Qualifiers
FH 11
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO200134840-A2.
XX
XX 17-MAY-2001.
XX
XX 10-NOV-2000; 2000WO-US030766.
XX
XX 10-NOV-1999; 99US-0164596P.
PR
XX (GLAX) GLAXO GROUP LTD.
PA (AFFY-) AFFYMETRIX INC.
XX
XX

XX Au K, Chen J, Patil N, Thomas D;
PI
XX
XX WPI; 2001-335945/35.
DR
XX
XX New polymorphic sites derived from the human genome are useful to
PT determine sites correlating with phenotypic traits, particularly disease,
PR and also in forensic and paternity testing.
XX
XX
PS Claim 85; Page 14; 43pp; English.
XX
XX The present invention relates to human oligonucleotides comprising a
CC single nucleotide polymorphic site (SNP: AAH8797-AAH89219). The present
CC sequence is one such oligonucleotide. The oligonucleotides can be used in
CC forensics, paternity testing, correlation of polymorphisms with
CC phenotypic traits, genetic mapping of phenotypic traits and marker
CC assisted breeding of animals and crop plants
CC
CC Revised record issued on 09-SEP-2004 : Correction to Feature Table Key
XX
XX
SQ Sequence 21 BP; 1 A; 10 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 836 TGATCTGCGCTGCGCTC 856
Db 1 TGAATCTGCGCTGCGCTC 21
|||||
|

RESULT 598
AAF74150
ID AAF74150 standard; DNA; 21 BP.
XX
XX AAF74150;
AC
XX
XX 30-APR-2001 (first entry)
DT
XX
XX
DE Primer #84.
XX
XX Solute carrier family 6 neurotransmitter transporter; serotonin 4; SLC6A4;
KW genotyping; allele specific oligonucleotide; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200109161-A1.
PN
XX
XX 08-FEB-2001.
PD
XX
XX 31-JUL-2000; 2000WO-US020638.
PF
XX
XX 29-JUL-1999; 99US-0146290P.
PR
XX
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX
XX Denton RR, Duda A, Nandabalan K, Sanchis A, Stephens JC;
PI WPI; 2001-123317/13.
XX
XX
DR
XX
XX New isolated polynucleotide comprising a polymorphic variant for the
PT solute carrier family 6 neurotransmitter transporter, serotonin member 4
PT gene for identifying drugs for treating disorders related to expression
PT of the protein.
XX
XX
XX Example 1; Page 39; 152pp; English.
PS
XX
XX The present invention relates to a polymorphic variant of a reference
CC sequence for the solute carrier family 6 neurotransmitter transporter,
CC serotonin member 4 (SLC6A4) gene or a fragment of it or a sequence
CC complementary to the first sequence. The invention is used in producing a
CC recombinant organism that can be used to express SLC6A4 for protein
CC structure analysis and binding studies. A composition comprising a

CC genotyping oligonucleotide is used to detect a polymorphism in the SLC6A4
CC gene
XX
XX
SQ Sequence 21 BP; 5 A; 3 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 391 AGTCTGGGATTACAGCGCTG 411
Db 1 AATGCTGGGATTACAGCGCTG 21
|||||
|

RESULT 599
ABO93614/C
ID ABO93614 standard; DNA; 21 BP.
XX
XX
XX ABO93614;
AC
XX
XX 16-OCT-2002 (first entry)
DT
XX
XX
DE Human DISC1/DISC2 PCR primer disc20 r2.
XX
XX Human; Disrupted in Schizophrenia 1; DISC1; neuroleptic; gene therapy;
KW neuropsychiatric disorder; schizoaffective disorder; bipolar disorder;
KW unipolar affective disorder; adolescent conduct disorder; schizophrenia;
KW PCR; primer; ss.
XX
XX
XX Homo sapiens.
OS
XX
XX WO200258637-A2.
PN
XX
XX 01-AUG-2002.
PD
XX
XX 23-JAN-2002; 2002WO-US002186.
PF
XX
XX 24-JAN-2001; 2001US-00770107.
PR
XX
XX (MILL-) MILLENIUM PHARM INC.
PA
XX
XX Meyer JM, Barrington-Martin R, Parker A, Barnes GT;
PI WPI; 2002-590791/63.
XX
XX
DR
XX
XX New human Disrupted-In-Schizophrenia (DISC) 1 and DISC2 genes containing
PT single nucleotide polymorphisms, useful for preventing or treating
PT neuropsychiatric disorders e.g. schizophrenia.
XX
XX
PS Claim 17; Fig 4; 169pp; English.
XX
XX
XX The invention relates to a novel Disrupted-In-Schizophrenia (DISC) 1
CC allelic variant polynucleotide. The polypeptides of the invention have
CC neuroleptic activity. The polynucleotides may have a use in gene therapy.
CC DISC1 or DISC2 nucleic acid molecules are useful for diagnosing or
CC treating a subject having a disease or disorder associated with specific
CC DISC1 or DISC2 alleles and/or aberrant DISC1 expression or activity e.g.
CC neuropsychiatric disorder such as schizoaffective, bipolar, unipolar
CC affective or adolescent conduct disorder or schizophrenia. Similarly, the
CC compound that inhibits DISC1 protein activity may be used in the method
CC for treating such neuropsychiatric disorders. The sequences shown in
CC ABO93575-ABO93658 represent the PCR primers used in the invention to
CC amplify the sequences of DISC2 and DISC2
XX
XX
SQ Sequence 21 BP; 4 A; 3 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 535 CTCTGCTGAGCTCCCAAG 555
Db 21 CTACTGCTGAGCTCCCAAG 1
|||||
|

RESULT 600
 ABS98164
 ID ABS98164 standard; DNA; 21 BP.
 XX
 AC ABS98164;
 XX
 DT 23-DEC-2002 (first entry)
 XX
 DE Human multidrug resistance gene polymorphic sequence #66.
 XX
 XX Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
 XX cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
 XX adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR112;
 XX aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
 XX cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
 XX epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
 XX glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
 XX HMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
 XX NADPH quinone oxidoreductase 2; NQO2; sulfoxotransferase thermolabile; STM;
 XX UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
 XX UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokininase receptor; UPA;
 XX multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
 XX multidrug resistance associated protein 3; cancer; prostate;
 XX acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
 XX altered drug metabolism; cardiovascular function; colorectal tumour;
 XX central nervous system; pulmonary; immunological; SNP;
 XX single nucleotide polymorphism.
 XX
 OS Homo sapiens.
 XX
 PN WO200257410-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 28-NOV-2001; 2001WO-US044838.
 XX
 PR 28-NOV-2000; 2000US-00724389.
 XX
 PA (DNAS-) DNA SCI LAB INC.
 XX
 PI Guida M, Hall J;
 XX
 DR WPI; 2002-698522/75.
 XX
 PT Isolated nucleic acid molecules having polymorphisms in known human genes
 PT e.g. cytochrome P450 and cathepsin S useful as genetic linkage markers
 PT for locating, identifying and characterizing the genes responsible for
 PT disorder-related traits.
 XX
 PS Example 22; Page 144; 714pp; English.
 XX
 CC This invention relates to the sequence of an isolated nucleic acid
 CC molecule comprising at least one base variation from that of a known
 CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
 CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
 CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
 CC inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating
 CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
 CC transferase (NNMT), (kallikrein 2) KLK2, nicotinamide-N-methyl
 CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
 CC sulfoxotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
 CC transferase (UGT2B15), urukininase receptor (UPA), multidrug resistance 1
 CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
 CC (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic
 CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
 CC The polymorphisms in the human genes cited in the invention are useful as
 CC genetic linkage markers for locating and characterizing the genes that
 CC are responsible for specific traits within the genome and eventually
 CC identifying the genes responsible for a variety of disorder-related

traits as a result of their e.g., overexpression, constitutive
 CC expression, mutation or underexpression, which may be used in diagnosing
 CC and/or treating the disorders. The nucleic acid molecules comprising the
 CC polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502E1,
 CC ARNT, EPHX2, GST12, NNMT, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
 CC metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
 CC used to screen for altered cardiovascular function. In COX2 for altered
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
 CC nervous system function, in FLAP and NNMT for altered pulmonary,
 CC immunological or haematological function, in KLK2 for altered serine
 CC protease activity in the prostate, in LTF for altered immunological or
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
 CC peripheral nervous system function. The present sequence represents a
 CC polymorphic DNA sequence of the invention
 XX
 SQ Sequence 21 BP; 5 A; 5 C; 7 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 2.0%; Score 19.4; DB 1; Length 21;
 Best Local Similarity 95.2%; Pred. No. 1.2e+03;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 868 GGATTACAGCGCTGAGCCACC 888
 DB 1 GGATTACAGGTGTGAGCCACC 21
 XX
 ID ADC42593
 XX
 AC ADC42593;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human FANCD2 PCR primer hFANCD2_exon7_F.
 XX
 KM cancer; Fanconi Anaemia; FA; BRCA; cytostatic; microarray;
 XX chemosensitising; ss; PCR; primer.
 XX
 OS Synthetic.
 XX
 PN WO2003039327-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 06-JUN-2002; 2002WO-US018153.
 XX
 PR 02-NOV-2001; 2001US-00998027.
 XX
 PR 02-NOV-2001; 2001WO-US045561.
 XX
 PA (DAND) DANA FARBER CANCER INST.
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 PI D'andrea AD, Taniguchi T, Timmers C, Grompe M, Fox EA;
 XX
 DR WPI; 2003-441436/41.
 XX
 PT Diagnosing or determining cancer or increased risk of cancer in a
 PT patient, by testing Fanconi Anemia/BRCA pathway gene or protein for a
 PT cancer-associated defect, that indicates cancer or increased risk of
 PT cancer.
 XX
 PS Example 14; Page 101; 160pp; English.
 XX
 CC The invention relates to a novel method of diagnosing or determining if a
 CC patient has cancer or is at increased risk of cancer, involving testing a
 CC Fanconi Anaemia (FA)/BRCA pathway gene or protein for the presence of a
 CC cancer-associated defect, where the presence of one or more cancer-
 CC associated defects is indicative of cancer or an increased risk of cancer
 CC in the patient. The method of the invention has cytostatic activity. The

CC method is useful for determining if a patient has cancer, or is at
CC increased risk of developing cancer, e.g. breast, ovarian or prostate
CC cancer. A microarray of the invention is useful for determining if a
CC patient has cancer, or is at increased risk of developing cancer, by
CC hybridizing a nucleic acid sample to the nucleic acid sequences from the
CC array, and detecting the presence of mutations in PA/BRCA pathway genes
CC in the nucleic acid sample from the patient, where detecting the presence
CC of mutations is indicative of a patient who has cancer, or is at
CC increased risk of developing cancer. A method of the invention is useful
CC for screening a chemosensitizing agent, and the agent obtained is useful
CC for treating a patient having a cancer. The present sequence is used in
CC the exemplification of the invention.

CC Sequence 21 BP; 5 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 966 AATCTCGCTCACTGCAACCT 986
DB 1 AATCTCGCTCACTGCAACCT 21

RESULT 602

ADE14130/C
ID ADE14130 standard; DNA; 21 BP.

XX ADE14130;

DT 29-JAN-2004 (first entry)

DE Optineurin promoter motif, repeat element or regulatory region #239.

KW Human; optineurin; de; ophthalmological; single nucleotide polymorphism;
KW SNP; glaucoma; progressive ocular hypertensive disorder;

KW glaucoma related disorder; motif; repeat element; regulatory region.

XX Homo sapiens.

OS US2003190617-A1.

PN 09-OCT-2003.

PD 06-MAR-2002; 2002US-00091281.

PF 06-MAR-2002; 2002US-00091281.

PR (SIEE/) SI E.

PA (RAYM/) RAYMOND V.

PA (MORI/) MORISSETTE J.

PI Raymond V, Morissette J, Si E;

XX WPI; 2003-864168/80.

DR New nucleic acid sequences of the optineurin gene are useful to detect
XX polymorphisms particularly single nucleotide polymorphisms in the
PT optineurin promoter to diagnose, prognose and treat glaucoma and related
PT disorders.

PS Claim 11; SEQ ID NO 241; 159pp; English.

CC The invention relates to an isolated nucleic acid (N1) comprising at
CC least 20 but not more than 1500 consecutive nucleotides of the optineurin
CC promoter appearing as ADE13890. Also included are the optineurin promoter
CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
CC detecting a single nucleotide polymorphism (SNP) in the optineurin
CC promoter, a host cell comprising the promoter operably linked to a
CC heterologous sequence, diagnosing or prognosing glaucoma in a sample
CC obtained from a cell or bodily fluid (comprising detecting a polymorphism
CC in a promoter region of the optineurin gene, associated with a glaucoma
CC phenotype), detecting a SNP sequence variation in a sample containing

CC DNA, detecting the presence of an optineurin promoter sequence variation
CC in a sample containing DNA, determining the presence or increased
CC susceptibility to glaucoma or to a progressive ocular hypertensive
CC disorder resulting in loss of visual field in a patient (or the severity
CC or progression of glaucoma in a patient, comprising providing of a selected
CC amplification reaction primers that direct amplification of a selected
CC nucleic acid region containing the variation within the optineurin
CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
CC obtaining a sample containing human genomic DNA, providing a nucleic acid
CC capable of detecting a SNP located within an optineurin promoter, and
CC detecting the polymorphism). The invention is used to diagnose and
CC prognose glaucoma and also to treat glaucoma related disorders. The
CC present sequence is an optineurin promoter motif, repeat element or
CC putative regulatory region.

CC Sequence 21 BP; 5 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 849 TCGGCTCCCAAGTCTGGG 869
DB 21 TCGGCTCCCAAGTCTGGG 1

RESULT 603

ADH59619
ID ADH59619 standard; DNA; 21 BP.

XX ADH59619;

DT 25-MAR-2004 (first entry)

DE Non-nucleotide probe of the invention #23.

KW non-nucleotide probe; Bacterial Artificial Chromosome clone; BAC; ss;
KW probe.

OS Synthetic.

PN WO2003027328-A2.

PD 03-APR-2003.

PF 24-SEP-2002; 2002WO-US030573.

PR 24-SEP-2001; 2001US-0324499P.

PA (BOST-) BOSTON PROBS INC.

PA (DAKO-) DAKOCYTOMATION DENMARK AS.

PI Kirszen NV, Hyldig-Nielsen JJ, Williams BF;

XX WPI; 2003-421160/39.

DR Non-nucleotide probe for suppressing binding of detectable nucleic acid
XX probes to undesired sequences, has aggregate nucleobase sequence
PT homologous to randomly distributed repeat sequence of genomic nucleic
PT acid.

PS Claim 10; SEQ ID NO 25; 103pp; English.

CC The present sequence represents a non-nucleotide probe. The probe is
CC useful for suppressing the binding of one or more detectable nucleic acid
CC probes, that are greater than 100 base pairs and that have been derived
CC from genomic nucleic acid, to one or more undesired sequences in an assay
CC for determining target genomic nucleic acid of a sample. The method
CC comprises contacting the sample with the mixture of probes (preferably
CC comprising 5-50 probes), contacting the sample with the one or more
CC detectable nucleic acid probes, and determining the target genomic
CC nucleic acid of the sample by determining the hybridization of the one or
CC more detectable nucleic acid probes to the target genomic nucleic acid of

XX AC ADH59605;
 XX DT 25-MAR-2004 (first entry)
 XX DE Non-nucleotide probe of the invention #9.
 XX KM non-nucleotide probe; Bacterial Artificial Chromosome clone; BAC; ss;
 XX KM probe.
 XX OS Synthetic.
 XX PN WO2003027328-A2.
 XX PD 03-APR-2003.
 XX PF 24-SEP-2002; 2002WO-US030573.
 XX PR 24-SEP-2001; 2001US-0324499P.
 XX PA (BOST-) BOSTON PROBES INC.
 XX PA (DAKO-) DAKOCYTOMATION DENMARK AS.
 XX PI Kirtsen NV, Hyldig-Nielsen JU, Williams BF;
 XX PI WPI; 2003-421160/39.
 XX PT Non-nucleotide probe for suppressing binding of detectable nucleic acid
 PT probes to undesired sequences, has aggregate nucleobase sequence
 PT homologous to randomly distributed repeat sequence of genomic nucleic
 PT acid.
 XX PS Claim 10; SEQ ID NO 11; 103bp; English.
 XX XX The present sequence represents a non-nucleotide probe. The probe is
 CC useful for suppressing the binding of one or more detectable nucleic acid
 CC probes, that are greater than 100 base pairs and that have been derived
 CC from genomic nucleic acid, to one or more undesired sequences in an assay
 CC for determining target genomic nucleic acid of a sample. The method
 CC comprises contacting the sample with the mixture of probes (preferably
 CC comprising 5-50 probes), contacting the sample with the one or more
 CC detectable nucleic acid probes, and determining the hybridization of the one or
 CC more detectable nucleic acid probes to the target genomic nucleic acid of
 CC the sample. The genomic nucleic acid is contained in a fixed tissue or a
 CC cell, and the sample is metaphase spreads, interphase nucleic or nucleic
 CC found in paraffin embedded tissue material or frozen tissue sections. The
 CC probe is also useful in comparing a sample of genomic nucleic acid with
 CC that of a control sample using a genomic nucleic acid reference array.
 CC The method comprises treating a sample of genomic nucleic acid and
 CC control genomic nucleic acid, which are differentially labelled, the
 CC array or both the sample and control genomic nucleic acid and the array
 CC with the mixture of the probe under suitable hybridization conditions,
 CC contacting the array with treated mixture of sample and control genomic
 CC nucleic acid under suitable hybridization conditions, and comparing the
 CC intensities of the signals from the differential labels of the array to
 CC that caused by hybridization of the probes to genomic nucleic acid, thus
 CC determining one or more variations in copy numbers of sequences in the
 CC sample as compared with the relative copy numbers of substantially
 CC identical sequences in the control. The hybridization of the genomic
 CC array is determined using an intercalating dye or a detectable antibody,
 CC or its fragment, that is specific for a nucleic acid/nucleic acid hybrid.
 CC The sample of genomic nucleic acid to be tested and the reference of
 CC nucleic acid are labelled with detectable moiety such that hybridization
 CC of the genomic array is determined by determining the presence, absence,
 CC amount or location of the detectable label on the one or more genomic
 CC arrays. The genomic array comprises nucleic acid that is prepared from
 CC Bacterial Artificial Chromosome (BAC) clones. The present sequence
 CC represents a non-nucleotide probe of the invention.
 XX Sequence 21 BP; 3 A; 8 C; 5 G; 5 T; 0 U; 0 Other;
 XX SQ

Query Match 2.0%; Score 19.4; DB 1; Length 21;

Best Local Similarity 95.2%; Pred. No. 1.2e+03;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 990 CCTCCCGGCGTCAGGATTC 1010
 Db 1 CCTCCCGGCGTCAAGGATTC 21
 RESULT 608
 ID ACAS4779
 ACAS4779 standard; DNA; 21 BP.
 XX AC ACAS4779;
 XX DT 05-JUN-2003 (first entry)
 XX DE Human NF-kappaB associated polynucleotide PCR primer #36.
 XX KM Human; nuclear factor-kappaB; NF-kappaB; immune disorder; cancer;
 KM inflammatory disorder; apoptosis; hepatic disorder; Hodgkin's lymphoma;
 KM haematopoietic tumour; hyper-igm syndrome; viral infection; asthma;
 KM hypohidrotic ectodermal dysplasia; human immunodeficiency virus; HIV;
 KM X-linked anhidrotic ectodermal dysplasia; al incontinentia pigmenti;
 KM influenza; rheumatoid arthritis; inflammatory bowel disease; colitis;
 KM atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
 KM experimental allergic encephalomyelitis; autoimmune disorder; wound;
 KM hyper immune activity; acute phase response; hypercongenital condition;
 KM birth defect; necrotic lesion; organ transplant rejection; pancreas;
 KM signal transduction; hyperproliferative disorder; diabetes mellitus;
 KM vitamin B12 malabsorption; neurological disorder; Huntington's chorea;
 KM Turner's syndrome; bacterial infection; cardiovascular disorder;
 KM infertility; psoriasis; haemolytic anaemia; antiinflammatory; anti-HIV;
 KM cytostatic; hepatotropic; vitruide; antineumatic; antiallergic;
 KM antiaslomatic; immunosuppressive; vulnery; antibacterial;
 KM neuroprotective; immunosuppressive; vulnery; antibacterial;
 KM antinfertility; antinaemic; antipsoriatic; cerebroprotective; cardiac;
 KM antidiabetic; antinaemic; antipsoriatic; cerebroprotective; cardiac;
 KM antidiabetic; PCR; primer; ss.
 XX OS Homo sapiens.
 XX PN WO200286076-A2.
 XX PD 31-OCT-2002.
 XX PF 19-APR-2002; 2002WO-US012636.
 XX PR 19-APR-2001; 2001US-0284962P.
 XX PR 26-APR-2001; 2001US-0286645P.
 XX PR 09-JUN-2002; 2002US-0346986P.
 XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX PI Carman J, Feder J, Nadler S;
 XX DT WPI; 2003-093119/08.
 XX PT Novel NF-kappaB-associated polypeptides and polynucleotides useful for
 PT diagnosing, treating and preventing cancer, hepatic disorders, aberrant
 PT apoptosis, viral infections, autoimmune disorders, asthma and stroke.
 XX Example 3; Page 341; 608bp; English.
 XX PS The present invention relates to the isolation of human nuclear factor-
 CC kappaB (NF-kappaB) associated polypeptides and polynucleotides. The NF-
 CC kappaB associated polypeptide and polynucleotide sequences are useful for
 CC preventing, treating or ameliorating various disorders including immune
 CC disorders, inflammatory disorders, cancer, disorders relating to
 CC aberrant apoptosis, hepatic disorders, Hodgkin's lymphomas,
 CC haematopoietic tumours, hyper-igm syndromes, hypohidrotic ectodermal
 CC dysplasia, X-linked anhidrotic ectodermal dysplasia, immunodeficiency, al
 CC incontinentia pigmenti, viral infections (e.g. those caused by human
 CC immunodeficiency virus (HIV), human T-cell lymphotropic virus (HTLV),
 CC hepatitis B, hepatitis C, Epstein Barr virus (EBV), influenza),

rheumatoid arthritis, inflammatory bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick syndrome, stroke, experimental allergic encephalomyelitis (EAE), autoimmune disorders, disorders related to hyper immune activity, disorders related to aberrant acute phase responses, hypercongenital conditions, birth defects, necrotic lesions, wounds, organ transplant rejection, disorders related to aberrant signal transduction, hyperproliferative disorders, diseases of the pancreas (e.g. diabetes mellitus, vitamin B12 malabsorption), neurological disorders (e.g. Huntington's chorea), Turner's syndrome, bacterial infections, cardiovascular disorders, infertility, psoriasis and haemolytic anaemia. The present sequence represents a PCR primer used in the examples of the present invention

Sequence 21 BP; 4 A; 2 C; 9 G; 6 T; 0 U; 0 Other;

Query Match	2.0%	Score 19.4;	DB 1;	Length 21;
Best Local Similarity	95.2%	Pred. No. 1.2e+03;		
Matches	20;	Conservative	0;	Mismatches 1;
			Indels	0;
			Gaps	0;

QY 476 TGAAGTCAGTGGTGTGATCA 496
|||
Db 1 TGAAGTCAGTGGTGTGATCA 21

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RESULT 609
AD123732
ID AD123732 standard; DNA; 21 BP.

AC	ADI23732;
XX	
DT	06-MAY-2004 (first entry)

XX Human LPDLR PCR primer #12.
DE
XX
XX
KW lipase; LPDL; lipDLR: lipase deficiency; atherosclerosis;
KW fatty liver disease; dyslipidemia; hypercholesterolemia;
KW hypertriglyceridemia; mixed dyslipidaemia; lipid deficient state;
KW hypoprotein deficient state; human; ss; PCR; primer.

OS Homo sapiens.

PN WO2003055995-A2.

PD 10-JUL-2003.

PF 23-DEC-2002; 2002WO-CA001998.

PR 21-DEC-2001; 2001US-0341786P.

XX XX

PA (WENX/) WEN X.

PA (STEW/) STEWART A K.
PA (TEIT/) TEIT I

PA (1501/) 1501 L.
PA (HEGE/) HEGET.E P A

XX (MEGE) MEGBLE K A.

PI Wen X, Stewart AK, Tsui L, Hegdele RA,

DR WPI; 2003-569444/53.

PT Novel isolated LDL or LDLR lipase polypeptides, useful for identifying
PT substances that bind to the protein and which are useful for treating
PT diseases associated with lipase function e.g. atherosclerosis and
PT hypercholesterolemia.

PS Disclosure; SEQ ID NO 68; 172pp; English.

The invention relates to an isolated mammalian (e.g., human or mouse) lipase polypeptide (polyp), e.g., LPDL (I) or LPDL polyp (II). (I) or (II) is useful for identifying substances which can bind with LPDL or LPDL polyp, and for identifying a compound that affects the binding of LPDL or LPDL polyp and an LPDL or LPDL binding polyp. (I) or (II) or their nucleic acid is useful for identifying a compound that affects LPDL or LPDL polyp activity or expression. (I) or (II) or their nucleic acid

is useful for detecting or monitoring a condition associated with increased or decreased LDL or Lp(a) expression or activity in an animal where the condition is lipase deficiency, atherosclerosis, fatty liver disease and dyslipidaemias, such as hypercholesterolemia.

hypertriglyceridemia, mixed (combined) dyslipidemia, lipid or lipoprotein deficiency, and/or any other tissue or plasma disorders of lipid or lipoprotein metabolism. The nucleic acid is useful for diagnosing the presence of or a predisposition for a disorder in a subject which involves detecting a germline alteration in the nucleic acid in the subject. An inhibitor is useful for modulating triglyceride activity by inhibiting expression or activity of (I) or (II). The nucleic acid is useful as a probe or primer. The present sequence is used in the exemplification of the invention.

Sequence 21 BP; 5 A; 3 C; 8 G; 5 T; 0 U; 0 Other;

Query Match	2.0%	Score 19.4;	DB 1;	Length 21;
Best Local Similarity	95.2%;	Pred. No. 1.2e+03;		
Matches	20;	Conservative	0;	Mismatches 1;
			Indels	0;
			Gaps	0;

QY 863 TGCTGGATTACAGCGCTGAG 883
|||||
Db 1 TGCTGGATTACAGCGCATGAG 21

Db 1 TGCTGGATTACAGCATGAG 21

RESULT 610
AD012329
ID AD012329 standard; DNA; 21 BP.

AC	ADO12329;
XX	
DT	15-JUL-2004 (first entry)

XX Single multiplex PCR primer #1701.
 DE
 XX
 KW ss; primer; simultaneous amplification;
 KW single multiplex polymerase chain reaction; multifactorial disease;
 KW genetic alteration; pharmacogenetic reaction; genotyping; polymorphism
 KW gene expression profiling.

OS Synthetic.

PN WO2004033649-A2.

PD 22-APR-2004

PF 07-OCT-2003; 2003WO-US031874.

PR 07-OCT-2002; 2002US-0417009P.

PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.

PI Li H, Li J;

DR WPI; 2004-340914/31.

PT Designing primers for simultaneous amplification of target DNA fragments
PT in a single multiplex polymerase chain reaction, for high throughput
PT multiplex DNA sequence amplification, comprises aligning two primers.

PS Disclosure; Page 41; 120pp; English

The invention relates to a method of designing primers for simultaneous amplification of target DNA fragments in a single multiplex polymerase chain reaction by aligning a first primer and a second primer. The method comprises: (a) aligning a first primer and a second primer; and (b) selecting the first primer where the first primer at its 3' end does not contain four or more bases that are perfectly matching to the 3' end sequence of the first primer or a second primer, the first primer at its 3' end does not contain seven or more bases that are perfectly matching except one mismatch to the 3' end sequence of the first primer or the second primer, the first primer at its 3' end does not contain six or more bases that are perfectly matching to a sequence anywhere of the

CC first primer or the second primer, and the first primer at its 3' end
CC does not contain eleven or more bases that are perfectly matching except
CC one mismatch to a sequence anywhere of the first primer or the second
CC primer. The method is useful for designing primers for simultaneous
CC amplification of target DNA fragments in a single multiplex polymerase
CC chain reaction. It is also useful in the identification of multiple genes
CC related to multifactorial diseases, the genome-scale detection of genetic
CC alterations, the studies in pharmacogenetic reactions, the genotyping
CC genetic polymorphisms in a large population, the gene expression
CC profiling in various samples and high throughput genotyping technologies.
CC This sequence corresponds to an example of a primer of the invention.
XX
SQ Sequence 21 BP; 4 A; 8 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 209 GGCTGCTCGAAGCTCCGAC 229
Db 1 GGCTGCTCGAAGCTCCGAC 21

RESULT 611
AA225156
ID AA225156 standard; DNA; 22 BP.
XX
AC AA225156;
XX
DT 13-DEC-1999 (first entry)
XX
DE Human short interspersed repetitive element PCR primer #14.
XX

KM Human; short interspersed repetitive element; SINE; PCR; primer;
KW Oncochrychnus; restriction primer; short interspersed repeated sequence;
KM eukaryote; restricted polymerase chain reaction fingerprinting;
XX identification; DNA specimen; discrimination; ss.
XX

OS Synthetic.
OS Homo sapiens.
XX

PN JP2913035-B1.
XX

PD 28-JUN-1999.
XX

PF 10-JUL-1998; 98BP-00195692.
XX

PR 10-JUL-1998; 98BP-00195692.
XX

PA (NORQ) NORINSUISANSHO SUIANCHO YOSHOKU KENKYUSHOCHO.
XX

DR WPI; 1999-583348/50.
XX

PT Restriction primer for distinguishing individuals with short interspersed
XX repeated sequence of eukaryotes by restricted polymerase chain reaction
XX fingerprinting.
XX

PS Claim 6; Page 3; 17pp; Japanese.
XX

CC The present invention describes a restriction primer for eukaryotic short
CC interspersed repeated sequences (SINE), which has one or more additional
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
CC the SINE. The annealing temperature of the primer to the DNA sequence is
CC kept higher than the fusion temperature of the primer during polymerase
CC chain reaction (PCR). The PCR fragments obtained are subjected to
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from
CC the electrophoresis band pattern, eukaryotic individuals are
CC distinguished. The primer is used for amplifying a eukaryotic
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be
CC used individual identification of humans for medical and legal
CC applications and ecological studies. DNA specimens in traces
CC (approximately 10 ng in mass) can be used for individual discrimination

CC of eukaryotes using the primer in a polymerase chain reaction (PCR).
CC AA225143 to AA225191 represent specifically claimed examples of primers
CC from the present invention
XX

SQ Sequence 22 BP; 7 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 869 GATTACAGGCGTAGCCACCA 889
Db 1 GATTACAGGCGTAGCCACCA 21

RESULT 612
AA225168
ID AA225168 standard; DNA; 22 BP.
XX
AC AA225168;
XX

DT 13-DEC-1999 (first entry)
XX
DE Human short interspersed repetitive element PCR primer #26.
XX

KM Human; short interspersed repetitive element; SINE; PCR; primer;
KW Oncochrychnus; restriction primer; short interspersed repeated sequence;
KM eukaryote; restricted polymerase chain reaction fingerprinting;
XX identification; DNA specimen; discrimination; ss.
XX

OS Synthetic.
OS Homo sapiens.
XX

PN JP2913035-B1.
XX

PD 28-JUN-1999.
XX

PF 10-JUL-1998; 98BP-00195692.
XX

PR 10-JUL-1998; 98BP-00195692.
XX

PA (NORQ) NORINSUISANSHO SUIANCHO YOSHOKU KENKYUSHOCHO.
XX

DR WPI; 1999-583348/50.
XX

PT Restriction primer for distinguishing individuals with short interspersed
XX repeated sequence of eukaryotes by restricted polymerase chain reaction
XX fingerprinting.
XX

PS Claim 6; Page 4; 17pp; Japanese.
XX

CC The present invention describes a restriction primer for eukaryotic short
CC interspersed repeated sequences (SINE), which has one or more additional
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
CC the SINE. The annealing temperature of the primer to the DNA sequence is
CC kept higher than the fusion temperature of the primer during polymerase
CC chain reaction (PCR). The PCR fragments obtained are subjected to
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from
CC the electrophoresis band pattern, eukaryotic individuals are
CC distinguished. The primer is used for amplifying a eukaryotic
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be
CC used individual identification of humans for medical and legal
CC applications and ecological studies. DNA specimens in traces
CC (approximately 10 ng in mass) can be used for individual discrimination
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).
CC AA225143 to AA225191 represent specifically claimed examples of primers
CC from the present invention
XX

SQ Sequence 22 BP; 6 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 1.3e+03;

XX Human; short interspersed repetitive element; SINE; PCR; primer;
 KW Oncohychnus; restriction primer; short interspersed repeated sequence;
 KW eukaryote; restricted polymerase chain reaction fingerprinting;
 KM identification; DNA specimen; discrimination; ss.

XX Synthetic.
 OS Homo sapiens.

XX JP2913035-B1.

XX 28-JUN-1999.

XX 10-JUL-1998; 98JP-00195692.

XX 10-JUL-1998; 98JP-00195692.

XX (NORO) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.

XX WPI; 1999-583348/50.

XX Restriction primer for distinguishing individuals with short interspersed
 PT repeated sequence of eukaryotes by restricted polymerase chain reaction
 PT fingerprinting.

XX Claim 6; Page 4; 17pp; Japanese.

XX The present invention describes a restriction primer for eukaryotic short
 CC interspersed repeated sequences (SINE), which has one or more additional
 CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
 CC the SINE. The annealing temperature of the primer to the DNA sequence is
 CC kept higher than the fusion temperature of the primer during polymerase
 CC chain reaction (PCR). The PCR fragments obtained are subjected to
 CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from
 CC the electrophoresis band pattern, eukaryotic individuals are
 CC distinguished. The primer is used for amplifying a eukaryotic
 CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
 CC polymerase chain reaction (PCR) fingerprinting. In particular it may be
 CC used in individual identification of humans for medical and legal
 CC applications and ecological studies. DNA specimens in traces
 CC (approximately 10 ng in mass) can be used for individual discrimination
 CC of eukaryotes using the primer in a polymerase chain reaction (PCR).
 CC AA25143 to AA25191 represent specifically claimed examples of primers
 CC from the present invention

SO Sequence 22 BP; 7 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.4; DB 1; Length 22;

Best Local Similarity 95.2%; Pred. No. 1.3e+03;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 869 GATTACAGCGGTGAGCCACCA 889

DB 1 GATTACAGCGGTGAGCCACCA 21

RESULT 616

AA25155 ID AA25155 standard; DNA; 22 BP.

XX AA25155;

XX 13-DEC-1999 (first entry)

XX Human short interspersed repetitive element PCR primer #13.

XX Human; short interspersed repetitive element; SINE; PCR; primer;
 KM Oncohychnus; restriction primer; short interspersed repeated sequence;
 KM eukaryote; restricted polymerase chain reaction fingerprinting;
 KM identification; DNA specimen; discrimination; ss.

XX Synthetic.
 OS Homo sapiens.

XX JP2913035-B1.

XX 28-JUN-1999.

XX 10-JUL-1998; 98JP-00195692.

XX 10-JUL-1998; 98JP-00195692.

XX (NORO) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.

XX WPI; 1999-583348/50.

XX Restriction primer for distinguishing individuals with short interspersed
 PT repeated sequence of eukaryotes by restricted polymerase chain reaction
 PT fingerprinting.

XX Claim 6; Page 3; 17pp; Japanese.

XX The present invention describes a restriction primer for eukaryotic short
 CC interspersed repeated sequences (SINE), which has one or more additional
 CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
 CC the SINE. The annealing temperature of the primer to the DNA sequence is
 CC kept higher than the fusion temperature of the primer during polymerase
 CC chain reaction (PCR). The PCR fragments obtained are subjected to
 CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from
 CC the electrophoresis band pattern, eukaryotic individuals are
 CC distinguished. The primer is used for amplifying a eukaryotic
 CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
 CC polymerase chain reaction (PCR) fingerprinting. In particular it may be
 CC used in individual identification of humans for medical and legal
 CC applications and ecological studies. DNA specimens in traces
 CC (approximately 10 ng in mass) can be used for individual discrimination
 CC of eukaryotes using the primer in a polymerase chain reaction (PCR).
 CC AA25143 to AA25191 represent specifically claimed examples of primers
 CC from the present invention

SO Sequence 22 BP; 8 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.4; DB 1; Length 22;

Best Local Similarity 95.2%; Pred. No. 1.3e+03;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 869 GATTACAGCGGTGAGCCACCA 889

DB 1 GATTACAGCGGTGAGCCACCA 21

RESULT 617

AA511629 ID AA511629 standard; DNA; 22 BP.

XX AA511629;

XX 24-OCT-2001 (first entry)

XX Human CYP2B6 allele sequencing primer seqCYP2B6-7F for exon 7.

XX CYP2B6; cytosolic; gene therapy; genotyping; cancer; metabolism; ss;
 KM human; cancer susceptibility; environmental carcinogen;
 KM sequencing primer.

XX Homo sapiens.

XX WO200159152-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-EP001456.

XX 09-FEB-2000; 2000EP-00102701.

XX (EPID-) EPIDAKROS BIOTECHNOLOGIE AG.

XX Zanger UM, Lang T;
XX WPI; 2001-502719/55.
XX
XX
XX New polynucleotide(s) of the polymorphic human CYP2B6 gene for the
XX detection and treatment of disorders i.e. cancer.
XX
XX Claim 36; Page 45; 83pp; English.
XX
XX The sequence represents a sequencing primer used to sequence an exon of
XX the human CYP2B6 gene. It is used for specific detection and genotyping
XX of CYP2B6 alleles in humans, determination of which is useful for the
XX optimization of therapies utilizing CYP2B6 substrates. Oligonucleotide
XX sequences are useful in detection of the individual predisposition to
XX several common cancers caused by environmental carcinogens, and diseases
XX treated with drugs that are targets of the CYP2B6 gene product, whose
XX metabolism is therefore dependent on CYP2B6. Cancer or susceptibility to
XX cancer can be diagnosed by detecting the presence of a molecular variant
XX of CYP2B6. From variants of the alleles, modulators of the activity can
XX be developed for use in treatment and prevention of CYP2B6-related
XX disorders
XX
XX Sequence 22 BP; 7 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 869 GATTACAGGCGGTGAGCCACCA 889
DB 1 GATTACAGGCGATGACCCACCA 21
RESULT 618
AAF93028/C
ID AAF93028 standard; DNA; 22 BP.
XX
XX AAF93028;
XX
XX 17-MAY-2001 (first entry)
XX
XX Polymorphic sequence for ABC1 polymorphic site #38.
XX
XX High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.
XX
XX Homo sapiens.
XX
XX WO200115676-A2.
XX
XX 08-MAR-2001.
XX
XX 01-SEP-2000; 2000WO-1B001492.
XX
XX 01-SEP-1999; 99US-0151977P.
XX
XX 15-MAR-2000; 2000US-00526193.
XX
XX 23-JUN-2000; 2000US-0213958P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX (XENO-) XENON GENETICS INC.
XX
XX
XX Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;
XX
XX WPI; 2001-244356/25.
XX
XX
XX Treating a lower than normal high density lipoprotein-cholesterol (HDL-C)
XX level, a higher than normal triglyceride level, or a cardiovascular
XX disease, by administering a compound that modulates LXR- or RXR-mediated
XX transcriptional activity.
XX
XX Disclosure; Fig 4; 317pp; English.
XX
XX The present invention relates to a method for treating a patient

CC diagnosed as having a lower than normal high density lipoprotein-
CC cholesterol (HDL-C) level, a higher than normal triglyceride level, or a
CC cardiovascular disease, involving administering a compound that modulates
CC LXR- or RXR-mediated transcriptional activity or ABC1 expression or
CC activity. The LXR gene product may be used in an assay to identify
CC compounds useful for the treatment of a disease or condition selected a
CC lower than normal HDL cholesterol level, a higher than normal
CC triglyceride level, and a cardiovascular disease
XX
XX Sequence 22 BP; 6 A; 2 C; 10 G; 3 T; 0 U; 1 Other;
SQ
Query Match 2.0%; Score 19.4; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 533 TCCTCTGCGCTGAGCTCCCA 554
DB 22 TTCTCTGCTGAGCTCCCA 1
RESULT 619
ADC24360
ID ADC24360 standard; DNA; 22 BP.
XX
XX ADC24360;
XX
XX 18-DEC-2003 (first entry)
XX
XX PCR primer for amplifying the BRCA1 gene #SEQ ID 50.
XX
XX DNA amplification; copy number; polymerase chain reaction; PCR; primer;
XX
XX 88.
XX
XX Synthetic.
XX
XX JP2002345466-A.
XX
XX 03-DEC-2002.
XX
XX 08-MAY-2001; 2001JP-00137858.
XX
XX 08-MAY-2001; 2001JP-00137858.
XX
XX
XX (TAKA-) TAKARA BIO KK.
XX
XX (KOKU-) KOKURITSU GAN CENT SOCHO.
XX
XX (YAK-) YAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
XX
XX WPI; 2003-460878/44.
XX
XX
XX Amplification of DNA maintaining genes and copy number of the sequence on
XX a genome, and their ratios in the resultant DNA fragment.
XX
XX Example 3; SEQ ID NO 50; 33pp; Japanese.
XX
XX The invention relates to a method for the amplification of DNA that
XX maintains genes and copy number of the sequence. This method is useful
XX for easy and operable amplification of DNA. The method was carried out by
XX fragmentation genomic DNA, preparation of blunt end of the fragmented
XX DNA, ligation of an adapter to the blunted DNA, PCR of the ligated DNA in
XX 2 steps, and confirmation of the amplified APC gene. The current sequence
XX represents a PCR primer used in an example from the invention.
XX
XX Sequence 22 BP; 7 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 387 CCAAGTGTGCGATTACAGG 407
DB 1 CCAAGTGTGCGATTACAGG 21

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RESULT 620
AAQ73576
ID AAQ73576 standard; DNA; 24 BP.
XX
XX AAQ73576;
AC
XX 25-MAR-2003 (revised)
DT 25-JUN-1995 (first entry)
XX
XX Enhancer element er-6 conserved basepair sequence.
DE
XX Enhancer element; carcinoma; tumor; cancer; SLP1 gene;
KW secretory leukoprotease-inhibitor gene; cytokeratin gene-8; ss.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH misc_difference 14 /*tag= a
FT /label= purine
FT misc_difference 16 /*tag= b
FT /label= pyrimidine
FT misc_difference 22 /*tag= c
FT /label= purine
XX
XX WO9421118-A1.
XX
XX 29-SEP-1994.
XX
XX 24-MAR-1994; 94WO-US003197.
XX
XX 24-MAR-1993; 93US-00035435.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Garver RI, Sorscher EJ;
XX
XX WPI; 1994-316537/39.
XX
XX DNA construct for treating human carcinoma - includes a cancer-
PT therapeutic gene under the control of a promoter and a gp. of enhancer
PT sequences.
XX
XX Claim 1; Fig 6; 54pp; English.
PS
XX This enhancer element is part of a DNA construct used for treating human
XX carcinoma which contains a cancer therapeutic protein under the control
CC of a promoter and 3 enhancer sequences in a specific 5'-3' order. This
CC enhancer element is derived from the flanking region of the human
CC epithelial cell cytokeratin-8 gene. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX Sequence 24 BP; 3 A; 8 C; 6 G; 4 T; 0 U; 3 Other;
SQ
Query Match 2.0%; Score 19.4; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 716 CCCAGCCTCTGAGTAGTGGA 739
DB 1 CCTCAGCCTCTGAGTAGTGGA 24

```

```

XX
DE Enhancer element er-6 conserved basepair sequence.
XX
XX Enhancer element; carcinoma; tumor; cancer; SLP1 gene;
KW secretory leukoprotease-inhibitor gene; cytokeratin gene-8; ss.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH misc_difference 14 /*tag= a
FT /label= purine
FT misc_difference 16 /*tag= b
FT /label= pyrimidine
FT misc_difference 22 /*tag= c
FT /label= purine
XX
XX WO9421118-A1.
XX
XX 29-SEP-1994.
XX
XX 24-MAR-1994; 94WO-US003197.
XX
XX 24-MAR-1993; 93US-00035435.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Garver RI, Sorscher EJ;
XX
XX WPI; 1994-316537/39.
XX
XX DNA construct for treating human carcinoma - includes a cancer-
PT therapeutic gene under the control of a promoter and a gp. of enhancer
PT sequences.
XX
XX Claim 1; Fig 6; 54pp; English.
PS
XX This enhancer element is part of a DNA construct used for treating human
XX carcinoma which contains a cancer therapeutic protein under the control
CC of a promoter and 3 enhancer sequences in a specific 5'-3' order. This
CC enhancer element is derived from the flanking region of the human
CC epithelial cell secretory leukoprotease-inhibitor gene. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
XX Sequence 24 BP; 3 A; 8 C; 6 G; 4 T; 0 U; 3 Other;
SQ
Query Match 2.0%; Score 19.4; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 716 CCCAGCCTCTGAGTAGTGGA 739
DB 1 CCTCAGCCTCTGAGTAGTGGA 24

```

```

RESULT 622
AAT63214
ID AAT63214 standard; DNA; 20 BP.
XX
XX AAT63214;
AC
XX 17-JUN-1997 (first entry)
DT
XX
XX Primer Alu 5' used in Inter-Alu PCR for PAC isolation.
DE
XX S182 gene; familial Alzheimer's disease; diagnosis; transgenic animal;
KW polymerase chain reaction; PCR; primer; artificial chromosome; PAC; ss.
XX
XX Synthetic.
OS
XX
XX WO9703999-A1.

```

```
XX 06-FEB-1997.
PD
XX
PF 26-JUN-1996; 96WO-US011065.
XX
XX 18-JUL-1995; 95US-0001500P.
PR 02-AUG-1995; 95US-0001800P.
XX
PA (UNITW ) UNIV WASHINGTON SCHOOL MED.
XX (USF-) UNIV SOUTH FLORIDA.
XX
PI Goate AM, Hardy JA;
XX
DR WPI; 1997-132571/12.
XX
PT New mutante of the S182 gene associated with familial Alzheimer's disease
PT - and related protein and transgenic animals, useful as models for
PT screening and assessing potential drugs.
XX
XX Example 2; Page 11; 26pp; English.
XX
CC Inter-Alu PCR was performed on YACs 905C2 and 763B11. Unpurified YAC DNA
CC was amplified with generate primers Alu 5' (AAT63214) and Alu 3'
CC (AAT63215). Genetic linkage strategies have placed a gene causing early
CC onset Alzheimer's disease (AD) on the long arm of chromosome 14 between
CC D14S289 and D14S61. The gene, S182 (see also AAT63207), was localised to
CC a 100 kb region between D14S77 and D14S668E (see also AAT63216-22). A
CC number of novel mutations in the S182 gene have been identified in
CC families multiply affected by early onset AD
XX
SQ Sequence 20 BP; 5 A; 4 C; 6 G; 3 T; 0 U; 2 Other;
XX
Query Match 1.9%; Score 19.2; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 868 GGATTACAGCGCTGAGCCAC 887
DB 1 GGATTACAGGRTGAGCCAC 20
XX
RESULT 623
ID AAA35956
XX AAA35956 strand; DNA; 24 BP.
XX
AC AAA35956;
XX
XX 26-JUL-2000 (first entry)
XX
DE Human genomic SNP allele specific oligonucleotide SEQ ID NO:13.
XX
XX Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis;
XX allele specific oligonucleotide; ASO; reduced complexity genome; RCG;
XX genomic classification; identification; DNA fingerprinting; ss.
XX tumour characterisation; hybridisation; ss.
XX
OS Homo sapiens.
XX
XX WO200018960-A2.
XX
XX 06-APR-2000.
XX
XX 24-SEP-1999; 99WO-US022283.
XX
XX 25-SEP-1998; 98US-0101757P.
XX
XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
XX Landers JE, Jordan B, Houseman DE, Charest A;
XX
XX WPI; 2000-293181/25.
XX
PT Detection of single nucleotide polymorphisms in genomes by preparation
```

```
PT and analysis of reduced complexity genomes, useful for genotyping,
PT fingerprinting and determining allele frequency of SNPs.
XX
XX Disclosure; Page 53; 11pp; English.
XX
XX A method has been developed for detecting the presence or absence of a
XX single nucleotide polymorphism (SNP) allele in a genomic sample. The
XX method comprises preparing a reduced complexity genome (RCG) from the
XX genomic sample and analysing the RCG for the presence or absence of a SNP
XX allele. The method can be used to characterise a tumour, to generate a
XX genomic pattern for an individual genome or to generate a genomic
XX classification code for a genome. The method can be used to assess
XX whether a subject is at risk for developing a disease or to identify a
XX set of SNP alleles associated with a disease. The method can also be used
XX to perform linkage analysis. AAA35944 to AAA35947 represent sequences
XX used in the exemplification of the present invention. AAA35948 to
XX AAA36632 represent nucleotide sequences containing SNPs
XX
SQ Sequence 24 BP; 6 A; 8 C; 6 G; 4 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 870 ATTACAGCGCTGAGCCACCGCC 893
DB 1 ATTAAAGCGCTGCCCGCCACGATGCC 24
XX
RESULT 624
ID AAA27180/C
XX AAA27180 standard; DNA; 24 BP.
XX
AC AAA27180;
XX
XX 11-SEP-2000 (first entry)
XX
DE Forward primer P2 for target sequence human P2 gene.
XX
XX P2; CXSC chemokine; Chromosome 5q31; gene therapy; asthma; PCR primer;
XX allergic rhinitis; urticaria; anaphylactic shock; hives; hay fever; human;
XX ss.
XX
OS Homo sapiens.
XX
XX WO200029621-A2.
XX
XX 25-MAY-2000.
XX
XX 12-NOV-1999; 99WO-US026931.
XX
XX 16-NOV-1998; 98US-00193320.
XX
XX (GENE-) GENELABS TECHNOLOGIES INC.
XX
XX Dolganov G, Novikov A;
XX
XX WPI; 2000-387825/33.
XX
XX Measuring target polynucleotide sequences in biological samples by
XX contracting sequence-selective primer pairs, forming conjugates with
XX adaptor molecules, polymerizing target-identifier dimers and quantifying
XX them.
XX
XX Disclosure; Page 99; 103pp; English.
XX
XX A novel method for simultaneously determining the level of a number of
XX target polynucleotides in a sample has been disclosed. The method
XX involves forming double stranded copies of the target sequence in direct
XX proportion to the target levels in the original sample. The target
XX sequence is copied using primer pairs designed to flank a defined region
XX in the target sequence. The double stranded copies are then cleaved and
XX reacted with either first or second adaptor sequences. The first and
```

second conjugate mixtures are then allowed to form dimers with each other through the target sequences. The adaptor sequences are then removed to leave target sequence dimers. These dimers are then polymerised to form dimer multimers. The relative abundances of target identifiers in the multimer allow expression levels to be determined. This method is useful for developing polynucleotide abundance level profiles for cells and tissues under various conditions, stages of development and disease states, particularly where the target polynucleotide is present at low levels. The method may also be used in the discovery and evaluation of candidate therapeutic agents and their effective dosage levels. In addition to the method described above, the invention also includes the polynucleotide and polypeptide of P2. P2 is thought to be a member of a novel chemokine family, denoted CX5C and may be associated with immune function. Compositions of the P2 polypeptide may be useful in the treatment of asthma, allergic rhinitis (hay fever), urticaria (hives), anaphylactic shock and conditions involving immune system hypersensitivity. The P2 polynucleotide to treat conditions using gene therapy. The human P2 gene has been localised to chromosome 5, within the cytokine gene cluster at 5q31. The present sequence is the forward primer P2 for target sequence human P2 gene

Sequence 24 BP; 4 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 676 CACTGCACTCTGCTCCCGGT 699

DB 24 CACTGCACTCTGCTCCCGGT 1

RESULT 625
AAH45660/C
ID AAH45660 standard; DNA; 24 BP.

AC AAH45660;

DT 24-SEP-2001 (first entry)

XX PCR primer specific for human protease regulatory protein 9 cDNA.

XX Protease regulatory protein 9; malignant tumour; haemopathy; cytostatic;

KM HIV infection; immunological disease; inflammation; haemostatic;

KM viroicide; immunomodulatory; PCR primer; ss.

OS Homo sapiens.

PN WO200149731-A1.

PD 12-JUL-2001.

XX 25-DEC-2000; 2000WO-CN000652.

XX 29-DEC-1999; 99CN-00127227.

PA (YTFU-) UNIV FUDAN.

PA (SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD.

PI Mao Y, Yie Y;

DR WPI; 2001-441850/47.

PT Human protease regulatory protein 9 and encoded polynucleotide, used in

PT diagnosis and treatment of malignant tumours, hemopathy, human

PT immunodeficiency virus infection, immunological diseases and

PS inflammation.

XX Example 3; Page 17; 35pp; Chinese.

XX This invention relates to human protease regulatory protein 9, and the

CC cDNA encoding it. The invention includes a vector containing the cDNA, a

CC host cell transformed with the vector, and an antibody directed against

the protein. The protein and polynucleotide sequences can be used in the diagnosis and treatment of malignant tumours, haemopathy, human immunodeficiency virus (HIV) infection, immunological diseases, and various inflammatory conditions. Use of the protein or polynucleotide or their agonists/antagonists causes cytostatic, haemostatic, viroicide or immunomodulatory activity. The present sequence represents a PCR primer specific for cDNA encoding human protease regulatory protein 9

Sequence 24 BP; 5 A; 2 C; 12 G; 5 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 968 TCTCGGCTCAGTCACTCTGCC 991

DB 24 TCTCGGCTCAGTCACTCTGCC 1

RESULT 626
AAH46154/C
ID AAH46154 standard; DNA; 24 BP.

AC AAH46154;

DT 12-SEP-2001 (first entry)

XX Cysteine protease 10 RT-PCR primer, SEQ ID NO:3.

KM Cysteine protease 10; human; recombinant production; malignant tumour;

KM cancer; blood disease; HIV infection; human immunodeficiency virus;

KM immune disorder; inflammatory condition; cytostatic; anti-HIV;

KM antiinflammatory; immunomodulator; reverse transcription-PCR;

KM RT-PCR primer; ss.

OS Homo sapiens.

PN WO200146442-A1.

PD 28-JUN-2001.

XX 18-DEC-2000; 2000WO-CN000608.

XX 22-DEC-1999; 99CN-00125682.

PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

PI Mao Y, Xie Y;

DR WPI; 2001-418079/44.

PT Cysteine protease 10 and encoded polynucleotide, applicable in diagnosis

PT and treatment of malignant tumor, hemopathy, HIV infection, immunological

PT diseases and various inflammation.

PS Example 3; Page 12; 35pp; Chinese.

XX This sequence represents cDNA encoding cysteine protease 10. The protein

CC has a molecular weight of 10 kD, and has homology with a cysteine

CC protease given in AAB73748 over a 51 amino acid stretch. The invention

CC relates to cysteine protease 10 (AAB73746), nucleic acids encoding it

CC (AAH46153), and a method for the recombinant production of cysteine

CC protease 10. The present invention additionally discloses an agonist of

CC cysteine protease 10 for therapeutic use, and an antibody which

CC specifically binds to cysteine protease 10. Cysteine protease 10, and

CC nucleotides which encode it may be used for treating a variety of

CC diseases, such as malignant tumours, blood diseases, HIV (human

CC immunodeficiency virus) infection, immune disorders and inflammatory

CC conditions. The protein may also be used to screen for modulators of its

CC activity or for peptide fingerprinting identification. The polynucleotide

CC can be used as a primer for nucleic acid amplification reactions or as a

CC probe for hybridisation reactions, or in producing gene chips or

CC microarrays. Sequences AAH46154-AAH46155 represent reverse transcription-

CC PCR (RT-PCR) primers used in an exemplification of the invention to
CC isolate human cysteine protease 10 cDNA
XX
SQ Sequence 24 BP; 7 A; 5 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 536 TCCTGCTCAGCCTCCAGTAGC 559
DB 24 TCTTGTCTCAGCCTCCAGTAGC 1

RESULT 627

AAH75665
ID AAH75665 standard; DNA; 24 BP.

XX AAH75665;

DT 08-NOV-2001 (first entry)

XX Human Pax protein 9 PCR primer 2.

XX Human; Pax protein 9; cytosolic; virucide; immunomodulatory;
XX antiinflammatory; haemostatic; anti-HIV; paired box domain; neoplasm;
XX human immunodeficiency virus; HIV; infection; immunological disease;
XX developmental disorder; growth developmental disturbance;
XX Waardenburger's syndrome; gene therapy; PCR primer; ss.

OS Homo sapiens.

XX WO200165584-A1.

XX 13-SEP-2001.

XX 26-FEB-2001; 2001WO-CN000198.

XX 07-MAR-2000; 2000CN-0011895.

XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2001-565571/63.

PT New human Pax protein 9 for diagnosing and treating developmental
PT disorders, malignant neoplasm, hemopathy, human immunodeficiency virus
PT infection, immunological diseases and various inflammations.

XX Example 2; Page 11; 35pp; Chinese.

CC The invention relates to the human Pax protein 9 with cytosolic,
CC virucide, immunomodulatory, antiinflammatory, haemostatic and anti-HIV
CC activity. The polypeptide and encoded polynucleotide, with paired box
CC domain, are applicable in diagnosis and treatment of malignant neoplasm,
CC haemopathy, human immunodeficiency virus (HIV) infection, immunological
CC diseases, various inflammations, developmental disorders, growth
CC developmental disturbance and Waardenburger's syndrome. The
CC polynucleotide is useful for gene therapy. The present sequence is that
CC of a human Pax protein 9 PCR primer, useful to the invention
XX
SQ Sequence 24 BP; 3 A; 0 C; 5 G; 16 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 170 TTTTCTTCTAGTACGATGAGTT 193
DB 1 TTTTCTTCTTCTAGTACGAGTT 24

RESULT 628
AAF92846
ID AAF92846 standard; DNA; 24 BP.

XX AAF92846;

DT 17-MAY-2001 (first entry)

XX Human ABC1 transcription factor binding site #9.

XX High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.

OS Homo sapiens.

XX WO200115676-A2.

XX 08-MAR-2001.

XX 01-SEP-2000; 2000WO-IB001492.

XX 01-SEP-1999; 99US-0151977P.

XX 15-MAR-2000; 2000US-00526193.

XX 23-JUN-2000; 2000US-0213958P.

XX (UTBR-) UNIV BRITISH COLUMBIA.

XX (XENO-) XENON GENETICS INC.

XX Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;

XX WPI; 2001-244356/25.

XX Treating a lower than normal high density lipoprotein-cholesterol (HDL-C)

XX level, a higher than normal triglyceride level, or a cardiovascular

XX disease, by administering a compound that modulates LXR- or RXR-mediated

XX transcriptional activity.

XX Disclosure; Fig 3; 317pp; English.

XX The present invention relates to a method for treating a patient
XX diagnosed as having a lower than normal high density lipoprotein-
XX cholesterol (HDL-C) level, a higher than normal triglyceride level, or a
XX cardiovascular disease, involving administering a compound that modulates
XX LXR- or RXR-mediated transcriptional activity or ABC1 expression or
XX activity. The LXR gene product may be used in an assay to identify
XX compounds useful for the treatment of a disease or condition selected a
XX lower than normal HDL cholesterol level, a higher than normal
XX triglyceride level, and a cardiovascular disease

XX Sequence 24 BP; 4 A; 6 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 208 AGGCTGTTCTGAACTCCGACT 231
DB 1 AGGTTGTTTGAAGTCTGACT 24

RESULT 629

AAH48397
ID AAH48397 standard; DNA; 24 BP.

XX AAH48397;

DT 15-SEP-2001 (first entry)

XX Fumarase 9 PCR primer 1.

XX Fumarase 9; cytosolic; antiviral; immunomodulatory; antiinflammatory;
XX cardiac; cancer; haemopathy; human immunodeficiency virus; HIV;
XX infection; immunological disease; inflammatory disease; PCR primer; ss.

OS Unidentified.
XX
XX WO200148176-A1.
XX
XX 05-JUL-2001.
XX
XX 18-DEC-2000; 2000WO-CN000612.
XX
XX 24-DEC-1999; 99CN-00125763.
XX
XX (BIOW-) BIOWINDOW GENE DEV LTD SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2001-418271/44.
XX
XX Fumarase 9 polynucleotide and polypeptide, useful in diagnosis and
PT treatment of malignant neoplasm, hemopathy, HIV infection, immunological
PT diseases and various inflammatory diseases.
XX
XX Example 3; Page 11, 34pp; Chinese.
XX
XX The invention relates to an isolated polypeptide of Fumarase 9 comprising
CC the 80 amino acid sequence defined in the specification, or its fragment,
CC analogue or derivative. The polypeptide and the polynucleotide encoding
CC it are useful in the diagnosis and treatment of malignant neoplasms,
CC haemopathy, HIV infection, immunological diseases and various
CC inflammatory diseases. The present sequence is a primer used to isolate a
CC polynucleotide encoding the polypeptide of the invention
XX
XX Sequence 24 BP; 12 A; 7 C; 2 G; 3 T; 0 U; 0 Other;
XX
XX
XX Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 607 TTTTAAATTTTGGACAGAGTC 630
DB 24 TTTTGGTTTGGTGGAGCGAGTC 1
XX
XX RESULT 630
AAF27674
XX AAF27674 standard; DNA; 24 BP.
XX
XX AAF27674;
XX
XX 02-APR-2001 (first entry)
XX
XX Primer #7.
XX
XX IL-1; interleukin; inflammation; infection; ss.
XX
XX Unidentified.
XX
XX WO200100880-A2.
XX
XX 04-JAN-2001.
XX
XX 30-JUN-2000; 2000WO-US018318.
XX
XX 30-JUN-1999; 99US-00345217.
XX
XX (INTE-) INTERLEUKIN GENETICS INC.
XX
XX Duff GW, Cox A, Camp NJ, Di Giovine FS;
XX
XX WPI; 2001-102903/11.
XX
XX Determining whether a subject has or is predisposed to disease associated
PT with IL-1 polymorphism involves determining presence of marker or allele
PT comprising IL-1 inflammatory haplotype.
XX

PS Claim 5; Page 48; 84pp; English.
XX
XX The present invention relates to a new method for determining whether a
CC subject has or is predisposed to developing a disease or condition that
CC is associated with an IL (interleukin)-1 inflammatory haplotype,
CC comprising detecting at least one allele of the haplotype, where the
CC presence of the allele indicates that the subject is predisposed to the
CC development or has the disease or condition. The method is useful for
CC determining whether a subject has or is predisposed to inflammatory
CC disease, a degenerative disease, an immunological disorder, an infectious
CC disease, trauma induced disease, or cancer. The above conditions
CC associated with an IL-1 inflammatory haplotype can be treated or
CC prevented by administering a therapeutic that compensates for a causative
CC mutation that is in linkage disequilibrium with at least one IL-1
CC polymorphism
XX
XX
XX Sequence 24 BP; 5 A; 7 C; 10 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 868 GGATTACAGCGGTGACCCACACG 891
DB 1 GGGATTACAGCGGTGACCCACCGG 24
XX
XX RESULT 631
AAH40034/c
XX AAH40034 standard; DNA; 24 BP.
XX
XX AAH40034;
XX
XX 14-AUG-2001 (first entry)
XX
XX SNP specific lower PCR primer SEQ ID 2630.
XX
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternally analysis; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200129262-A2.
XX
XX 26-APR-2001.
XX
XX 13-OCT-2000; 2000WO-US028436.
XX
XX 15-OCT-1999; 99US-0160096P.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX Picoult-Newburg L, Pohl M;
XX
XX WPI; 2001-290930/30.
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
XX Claim 1; Page 64; 83pp; English.
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
XX
XX The oligonucleotides are useful for genotyping a nucleic acid sample by

CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Leisch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence

XX Sequence 24 BP; 6 A, 6 C, 5 G, 7 T, 0 U, 0 Other;

XX Query Match 1.9%; Score 19.2; DB 1; Length 24;

XX Best Local Similarity 87.5%; Pred. No. 1.4e+03;

XX Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 851 GGCTTCCCAAGTCTGGATTAC 874

DB 24 GGACTCTTAAGTCTGGAATTAC 1

RESULT 632

AAH37609

ID AAH37609 standard; DNA; 24 BP.

AC AAH37609;

XX 14-AUG-2001 (first entry)

XX SNP specific upper PCR primer. SEQ ID 405.

XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNRP; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
XX Leisch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; PCR primer; ss.

OS Homo sapiens.

XX WO200129262-A2.

XX 26-APR-2001.

XX 13-OCT-2000; 2000WO-US028436.

XX 15-OCT-1999; 99US-0160096P.

XX (ORCH-) ORCHID BIOSCIENCES INC.

XX Picoult-Newburg L, Pohl M;

XX WPI; 2001-290930/30.

XX New genotyping oligonucleotide, useful for detecting the presence,
XX PT absence or identity of single polynucleotide polymorphism in a nucleic
XX acid sample.

XX Claim 1; Page 52; 83pp; English.

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
XX primer extension (SNPE) primers, and the sequences of regions flanking
XX sites of single nucleotide polymorphisms SNPs. The present invention
XX includes kits for determining the presence or absence of a SNP, using the
XX oligonucleotides of the invention. The PCR primers are used to amplify a
XX SNP flanking sequence, the SNPE primer is used as a genotyping primer.

CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Leisch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence

XX Sequence 24 BP; 4 A, 8 C, 3 G, 9 T, 0 U, 0 Other;

XX Query Match 1.9%; Score 19.2; DB 1; Length 24;

XX Best Local Similarity 87.5%; Pred. No. 1.4e+03;

XX Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 670 TTGGCTACTGCAACTCTGCTC 693

DB 1 TTGGCTTACTGCAACTCTTACTC 24

RESULT 633

AAF81133/C

ID AAF81133 standard; DNA; 24 BP.

AC AAF81133;

XX 02-MAY-2001 (first entry)

XX PCR primer used to amplify PTGS2 exon 9 SEQ ID 239.

XX Human; prostaglandin-endoperoxide synthase 2; PTGS2; cyclooxygenase 2;
XX single nucleotide polymorphism; SNP; immune-related disorder; arthritis;
XX inflammation; PCR primer; ss.

OS Homo sapiens.

XX WO200107662-A1.

XX 01-FEB-2001.

XX 24-JUL-2000; 2000WO-US020114.

XX 22-JUL-1999; 99US-0145170P.

XX (GENA-) GENA1SSANCE PHARM INC.

XX Denton RR, Nandabalan K, Sanchis A, Stephens JC, Tanguay DA;

XX WPI; 2001-182805/18.

XX New nucleic acid containing polymorphisms in the cyclooxygenase-2 gene,
XX PT for gene therapy of inflammation and for establishing a genotype or
XX haplotype.

XX Example 1b; Page 39; 118pp; English.

XX This invention relates to a polynucleotide sequence that is a polymorphic
XX variant of the human prostaglandin-endoperoxide synthase 2 (PTGS2) gene
XX also referred to as cyclooxygenase 2. The human PTGS2 gene sequence
XX AAF80896 contains 27 single nucleotide polymorphisms (SNPs). AAF80896 and
XX AAF80897 represent human PTGS2 gene and coding sequence, and the PTGS2
XX protein is represented by AAF82199. The invention includes PCR and
XX sequencing primers, and probes represented in AAF80898 - AAF81151 which
XX are used to isolated and characterise the PTGS2 gene sequence, and to

CC locate the positions of the SNPs. PTGS2 proteins and polynucleotide
CC sequences are used to express variant PTGS2 proteins, for structural
CC analysis or drug-binding studies and also in gene therapy (either
CC expressing PTGS2 or inhibitory RNA). Antibodies raised against PTGS2 are
CC useful for diagnosis, prognosis and therapy and analysis of the new, and
CC known, polymorphisms and used to determine between a particular trait, e.g. a
CC especially for determining association between PTGS2 haplotype and genotype.
CC clinical response to drugs that target PTGS2 but also disease
CC susceptibility, severity or stage. Anti-PTGS2 antibodies are particularly
CC used for developing diagnostic tests and treatments for immune-related
CC disorders such as arthritis and inflammation. The polymorphisms may also
CC be used to study expression and biological function of PTGS2. Transgenic
CC animals that express PTGS2 are used to study expression of PTGS2
CC isogenes, for in vivo drug screening and testing, and for assessing
CC effects of therapeutic agents

XX Sequence 24 BP; 7 A; 4 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 710 CTCTGCCCCAGCTCTGTAGTAG 733
DB 24 CTCTGCTCTCACTCTCTGAGTAG 1

RESULT 634
AA164727/C
ID AA164727 standard; DNA; 24 BP.

AC AA164727;
XX 07-DEC-2001 (first entry)

DE Human line 1-12 PCR primer 1.

XX Human; line 1-12; cytostatic; virucidal; immunomodulatory;
KM antiinflammatory; haemostatic; malignant tumour; HIV; infection;
KW human immunodeficiency virus; immunological disease; PCR primer; ss.

XX Homo sapiens.

XX WO200173068-A1.

XX 04-OCT-2001.

XX 26-MAR-2001; 2001WO-CN000495.

XX 27-MAR-2000; 2000CN-00115143.

XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX Mao Y, Xie Y;

XX WPI; 2001-597126/67.

PT Line 1-12 and encoded polynucleotide, used in diagnosis and treatment of
PT malignant tumors, hemopathy, human immunodeficiency virus infection,
PT immunological diseases and inflammation.

XX Example 3; Page 16; 33pp; Chinese.

XX The invention relates to human line 1-12 with cytostatic, virucidal,
CC immunomodulatory, antiinflammatory and haemostatic activity. The protein
CC and encoding polynucleotide are used in diagnosis and treatment of
CC malignant tumour, haemopathy, human immunodeficiency virus (HIV)
CC infection, immunological diseases and various inflammations. The present
CC sequence is that of a human line 1-12 PCR primer, useful to the invention

XX Sequence 24 BP; 5 A; 4 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;

Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 976 CACTGCAACTCTGCTCTCCGGGC 999
DB 24 CACTGCAACTCTGCTCTCTGAGAC 1

RESULT 635

AB083629
ID AB083629 standard; DNA; 24 BP.

XX AB083629;

XX 26-JAN-2003 (first entry)

XX Human mPer3-10.01 PCR primer 1 SEQ ID NO:3.

XX Human; mPer3-10.01; vegetative nervous dysfunction; psychic disease;
KW endocrinopathy; growth development disturbance disease; tumour;
KW PCR primer; ss.

XX Homo sapiens.

XX CN1345805-A.

XX 24-APR-2002.

XX 26-SEP-2000; 2000CN-00125425.

XX 26-SEP-2000; 2000CN-00125425.

XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX Mao Y, Xie Y;

XX WPI; 2002-539321/58.

XX Novel polypeptide-human mPer 3-10.01 and polynucleotide for encoding the
PT polypeptide.

XX Example 2; Page 17 (Disclosure); 33pp; Chinese.

XX The present invention describes human mPer3-10.01 (1). Also described is
CC a method for producing (1) using DNA recombination technology. (1) can be
CC used in the treatment of several diseases, such as vegetative nervous
CC dysfunction, psychic disease, endocrinopathy, growth development
CC disturbance disease and tumours. The present sequence represents a PCR
CC primer for (1), which is used in an example from the present invention

XX Sequence 24 BP; 4 A; 8 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 930 TCTCACTCTGTACCCAGCTGGA 953
DB 1 TCTCACTCTGTCCCAAGCTGGA 24

RESULT 636

ABV76754
ID ABV76754 standard; DNA; 24 BP.

XX ABV76754;

XX 28-MAR-2003 (first entry)

XX Human sailor transposase 9.35 RT-PCR primer, SEQ ID NO:3.

XX Human; sailor transposase 9.35; recombinant production; gene therapy;
KW cancer; tumour; HIV infection; human immunodeficiency virus; cytostatic;

KM reverse transcription-PCR; RT-PCR; primer; ss.
XX Homo sapiens.
XX CN1360027-A.
XX PD 24-JUL-2002.
XX PF 20-DEC-2000; 2000CN-00135114.
XX PR 20-DEC-2000; 2000CN-00135114.
XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX Mao Y, Xie Y;
XX WPI; 2002-733652/80.
XX DR WPI; 2002-733652/80.
XX PT Polypeptide-human sailor transposase 9.35 and polynucleotide for coding
XX it.
XX PS Example 2; Page 17 (Disclosure); 32pp; Chinese.
XX CC The invention relates to human sailor transposase 9.35 (ABP58531) and
XX CC nucleic acids encoding it (ABV76753). The protein has a molecular weight
XX CC of 9.35 kD. The invention also relates to a method for the recombinant
XX CC production of the protein, an antagonist of the protein, and the use of
XX CC the protein, gene and antagonist in therapeutic applications. Sailor
XX CC transposase 9.35 can be used in the treatment of a variety of diseases
XX CC such as cancer and HIV (human immunodeficiency virus) infection.
XX CC Sequences ABV76754-ABV76755 represent reverse transcription-PCR (RT-PCR)
XX CC primers used in an exemplification of the invention to isolate human
XX CC sailor transposase 9.35 cDNA
XX SQ Sequence 24 BP; 6 A; 9 C; 6 G; 3 T; 0 U; 0 Other;
SQ Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 868 GGATTACAGCGCTGAGCCACCG 891
DB 1 GGATTACAGCGCTGAGCCACCG 24
RESULT 637
AB084159
ID AB084159 standard; DNA; 24 BP.
XX AC AB084159;
XX DT 19-FEB-2003 (first entry)
XX DE Human transcription regulatory factor 16.06 PCR primer SEQ ID NO:4.
XX KW Human; transcription regulatory factor 16.06; tumour; PCR primer; ss;
XX KW embryonic development malformation; protein metabolic disorder disease.
XX OS Homo sapiens.
XX PN CN1352077-A.
XX PD 05-JUN-2002.
XX PF 02-NOV-2000; 2000CN-00127179.
XX PR 02-NOV-2000; 2000CN-00127179.
XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX PI Mao Y, Xie Y;
XX DR WPI; 2002-637132/69.

XX New polypeptide-human transcription regulatory factor 16.06 and
XX PT polynucleotide for encoding the polypeptide, embryonic development
XX PT malformation, tumour, and protein metabolic disorder disease.
XX PS Example 2; Page 18 (Disclosure); 34pp; Chinese.
XX CC The present invention describes human transcription regulatory factor
XX CC 16.06 (I). Also described is a DNA recombination process used to produce
XX CC (I). (I) can be used for treating various diseases, such as embryonic
XX CC development malformation, tumours and protein metabolic disorder disease.
XX CC The present sequence represents a PCR primer for (I), which is used in an
XX CC example from the present invention
XX SQ Sequence 24 BP; 4 A; 8 C; 6 G; 6 T; 0 U; 0 Other;
SQ Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 924 ATGGATCTCACTCTGTACCCAG 947
DB 1 ATGGATCTCACTCTGTACCCAG 24
RESULT 638
ABV72841
ID ABV72841 standard; DNA; 24 BP.
XX AC ABV72841;
XX DT 30-DEC-2002 (first entry)
XX DE Human alpha 2,3-sialyltransferase 9.90 PCR primer 1.
XX KW Human; alpha 2,3-sialyltransferase 9.90; immunological defect; tumour;
XX KW inflammation; PCR; primer; ss.
XX OS Homo sapiens.
XX PN CN1352272-A.
XX PD 05-JUN-2002.
XX PF 10-NOV-2000; 2000CN-00127416.
XX PR 10-NOV-2000; 2000CN-00127416.
XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX PI Mao Y, Xie Y;
XX WPI; 2002-628720/68.
XX DR WPI; 2002-628720/68.
XX PT New polypeptide-human alpha 2,3-sialyltransferase 9.90 for treating
XX PT immunological defect, various tumours and various inflammations.
XX PS Example 2; Page 19 (Disclosure); 33pp; Chinese.
XX CC The invention relates to the novel human alpha 2,3-sialyltransferase
XX CC 9.90, and the polynucleotide encoding it. The polypeptide is useful for
XX CC treating various diseases, such as an immunological defect, various
XX CC tumours and various inflammations. The invention also discloses the
XX CC antagonist resisting the polypeptide and its treatment effect. The
XX CC present sequence represents a PCR primer used to amplify the human
XX CC alpha 2,3-sialyltransferase 9.90 gene of the invention
XX SQ Sequence 24 BP; 4 A; 7 C; 5 G; 8 T; 0 U; 0 Other;
SQ Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 636 GGGTTCAGTATTTCTCTGCCCC 719
 DB 1 GAGTTCAGTATTTCTCTGCCCTC 24

RESULT 639

ABZ20663
 ID ABZ20663 standard; DNA; 24 BP.

AC ABZ20663;

DT 03-MAR-2003 (first entry)

DE Human G protein subunit 9-02 coding sequence PCR primer #2.

XX Human; G protein subunit 9.02; cancer; constipation; diarrhoea; cough;

KM cardiac asthma; colic; psychic disease; PCR; primer;

KW morphine analgesic acute poisoning; ss.

XX Homo sapiens.

XX CN1345751-A.

XX 24-APR-2002.

XX 26-SEP-2000; 2000CN-00125456.

XX 26-SEP-2000; 2000CN-00125456.

XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX Mao Y, Xie Y;

XX WPI; 2002-675773/73.

XX Novel polypeptide-human G protein subunit 9.01.

XX Example 2; Page 19 (Disclosure); 34pp; Chinese.

CC The present invention provides the protein and coding sequences of human
 CC G protein subunit 9.02. The sequences can be used in the treatment of
 CC cancers, coughs, cardiac asthma, diarrhoea, constipation, colic, psychic
 CC disease and morphine analgesic acute poisoning. The present sequence is
 CC a PCR primer used to isolate the coding sequence of the invention

XX Sequence 24 BP; 4 A; 8 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;

Best Local Similarity 87.5%; Pred. No. 1.4e+03;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 924 ATGGAATTCACCTCTGTTACCCG 947
 DB 1 ACGGAGTCTCCTCTGTTGCCAG 24

RESULT 640

ABX14631/C
 ID ABX14631 standard; DNA; 24 BP.

AC ABX14631;

DT 04-MAR-2003 (first entry)

DE Guanosine triphosphatase activator protein 10.12 RT-PCR primer #1.

XX ss; guanosine triphosphatase activator protein 10.12; PCR; primer;

KM malignant tumour; inflammation; immunological disease; haemopathy;

KW human immunodeficiency virus infection; HIV; RT-PCR;

XX reverse transcriptase PCR.

XX Unidentified.

PN CN1352022-A.

XX 05-JUN-2002.

XX 10-NOV-2000; 2000CN-00127330.

XX 10-NOV-2000; 2000CN-00127330.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2002-714410/78.

XX New polypeptide-guanosine triphosphatase activator protein 10.12 and

XX polynucleotide for encoding such polypeptide.

XX Example 2; Page 17 (disclosure); 33pp; Chinese.

XX The present invention discloses a new kind of polypeptide, guanosine

XX triphosphatase activator protein 10.12, polynucleotides encoding this

XX polypeptide and DNA recombination process to produce the polypeptide. The

XX present invention also discloses applying the polypeptide in treating

XX various diseases, such as malignant tumours, inflammations, immunological

XX diseases, haemopathy and human immunodeficiency virus (HIV) infection.

XX The present invention also discloses the antagonist resisting the

XX polypeptide and its treatment effect. The present invention also

XX discloses the application of the polynucleotides for encoding guanosine

XX triphosphatase activator protein 10.12. The present sequence is a reverse

XX transcribed (RT)-PCR primer used to isolate nucleic acids encoding

XX guanosine triphosphatase activator protein 10.12

XX Sequence 24 BP; 5 A; 5 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;

Best Local Similarity 87.5%; Pred. No. 1.4e+03;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 203 TGGTCAGGCTGCTCTGCACTCCG 226
 DB 24 TGCCCGAGCTGCTCTGCACTCCG 1

DE Ras GTP enzyme-activating protein 20.68 RT-PCR primer, SEQ ID NO:3.

XX Ras GTP enzyme-activating protein 20.68; cancer suppressor protein-20.68;

XX recombinant production; gene therapy; cancer; tumour; HIV infection;

KM human immunodeficiency virus; cytostatic; reverse transcription-PCR;

XX RT-PCR; primer; ss.

XX Unidentified.

XX CN1363596-A.

XX 14-AUG-2002.

XX 05-JAN-2001; 2001CN-00105082.

XX 05-JAN-2001; 2001CN-00105082.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2002-742044/81.

XX Polypeptide-cancer suppressor protein-20.68 and polynucleotide for coding
PT it.
XX
PS Example 2; Page 17 (Disclosure); 33pp; Chinese.
XX
CC The invention relates to Ras GTP enzyme-activating protein 20.68
CC (AB59833) and nucleic acids encoding it (ABV76760). The protein has a
CC molecular weight of 20.68 kD and is also referred to as cancer suppressor
CC protein-20.68. The invention also relates to a method for the recombinant
CC production of the protein, an antagonist of the protein, and the use of
CC the protein, gene and antagonist in therapeutic applications. Ras GTP
CC enzyme-activating protein 20.68 can be used in the treatment of a variety
CC of diseases such as cancer and HIV (human immunodeficiency virus)
CC infection. Sequences ABV76761-ABV76763 represent reverse transcription-
CC PCR (RT-PCR) primers used in an exemplification of the invention to
CC isolate Ras GTP enzyme-activating protein 20.68 cDNA
SQ
Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1004 GCGATTCTCTGCTCTCAGCCTCC 1027
DB 24 GTGATTCTCTCTCTCAGCCTCC 1
RESULT 642
ABV99633
ID ABV99633 standard; DNA; 24 BP.
XX
AC ABV99633;
XX
DT 03-FEB-2003 (first entry)
XX
DE Human natriuretic peptide receptor 11.66 PCR primer SEQ ID NO 4.
XX
KM Human; natriuretic peptide receptor 11.66; receptor; tumour; haemopathy;
KM HIV; human immunodeficiency virus; infection; immunological disease;
KM inflammation; PCR; primer; ss.
OS Homo sapiens.
XX
PN CN1352083-A.
XX
PD 05-JUN-2002.
XX
PF 02-NOV-2000; 2000CN-00127189.
XX
PR 02-NOV-2000; 2000CN-00127189.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-644453/70.
XX
PT New polypeptide-human natriuretic peptide 11.66 and polynucleotide for
PT encoding the polypeptide, useful for treating malignant tumors,
PT hemopathy, HIV infection, immunological diseases and various
PT inflammations.
XX
PS Example 2; Page 16 (Disclosure); 31pp; Chinese.
XX
CC The invention relates to human natriuretic peptide receptor 11.66. The
CC polypeptide is useful for treating various diseases, such as malignant
CC tumours, haemopathy, HIV infection, immunological diseases and various
CC inflammations. The present sequence is that of a human natriuretic
CC peptide receptor 11.66 PCR primer useful in examples of the invention
SQ Sequence 24 BP; 3 A; 7 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 924 ATGGAATCTCACTGTGTACCCAG 947
DB 1 ATGGAATCTCACTGTGTACCCAG 24
RESULT 643
AAS20139
ID AAS20139 standard; DNA; 24 BP.
XX
AC AAS20139;
XX
DT 09-APR-2002 (first entry)
XX
DE Human phytochrome 12 RT-PCR primer #1.
XX
KM Human; ss; phytochrome 12; malignant tumour; haemopathy;
KM human immunodeficiency virus infection; HIV; immunological disease;
KM inflammation; RT-PCR; primer.
OS Homo sapiens.
XX
PN WO200192316-A1.
XX
PD 06-DEC-2001.
XX
PF 21-MAY-2001; 2001WO-CN000834.
XX
PR 24-MAY-2000; 2000CN-00115823.
XX
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-083184/11.
XX
KM phytochrome 12 and encoding polynucleotide, used in diagnosis and
KM treatment of malignant tumors, hemopathy, human immunodeficiency virus
KM infection, immunological diseases and inflammation.
OS Homo sapiens.
XX
PN CN1352083-A.
XX
PD 05-JUN-2002.
XX
PF 02-NOV-2000; 2000CN-00127189.
XX
PR 02-NOV-2000; 2000CN-00127189.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-644453/70.
XX
PT New polypeptide-human natriuretic peptide 11.66 and polynucleotide for
PT encoding the polypeptide, useful for treating malignant tumors,
PT hemopathy, HIV infection, immunological diseases and various
PT inflammations.
XX
PS Example 2; Page 17; 36pp; Chinese.
XX
CC The invention relates to an isolated polypeptide of phytochrome 12, the
CC cDNA encoding it, and its fragment, analogue or derivative. Also included
CC are vectors expressing protein, a host cell comprising the vector, the
CC isolation of modulators of the protein and an anti-phytochrome 12
CC antibody. The protein and nucleic acid are used in diagnosis and
CC treatment of a malignant tumour, haemopathy, human immunodeficiency virus
CC (HIV) infection, immunological diseases and various inflammations. The
CC present sequence is an RT-PCR (reverse transcriptase PCR) primer used to
CC isolate the cDNA encoding the phytochrome 12
SQ Sequence 24 BP; 4 A; 8 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1001 CAAGGATTCCTGCTCTCAGCCT 1024
DB 1 CAAGGATTCCTGCTCTCAGCCT 24
RESULT 644
ABI99962
ID ABI99962 standard; DNA; 24 BP.
XX
AC ABI99962;
XX

DT 31-MAY-2002 (first entry)
 XX Human phosphatidic acid phosphatase 2-12 RT-PCR primer, SEQ ID NO:4.
 DE
 XX
 XX Human; phosphatidic acid phosphatase 2-12; recombinant production;
 KM cancer; HIV infection; human immunodeficiency virus; gene therapy;
 KM cytosolic; anti-HIV; reverse transcription-PCR; RT-PCR; primer; ss.
 XX Homo sapiens.
 OS
 XX CN1325990-A.
 PN
 XX
 XX 12-DEC-2001.
 PD
 XX
 XX 31-MAY-2000; 2000CN-00116248.
 PF
 XX
 XX 31-MAY-2000; 2000CN-00116248.
 PR
 XX
 XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 PA
 XX
 XX Mao Y, Xie Y;
 PI
 XX WPI, 2002-196710/26.
 DR
 XX
 XX New polypeptide-human phosphatidic acid phosphatase 2-12 for treating
 PT diseases such as cancer and human immunodeficiency virus infection.
 PS
 XX Example 2; Page 17 (disclosure); 34pp; Chinese.
 XX
 XX The invention relates to human phosphatidic acid phosphatase 2-12
 CC (AAM49149) and to nucleic acids encoding it (AB199960). The protein has a
 CC molecular weight of 12 kb. The invention also relates to a method for the
 CC recombinant production of the protein, an antagonist of the protein, and
 CC the use of the protein, gene and antagonist in therapeutic applications.
 CC Phosphatidic acid phosphatase 2-12 can be used in the treatment of a
 CC variety of diseases such as cancer and HIV (human immunodeficiency virus)
 CC infection. Sequences AB199961-AB199962 represent reverse transcription-
 CC PCR (RT-PCR) primers used in an exemplification of the invention to
 CC isolate human phosphatidic acid phosphatase 2-12 cDNA
 XX
 XX Sequence 24 BP; 6 A; 3 C; 6 G; 9 T; 0 U; 0 Other;
 SQ
 Query Match 1.9%; Score 19.2; DB 1; Length 24;
 Best Local Similarity 87.5%; Pred. No. 1.4e+03;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 310 TTTGTGTTAGAAACAGGCTTTCAC 333
 DB 1 TTTTGTAGTAGACACAGGCTTTCAC 24
 RESULT 645
 AAI72742
 ID AAI72742 standard; DNA; 24 BP.
 XX
 XX AAI72742;
 AC
 XX
 XX 03-JUL-2002 (first entry)
 DT
 XX
 XX Human cytokine receptor 15 PCR primer #1.
 DE
 XX
 XX Gene; human cytokine receptor 15; malignant tumour; haemopathy;
 KM human immunodeficiency virus; HIV; inflammation; gene therapy; PCR;
 KM primer; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200183536-A1.
 PN
 XX
 XX 08-NOV-2001.
 PD
 XX
 XX 23-APR-2001; 2001WO-CN000577.
 PF
 XX

PR 27-APR-2000; 2000CN-00115491.
 XX
 XX (BIOV-) BIOWINDOW GENE DEV INC SHANGHAI.
 PA
 XX
 XX Mao Y, Xie Y;
 PI
 XX
 XX WPI, 2002-026253/03.
 DR
 XX
 XX Cytokine receptor 15 and encoded polynucleotide, applicable in diagnosis
 PT and treatment of developmental disorders, cancer, hemopathy, HIV
 PT infection, immunological diseases and various inflammations.
 XX
 XX Example 3; Page 12; 38pp; Chinese.
 PS
 XX
 XX The present invention relates to human cytokine receptor 15 (see
 CC AAB47984). Human cytokine receptor 15, and the DNA encoding it, are used
 CC in diagnosis and treatment of malignant tumour, haemopathy, human
 CC immunodeficiency virus (HIV) infection, immunological diseases and
 CC various inflammations. This sequence is a PCR primer which was used in an
 CC example from the invention
 XX
 XX Sequence 24 BP; 7 A; 2 C; 7 G; 8 T; 0 U; 0 Other;
 SQ
 Query Match 1.9%; Score 19.2; DB 1; Length 24;
 Best Local Similarity 87.5%; Pred. No. 1.4e+03;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 179 AGTAGATGATGAGTTTCATGT 202
 DB 1 AGTAGATGATGAGTTTCATGT 24
 RESULT 646
 AAL43822
 ID AAL43822 standard; DNA; 24 BP.
 XX
 XX AAL43822;
 AC
 XX
 XX 19-SEP-2002 (first entry)
 DT
 XX
 XX Human oncogene protein 11-66 PCR primer 1.
 DE
 XX
 XX Human; ss; gene therapy; oncogene protein 11.66; malignant tumour;
 KM haemopathy; development disturbance; HIV; immunological disease;
 KM inflammation; PCR; primer.
 XX
 XX Homo sapiens.
 OS
 XX CN1333235-A.
 PN
 XX
 XX 30-JAN-2002.
 PD
 XX
 XX 07-JUL-2000; 2000CN-00119427.
 PF
 XX
 XX 07-JUL-2000; 2000CN-00119427.
 PR
 XX
 XX (SHAN-) SHANGHAI BIODOR GENE DEV CO LTD.
 PA
 XX
 XX Mao Y, Xie Y;
 PI
 XX
 XX WPI, 2002-305565/35.
 DR
 XX
 XX Novel polypeptide-oncoprotein 11.66 and polynucleotide for encoding said
 PT polypeptide.
 PT
 XX
 XX Example 2; Page 18 (disclosure); 33pp; Chinese.
 PS
 XX
 XX The invention comprises the amino acid and coding sequence of the human
 CC oncogene protein 11.66. The oncogene protein 11.66 DNA and protein
 CC sequences are useful for treating malignant tumour, haemopathy,
 CC development disturbance, HIV infection, immunological disease and various
 CC inflammations. The present DNA sequence represents a human oncogene
 CC protein 11.66 PCR primer

```
XX SQ Sequence 24 BP; 4 A; 4 C; 8 G; 8 T; 0 U; 0 Other;
Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 181 TAGAGATGAGATTCTCCATGTTG 204
      |||||
DB 1 TCGAGATGAGATTCTCCATGTTG 24

RESULT 647
ABSS5854
ID ABSS5854 standard; DNA; 24 BP.
XX AC ABSS5854;
XX DT 23-DEC-2002 (first entry)
XX DE Human SOX3 protein 13.31 cDNA RT-PCR primer #1.
XX KM Human; SOX3 protein 13.31; primer; ss; malignant tumour; haemopathy;
XX KW HIV infection; human immunodeficiency virus; immunological disease;
XX KM inflammation; RT-PCR; reverse transcriptase.
XX OS Homo sapiens.
XX PN CN1352146-A.
XX PD 05-JUN-2002.
XX PF 10-NOV-2000; 2000CN-00127333.
XX PR 10-NOV-2000; 2000CN-00127333.
XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX PI Mao Y, Xie Y;
XX DR WPI; 2002-708125/77.
XX PT New polypeptide-human SOX3 protein 13.31.
XX PS Example 2; Page 16 (Disclosure); 32pp; Chinese.
XX CC The invention relates to the human SOX3 protein 13.31 and the
XX CC polynucleotide encoding it. The polypeptide is used in treating various
XX CC diseases, such as malignant tumours, haemopathy, HIV infection,
XX CC immunological diseases and various inflammations. This sequence
XX CC represents a reverse transcriptase PCR (RT-PCR) primer used in isolation
XX CC of cDNA encoding the human SOX3 protein 13.31
XX SQ Sequence 24 BP; 8 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 868 GGATTACAGCGCTGAGCCACACG 891
      |||||
DB 1 GGATTACAGCATGAGCCACCATG 24

RESULT 648
ABL40967
ID ABL40967 standard; DNA; 24 BP.
XX AC ABL40967;
XX DT 03-JUL-2002 (first entry)
XX DE Polypeptide-hexokinase protein cDNA isolating primer 2.
```

```
XX KM Polypeptide-hexokinase protein; cytosolic; haemostatic; virucide;
XX KW immunomodulatory; antiinflammatory; RT-PCR; primer; ss.
XX OS Synthetic.
XX PN WO200220795-A1.
XX PD 14-MAR-2002.
XX PF 02-JUL-2001; 2001WO-CN001115.
XX PR 07-JUL-2000; 2000CN-00117013.
XX PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX PI Mao Y, Xie Y;
XX DR WPI; 2002-258030/30.
XX DE Polypeptide-hexokinase protein and encoding polynucleotide, used in
XX PT diagnosis and treatment of malignant tumors, hemopathy, human
XX PT immunodeficiency virus infection, immunological diseases and
XX PT inflammation.
XX PS Example 2; Page 11; 35pp; Chinese.
XX CC The invention relates to a novel polypeptide-hexokinase protein. The
XX CC protein can be expressed by standard recombinant methodology. The novel
XX CC polypeptide and encoding polynucleotides are used in diagnosis and
XX CC treatment of malignant tumour; haemopathy, human immunodeficiency virus
XX CC (HIV) infection, immunological diseases and various inflammations. The
XX CC present sequence represents the polypeptide-hexokinase protein cDNA
XX CC isolating RT-PCR primer
XX SQ Sequence 24 BP; 3 A; 2 C; 9 G; 10 T; 0 U; 0 Other;
Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 174 TTTTATGATGAGATGGAGTTTCTC 197
      |||||
DB 1 TTTTATGATGAGATGGAGTTTCTC 24

RESULT 649
ABS57191
ID ABS57191 standard; DNA; 24 BP.
XX AC ABS57191;
XX DT 30-JAN-2003 (first entry)
XX DE Amylase 9.35 specific RT-PCR primer, #2.
XX KM Amylase 9.35; RT-PCR; ss; tumour; haemopathy; antagonist; HIV;
XX KW human immunodeficiency virus; immunological disease; inflammation;
XX KM reverse transcription; primer.
XX OS Unidentified.
XX PN CN1345971-A.
XX PD 24-APR-2002.
XX PF 29-SEP-2000; 2000CN-00125588.
XX PR 29-SEP-2000; 2000CN-00125588.
XX PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX PI Mao Y, Xie Y;
```


XX WPI; 2002-539369/58.
DR
XX New polypeptide-amylose 9.35 for treating malignant tumor, hemopathy,
PT human immunodeficiency virus infection, immunological disease and various
PT inflammations.
XX
XX Example 2; Page 15 (disclosure); 31pp; Chinese.
XX
XX The present invention discloses a novel amylose 9.35, polynucleotide
CC coding for the polypeptide and method for producing this polypeptide by
CC using DNA recombination technology. The invention also discloses the
CC method for curing several diseases, such as malignant tumor, haemopathy,
CC human immunodeficiency virus (HIV) infection, immunological diseases and
CC various inflammations by using the polypeptide. The invention also
CC discloses an antagonist for resisting said polypeptide and its
CC therapeutic action and also discloses the application of the
CC polynucleotide for coding this novel amylose 9.35. The sequence presented
CC is the reverse transcription (RT)-PCR primer, #2, which was used to
CC isolate amylose 9.35 cDNA
XX
SQ Sequence 24 BP; 4 A; 8 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 924 ATGGATCTCATCTCTTACCCAG 947
DB 1 ATGGAGTCTCATCTCTGTGACCCG 24
RESULT 650
AB081233/C
ID AB081233 standard; DNA; 24 BP.
XX
XX AB081233;
AC
XX
DT 05-DEC-2002 (first entry)
XX
DE Human 14273 probe.
XX
XX Human; 14273; metabolic disorder; obesity; diabetes; anorexia; cachexia;
KM anorectic; antidiabetic; anabolic; transgenic animal; gene therapy;
KM probe; ss.
XX
XX Homo sapiens.
OS
XX
PN WO200267868-A2.
XX
PD 06-SEP-2002.
XX
XX 26-FEB-2002; 2002WO-US006131.
PF
XX 26-FEB-2001; 2001US-0271655P.
PR
XX (MILL-) MILENNIUM PHARM INC.
PA
XX Gimeno R, Tsai F;
PI
XX WPI; 2002-698629/75.
DR
XX Identifying a nucleic acid associated with a metabolic disorder, useful
PT for diagnosing metabolic disorders, e.g. obesity, comprises contacting
PT the sample with a probe comprising at least 25 contiguous nucleotides of
PT the 14273 gene.
XX
XX Example 1; Page 61; 95pp; English.
PS
XX The present sequence is a probe, created by PCR, for human 14273 (see
CC AB081226), a nucleic acid associated with metabolic disorders. The probe
CC was used to examine the expression profile of human 14273 in different
CC tissues. It was found that 14273 molecules are expressed at high levels.

CC in adipose tissue, e.g. white adipose tissue and brown adipose tissue, as
CC well as in pancreatic islets. They are upregulated during exposure to
CC cold (i.e. under conditions that affect brown or white adipocyte
CC metabolism) and downregulated in genetic models of obesity. The present
CC invention provides 14273 nucleic acids, polypeptides and antibodies
CC useful for the diagnosis and treatment of metabolic disorders including
CC obesity, anorexia, cachexia and diabetes. Also provided are methods for
CC identifying a subject having a metabolic disorder, for identifying a
CC compound capable of modulating metabolic activity, methods for modulating
CC metabolic activity or adipocyte activity (hyperplastic growth,
CC hypertrophic growth or lipogenesis), methods for modulating lipogenesis
CC or lipolysis in a subject, and a method for regulating endogenous glucose
CC levels
XX
SQ Sequence 24 BP; 5 A; 6 C; 8 G; 5 T; 0 U; 0 Other;
Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 956 GCATGCGCAATCTCGCTCACT 979
DB 24 GCATGCGCAGATCTCGCTCACT 1
RESULT 651
ABK50651/C
ID ABK50651 standard; DNA; 24 BP.
XX
XX ABK50651;
AC
XX
DT 30-JUL-2002 (first entry)
XX
DE Human Parkinson's syndrome associated protein 11.11, RT-PCR primer #1.
XX
XX Human; Parkinson's syndrome associated protein 11.11; cancer;
KM human immunodeficiency virus; HIV infection; reverse transcriptase-PCR;
KM RT-PCR; primer; ss.
XX
XX Homo sapiens.
OS
XX
PN CN1331232-A.
XX
PD 16-JAN-2002.
XX
XX 30-JUN-2000; 2000CN-00116961.
PF
XX 30-JUN-2000; 2000CN-00116961.
PR
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
XX MAO Y, XIE Y;
PI
XX WPI; 2002-292874/34.
DR
XX New polypeptide-human Parkinsons syndrome associated protein 11.11 for
PT treating diseases such as cancer and human immunodeficiency virus
PT infection.
XX
XX Example 2; Page 17 (disclosure); 34pp; Chinese.
PS
XX The present invention relates to the isolation of human Parkinson's
CC syndrome associated protein 11.11, and the polynucleotide encoding it.
CC Also described is a process for preparing the polypeptide by DNA
CC recombination and the application of the polypeptide and polynucleotide
CC in treating various diseases such as cancer and human immunodeficiency
CC virus (HIV) infection. Antagonist against the polypeptide can also be
CC used in treating such diseases. The present sequence for reverse
CC transcriptase (RT)-PCR primer #1 is used with RT-PCR primer #2 (ABK50652)
CC for isolating cDNA encoding human Parkinson's syndrome associated protein
CC 11.11
XX
SQ Sequence 24 BP; 8 A; 6 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 925 TGGATCTCACTCTGTACCCAGG 948
DB 24 TGGAGCTCACTCTTTGCCAGG 1

RESULT 652
AB04729/C
ID ABA04729 standard; DNA; 24 BP.
XX
XX ABA04729;
AC
XX
XX 01-MAR-2002 (first entry)
DT
XX
XX Human ubiquitin-binding enzyme 9 PCR primer #1.
DE
XX
XX Human; cytostatic; haemostatic; virocid; immunomodulatory; PCR primer;
KW antiinflammatory; gene therapy; ubiquitin-binding enzyme 9; tumour;
KW haemopathy; HIV infection; immunological disease; inflammation; ss.
XX
XX Homo sapiens.
OS
XX WO200188142-A1.
PN
XX 22-NOV-2001.
PD
XX
XX 08-MAY-2001; 2001WO-CN000731.
PF
XX
XX 09-MAY-2000; 2000CN-00115634.
PR
XX
XX (SHAN-) SHANGHAI BOWINDOW GENE DEV INC.
PA
XX
XX Mao Y, Xie Y;
PI
XX
XX WPI; 2002-055699/07.
DR
XX
XX Human ubiquitin-binding enzyme 9A and encoding polynucleotide, used in
PT diagnosis and treatment of malignant tumors, hemopathy, human
PT immunodeficiency virus infection, immunological diseases and
PT inflammation.
XX
XX
XX Example 2; Page 18; 35pp; Chinese.
PS
XX The present invention relates to human ubiquitin-binding enzyme 9 (see
CC AAM47737). The enzyme and its coding sequence are useful in the diagnosis
CC and treatment of malignant tumors, haemopathy, HIV infection,
CC immunological diseases and various inflammations. The present sequence is
CC a PCR primer, which was used in an example from the present invention
XX
XX
SQ Sequence 24 BP; 3 A; 9 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 874 CAGGCGTGAGCCACACGCCCGGC 897
DB 24 CAGGCGTGAGCCACTGTGCCCGC 1

RESULT 653
AB077823
ID AB077823 standard; DNA; 24 BP.
XX
XX
XX ABO77823;
AC
XX
XX 20-DEC-2002 (first entry)
DT
XX
XX Human protein phosphatase 13.64 RT-PCR primer, SEQ ID NO.3.
DE

XX
XX Human; protein phosphatase 13.64; recombinant production; gene therapy;
KW female genital development disorder; abnormal female sex characteristic;
KW female genital tract tumour; oestrogen-related metabolic abnormality;
KW cytostatic; gynaecological; reverse transcription-PCR; RT-PCR; primer;
KW ss.
XX
XX Homo sapiens.
OS
XX CN1352290-A.
PN
XX
XX 05-JUN-2002.
PD
XX
XX 10-NOV-2000; 2000CN-00127328.
PF
XX
XX 10-NOV-2000; 2000CN-00127328.
PR
XX
XX 10-NOV-2000; 2000CN-00127328.
PA
XX
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
PI
XX
XX Mao Y, Xie Y;
PI
XX
XX WPI; 2002-667814/72.
DR
XX
XX The invention relates to human protein phosphatase 13.64 (ABB93687) and
CC nucleic acids encoding it (AB077822). The protein has a molecular weight
CC of 13.64 kD. The invention also relates to a method for the recombinant
CC production of the protein, an antagonist of the protein, and the use of
CC the protein, gene and antagonist in therapeutic applications. Protein
CC phosphatase 13.64 can be used in the treatment of a variety of diseases
CC such as disorders of female genital development, abnormal female sex
CC characteristics, tumours of the female genital tract and oestrogen-
CC related metabolic abnormalities. Sequences AB077823-AB077824 represent
CC reverse transcription-PCR (RT-PCR) primers used in an exemplification of
CC the invention to isolate human protein phosphatase 13.64 cDNA
XX
XX
SQ Sequence 24 BP; 4 A; 3 C; 9 G; 8 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 180 GTAGAGATGAGATTCTTCATGTT 203
DB 1 GTAGAGATGGGTTTCAACCGTGT 24

RESULT 654
ADE14009
ID ADE14009 standard; DNA; 24 BP.
XX
XX
XX ADE14009;
AC
XX
XX 29-JAN-2004 (first entry)
DT
XX
XX Optineurin promoter motif, repeat element or regulatory region #118.
DE
XX
XX Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
KW SNP; glaucoma; progressive ocular hypertensive disorder;
KW glaucoma related disorder; motif; repeat element; regulatory region.
XX
XX Homo sapiens.
OS
XX
XX US2003190617-A1.
PN
XX
XX 09-OCT-2003.
PD
XX

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PF 06-MAR-2002; 2002US-00091281.
XX
XX 06-MAR-2002; 2002US-00091281.
XX
XX (SIEE/) SI E.
XX (RAYM/) RAYMOND V.
XX (MORI/) MORISSETTE J.
XX
XX Raymond V, Morissette J, Si E;
XX
XX WPI; 2003-864168/80.
XX
XX New nucleic acid sequences of the optineurin gene are useful to detect
XX polymorphisms particularly single nucleotide polymorphisms in the
XX optineurin promoter to diagnose, prognose and treat glaucoma and related
XX disorders.
XX
XX Claim 1; SEQ ID NO 120; 159pp; English.
XX
XX The invention relates to an isolated nucleic acid (N1) comprising at
XX least 20 but not more than 1500 consecutive nucleotides of the optineurin
XX promoter appearing as AD313890. Also included are the optineurin promoter
XX operably linked to a heterologous nucleic acid, a nucleic acid capable of
XX detecting a single nucleotide polymorphism (SNP) in the optineurin
XX promoter, a host cell comprising the promoter operably linked to a
XX heterologous sequence, diagnosing or prognosing glaucoma in a sample
XX obtained from a cell or bodily fluid (comprising detecting a polymorphism
XX in a promoter region of the optineurin gene, associated with a glaucoma
XX phenotype), detecting a SNP sequence variation in a sample containing
XX DNA, detecting the presence of an optineurin promoter sequence variation
XX in a sample containing DNA, determining the presence or increased
XX susceptibility to glaucoma or to a progressive ocular hypertensive
XX disorder resulting in loss of visual field in a patient (or the severity
XX or progression of glaucoma in a patient, comprising providing
XX amplification reaction primers that direct amplification of a selected
XX nucleic acid region containing the variation within the optineurin
XX promoter and amplifying the DNA) and detecting a polymorphism (comprising
XX obtaining a sample containing human genomic DNA, providing a nucleic acid
XX capable of detecting a SNP located within an optineurin promoter, and
XX detecting the polymorphism). The invention is used to diagnose and
XX prognose glaucoma and also to treat glaucoma related disorders. The
XX present sequence is an optineurin promoter motif, repeat element or
XX putative regulatory region.
XX
XX Sequence 24 BP; 7 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 19.2; DB 1; Length 24;
XX Best Local Similarity 87.5%; Pred. No. 1.4e+03;
XX Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1020 AGCCTCCAGAGAGCTGGATTAC 1043
XX ||||| ||||| ||||| |||||
XX 1 AGCCTCTCAGTACTGAGATTAC 24
XX
XX RESULT 655
XX AAT94763
XX ID AAT94763 standard; DNA; 19 BP.
XX
XX AC AAT94763;
XX
XX XX 25-MAR-2003 (revised)
XX DT 18-FEB-1998 (first entry)
XX
XX DE Human progesterone receptor gene primer.
XX
XX XX Human; progesterone receptor; breast cancer; ovarian cancer; mutant;
XX KW antibody; mutation; primer; ss.
XX
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX PN US5683985-A.
```

```
XX
XX PD 04-NOV-1997.
XX
XX PF 03-DEC-1996; 96US-00759873.
XX
XX PR 12-APR-1996; 96US-00629939.
XX
XX PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
XX PI Kieback DG;
XX
XX DR WPI; 1997-548981/50.
XX
XX PT Diagnosis of increased risk for breast or ovarian cancer - by immunoassay
XX for mutant progesterone receptor protein.
XX
XX PS Disclosure; Col 7; 26pp; English.
XX
XX CC The present sequence represents a primer used in the detection of an Alu
XX insertion sequence in intron G in the human progesterone receptor gene.
XX CC The present invention has developed a novel method for diagnosing an
XX increased risk for breast or ovarian cancer. The method involves assaying
XX a sample containing human progesterone receptor protein (hPR) with an
XX antibody that distinguishes wild-type hPR from a mutant hPR having a Val-
XX to-Leu substitution at amino acid 660, where the presence of such a
XX mutant indicates an increased risk for breast or ovarian cancer.
XX CC Detection of the G-to-T point mutation gives an odds ratio for ovarian
XX cancer of 3.1 (sensitivity 46%, specificity 78%) and an odds ratio for
XX breast cancer of 2.0 (sensitivity 36%, specificity 78%). (Updated on 25-
XX MAR-2003 to correct PF field.)
XX
XX SQ Sequence 19 BP; 6 A; 2 C; 7 G; 4 T; 0 U; 0 Other;
XX
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Query Match 1.9%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 389 AAGTGTGGATTACAGG 407
XX ||||| ||||| ||||| |||||
XX 1 AAGTGTGGATTACAGG 19
XX
```

```
RESULT 656
AAT84754
ID AAT84754 standard; DNA; 19 BP.
XX
XX AC AAT84754;
XX
XX DT 04-NOV-1997 (first entry)
XX
XX DE FISH primer for human progesterone receptor intron G.
XX
XX KW Breast; ovarian cancer; diagnosis; risk; predisposition; human;
XX KW detection; point mutation; progesterone; receptor; FISH; primer;
XX KW Alu insertion; intron G; fluorescent in situ hybridisation; ss.
XX
XX OS Synthetic.
XX
XX PN US5645995-A.
XX
XX PD 08-JUL-1997.
XX
XX PF 12-APR-1996; 96US-00629939.
XX
XX PR 12-APR-1996; 96US-00629939.
XX
XX PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
XX PI Kieback DG;
XX
XX DR WPI; 1997-362926/33.
XX
XX PT Diagnosis of increased risk of breast or ovarian cancer - by detecting
```

PT point mutation in codon 660 of exon 4 of human progesterone receptor
PR gene.
XX
XX
PS Claim 18; Col 19-20; 26pp; English.
XX
CC Increased risk of breast or ovarian cancer can be diagnosed by detecting
CC a G to T point mutation at the 1st nucleotide of codon 660 in exon 4 of
CC the human progesterone receptor (PR) gene, i.e. nucleotide 2153 of
CC AAT84747. The odds ratio is 3.1 (sensitivity 46%, specificity 78%) for
CC ovarian cancer, and 2.0 (sensitivity 36%, specificity 78%) for breast
CC cancer. The method may also include detecting a C to T point mutation at
CC the 3rd nucleotide of codon 770 in exon 5 of the human PR gene, i.e.
CC nucleotide 2485 of AAT84747, and/or an Alu insertion in codon 897 of
CC intron G, i.e. AAT84749 inserted between nucleotides 120 and 121 of
CC AAT84748. The mutation in exon 4 can be detected by digesting a test
CC nucleic acid with BstI, and detecting the loss of a BstI restriction
CC site. The mutation in exon 5 can be detected by digesting a test nucleic
CC acid with NlaIII and detecting the addition of a NlaIII restriction site.
CC The mutation in intron G can be detected by digesting a test nucleic acid
CC with TaqI and detecting a 1.9 kb DNA fragment, by PCR using the primers
CC AAT84750-53, by FISH using AAT84754 or by Southern blotting using a probe
CC comprising the Alu insertion AAT84749
XX
SQ Sequence 19 BP; 6 A; 2 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 1.9%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 389 AAAGTCTGGGATTACAGG 407
DB 1 AAAGTCTGGGATTACAGG 19
|||||
RESULT 657
AAH38421
ID AAH38421 standard; DNA; 19 BP.
XX
XX
AC AAH38421;
XX
DT 14-AUG-2001 (first entry)
XX
XX
DE SNP specific upper PCR primer SEQ ID 1217.
XX
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Leisch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028436.
XX
PR 15-OCT-1999; 99US-0160096P.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
PS Claim 1; Page 56; 83pp; English.

CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Leisch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic, such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence
XX
SQ Sequence 19 BP; 3 A; 9 C; 2 G; 5 T; 0 U; 0 Other;
Query Match 1.9%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 675 TCACTGCAACCTCTGCTC 693
DB 1 TCACTGCAACCTCTGCTC 19
|||||
RESULT 658
AAH38469
ID AAH38469 standard; DNA; 19 BP.
XX
XX
AC AAH38469;
XX
DT 14-AUG-2001 (first entry)
XX
XX
DE SNP specific upper PCR primer SEQ ID 1265.
XX
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Leisch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028436.
XX
PR 15-OCT-1999; 99US-0160096P.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
PS Claim 1; Page 56; 83pp; English.

Query Match 1.9%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 384 CTCGCCAAGTCTGGGATT 402
DB 19 CTCGCCAAGTCTGGGATT 1

RESULT 661

ADL25033
ID ADL25033 standard; DNA, 19 BP.

AC ADL25033;
XX

DT 20-MAY-2004 (first entry)
XX

DE Intestinal epithelium/peyer's patch M cell-associated PCR primer #178.
XX

XX Intestinal epithelium cell development; peyer's patch M cell development;
XX inflammatory bowel disease; glutenenteropathy; infectious disease;

KM autoimmune disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;
XX Grave's disease; multiple sclerosis; allergy; asthma; diabetic mellitus;

KM immune system disorder; hypersensitivity; anaphylaxis;
XX blood group incompatibility; ss; human; PCR; primer.

OS Homo sapiens.
XX

FN WO200280852-A2.
XX

PD 17-OCT-2002.
XX

PF 04-APR-2002; 2002WO-US010873.
XX

PR 04-APR-2001; 2001US-0281416P.
XX

PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX

PI Brayden DJ, Byrne D, O'mahony DJ, Evans CF, Mah SP, Lo DD;
XX WPI; 2003-075470/07.

DR Novel isolated or purified polypeptide encoded by genes associated with
XX intestinal epithelium or M cell development, differentiation or function,
XX useful for treating autoimmune diseases and infectious diseases.

PS Disclosure, SEQ ID NO 543; 152pp; English.
XX

CC The invention comprises DNA sequences which are associated with
XX intestinal epithelium and peyer's patch M cells. The DNA sequences of the
XX invention are useful for assessing, modifying, modulating or regulating
XX intestinal epithelium or M cell development. The DNA sequences of the
XX invention are also useful in the treatment of: inflammatory bowel
XX disease, glutenenteropathy, infectious diseases, autoimmune diseases
XX (e.g. haemolytic anaemia, rheumatoid arthritis, dermatitis, Grave's
XX disease, multiple sclerosis, allergy, asthma and diabetic mellitus),
XX diseases or disorders of the immune system, hypersensitivity,
XX anaphylaxis, and blood group incompatibility. The present DNA sequence
XX represents a PCR primer that was used to amplify an intestinal
XX epithelium/peyer's patch M cell-associated DNA sequence of the invention.

CC Sequence 19 BP; 3 A; 5 C; 7 G; 4 T; 0 U; 0 Other;
XX

Query Match 1.9%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 638 TGTACCCAGGCTGGAGTG 656
DB 1 TGTACCCAGGCTGGAGTG 19

RESULT 662

ADM32300/C
ID ADM32300 standard; DNA, 19 BP.
XX

AC ADM32300;
XX

DT 20-MAY-2004 (first entry)
XX

DE Human interleukin-18 gene polymorphism related probe, SEQ ID NO 57.
XX

XX human interleukin-18; IL-18; adult onset still disease; gene;
XX single nucleotide polymorphism; ss; probe.

OS Homo sapiens.
XX

OS Synthetic.
XX

PN JP2004049136-A.
XX

PD 19-FEB-2004.
XX

PF 22-JUL-2002; 2002JP-00212550.
XX

PR 22-JUL-2002; 2002JP-00212550.
XX

PA (SUGI/) SUGIURA S.
XX (HYUB-) HYUBBITO GENOMICS KK.

DR WPI; 2004-174121/17.
XX

PT Detecting gene polymorphism in interleukin-18 gene of human, useful for
XX detecting adult onset still disease.

PS Claim 6; SEQ ID NO 57; 61pp; Japanese.
XX

CC The invention relates to a novel method for detecting a gene polymorphism
CC in a human interleukin (IL)-18 gene. The method involves detecting a 9
CC base insertion between -6311 position and -6310 position, a polymorphism
CC at positions -5890, -5316, -4762, -4675, -3268, -689 and -640 of a
CC polynucleotide which consists of a fully defined sequence of 6640 base
CC pairs as given in the specification, where in the 6640bp polynucleotide,
CC the position 6575 is set to +1 from which numbering is performed. The
CC method is useful for detecting gene polymorphism in IL-18 gene of human
CC and for detecting adult onset still disease. This polynucleotide sequence
CC represents a probe of the human interleukin-18 gene of the invention.

CC Sequence 19 BP; 4 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
XX

Query Match 1.9%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 GGTGTCGGAAGTCCCGA 228
DB 19 GGTGTCGGAAGTCCCGA 1

RESULT 663

ADO80008
ID ADO80008 standard; DNA, 19 BP.

AC ADO80008;
XX

DT 26-AUG-2004 (first entry)
XX

DE CENPCL extend primer #59.
XX

XX Cytostatic; Gene therapy; breast cancer; human; DGL; KIA0783; DPF3;
XX CENPCL; SNP; single nucleotide polymorphism; centromere protein C1;
XX Centromere autoantigen C1; chromosome 4q12-q13.3; extend; primer; ss.

OS Homo sapiens.
XX

PN WO2004047514-A2.
XX

PD 10-JUN-2004.
 XX
 XX 25-NOV-2003; 2003WO-US037943.
 PF
 XX 25-NOV-2002; 2002US-0429136P.
 PR 24-JUL-2003; 2003US-0490234P.
 XX
 XX (SEQU-) SEQUENOM INC.
 XX
 XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
 PI WPI; 2004-441037/41.
 DR
 XX Identifying a subject at risk of breast cancer by detecting the presence
 XX of polymorphic variations in the DLG1, KIA0783, DP3 or CENPC1 regions
 PT which are associated with breast cancer in a nucleic acid sample from a
 PT subject.
 PS Example 6; Page 91; 227pp; English.
 XX
 XX The present invention relates to a method for identifying a subject at
 CC risk of breast cancer. The method comprising detecting the presence or
 CC absence of one or more polymorphic variations associated with breast
 CC cancer in a nucleic acid sample from a subject. The nucleic acid sample
 CC comprises the DLG1 region (ADO79402), KIA0783 region (ADO79403), DP3
 CC region (ADO79404) or CENPC1 region (ADO79405). The gene DLG1 (discs,
 CC large homolog 1 (Drosophila)) is also known as synapse-associated protein
 CC 97, hdlg or SAP97. DLG1 has been mapped to chromosomal position 3q29. The
 CC gene KIA0783 is also known as PHF14 and PHD finger protein 14. KIA0783
 CC has been mapped to chromosomal position 7p21.3. The KIA0783 protein is a
 CC novel gene with unknown function, however, being a zinc finger protein,
 CC it likely to be a transcription factor. The gene DP3 (D4, zinc and
 CC double PHD fingers, family 3) is also known as CERD4, cer-d4, PLJ14079
 CC and 281040303Rik. DP3 is a Rho family guanine-nucleotide exchange
 CC factor. DP3 has been mapped to chromosomal position 14q24.3-q31.1. The
 CC gene CENPC1 (centromere protein C1) is also known as Centromere
 CC autoantigen C1. CENPC1 has been mapped to chromosomal position 4q12-
 CC q13.3. CENPC1 is a centromere autoantigen and a component of the inner
 CC kinetochore plate. The CENPC1 protein is required for maintaining proper
 CC kinetochore size and a timely transition to anaphase. The method is
 CC useful for identifying a subject at risk of breast cancer, for early
 CC diagnosis, prevention and treatment of breast cancer, to analyze and
 CC predict a response to a breast cancer treatment, and in clinical drug
 CC trials. The present sequence was used in an example from the invention.
 XX
 SO Sequence 19 BP; 6 A; 2 C; 7 G; 4 T; 0 U; 0 Other;
 Query Match 1.9%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 389 AAGTGTGGATTACAG 407
 DB 1 AAGTGTGGATTACAG 19
 RESULT 664
 AAV85791
 ID AAV85791 standard; DNA; 20 BP.
 XX
 XX AAV85791;
 XX
 XX 10-FEB-1999 (first entry)
 DT
 XX LRP5 exon primer 58-7 1r.
 DE
 XX LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis;
 XX insulin dependent diabetes mellitus; autoimmune disease;
 KW glomerulonephritis; inflammation; viral infection; osteoporosis;
 KW hypercholesterolemia; Alzheimer's disease; low density lipoprotein;
 KM PCR primer; ss.
 XX
 XX Synthetic.

OS Homo sapiens.
 XX
 XX WO9846743-A1.
 PN
 XX 22-OCT-1998.
 PD
 XX 15-APR-1998; 98WO-GB001102.
 PF
 XX 15-APR-1997; 97US-0043553P.
 PR 05-JUN-1997; 97US-0048740P.
 XX
 XX (MELT) MELTCOME TRUST LTD.
 PA (MERT) MERT & CO INC.
 XX
 XX Todd JA, Hess JW, Caskey CT, Cox RD, Gerhold D, Hammond H;
 PI Hey P, Kawaguchi Y, Merriman TR, Metzger ML, Nakagawa Y;
 PI Phillips MS, Twells RCU;
 XX
 DR WPI; 1998-594573/50.
 XX
 XX New isolated LDL-receptor related protein - used to develop products for
 PT treating, e.g. elevated triglyceride levels, diabetes, autoimmune
 PT disorders, inflammation or Alzheimer's disease.
 PS Claim 12; Page 106; 200pp; English.
 XX
 XX The present invention describes LRP5 (low density lipoprotein (LDL)
 CC receptor related protein, previously designated LRP-3). AAV85587 to
 CC AAV85822 represent exon primers used for obtaining LRP5 cDNA. Nucleic
 CC acid molecules (NMs) encoding LRP5 can be used for determining if an
 CC individual is susceptible to insulin dependent diabetes mellitus (IDDM).
 CC The NMs or proteins can be used for reducing triglyceride levels in the
 CC serum of an individual. Therapies that affect LRP5 may also be useful in
 CC the treatment of autoimmune diseases such as glomerulonephritis, diseases
 CC and disorders involving disruption of endocytosis and/or antigen
 CC presentation, cytokine clearance and/or inflammation, viral infection,
 CC pathogenic bacterial toxin contamination, elevation of free fatty acids
 CC or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's
 CC disease and cardiovascular disease. Products from the present invention
 CC can also be used for detection, diagnosis and drug screening
 XX
 SO Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 1.9%; Score 19; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 668 TCTTGCTCACTGCACCT 686
 DB 2 TCTTGCTCACTGCACCT 20
 RESULT 665
 AAV85869
 ID AAV85869 standard; DNA; 20 BP.
 XX
 XX AAV85869;
 XX
 XX 10-FEB-1999 (first entry)
 DT
 XX LRP5 SNP primer 58-7 1r.
 DE
 XX LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis;
 XX insulin dependent diabetes mellitus; autoimmune disease;
 KW glomerulonephritis; inflammation; viral infection; osteoporosis;
 KW hypercholesterolemia; Alzheimer's disease; low density lipoprotein;
 KM PCR primer; ss.
 XX
 XX Synthetic.
 OS Homo sapiens.
 XX
 XX WO9846743-A1.

```

PD 22-OCT-1998.
XX
XX 15-APR-1998; 98WO-GB001102.
XX
XX 15-APR-1997; 97US-0043553P.
PR 05-JUN-1997; 97US-0048740P.
XX
XX (WELL ) WELLCOME TRUST LTD.
PA (MERI ) MERCK & CO INC.
XX
PI Todd JA, Hess JW, Caskey CT, Cox RD, Gerhold D, Hammond H;
PI Hey P, Kawaguchi Y, Merriman TR, Metzker ML, Nakagawa Y;
PI Phillips MS, Twells RCJ;
XX
XX WPI; 1998-594573/50.
XX
XX New isolated LDL-receptor related protein - used to develop products for
PT treating, e.g. elevated triglyceride levels, diabetes, autoimmune
PT disorders, inflammation or Alzheimer's disease..
XX
PS Claim 12; Page 111; 200pp; English.
XX
XX The present invention describes LRP5 (low density lipoprotein (LDL)
XX receptor related protein, previously designated LRP-3). AAV85823 to
XX AAV85900 represent SNP primers used for obtaining LRP5 cDNA. Nucleic acid
XX molecules (NMs) encoding LRPs can be used for determining if an
XX individual is susceptible to insulin dependent diabetes mellitus (IDDM).
XX The NMs or proteins can be used for reducing triglyceride levels in the
XX serum of an individual. Therapies that affect LRPs may also be useful in
XX the treatment of autoimmune diseases such as glomerulonephritis, diseases
XX and disorders involving disruption of endocytosis and/or antigen
XX presentation, cytokine clearance and/or inflammation, viral infection,
XX pathogenic bacterial toxin contamination, elevation of free fatty acids
XX or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's
XX disease and cardiovascular disease. Products from the present invention
XX can also be used for detection, diagnosis and drug screening
XX
SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 668 TCCTGGCTCAGTCAACCT 686
DB 2 TCCTGGCTCAGTCAACCT 20

RESULT 666
AAZ37713/C
ID AAZ37713 standard; DNA; 20 BP.
XX
XX AAZ37713;
AC
XX
XX 07-JAN-2000 (first entry)
DT
XX
XX Human mdm2 phosphorothioate oligodeoxynucleotide #243.
DE
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
KW hyperproliferation; blood cancer; brain cancer; breast cancer;
KW lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;
KW restenosis; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9949065-A1.
XX
XX 30-SEP-1999.
XX
XX 26-MAR-1999; 99WO-US006702.
XX
XX
XX

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PR 26-MAR-1998; 98US-00048810.
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowseart LM;
XX
XX WPI; 1999-610754/52.
XX
XX New antisense compounds used to treat eg. hyperproliferative conditions.
XX
PS Example 9; Page 54; 157pp; English.
XX
XX AAZ37473-237738 represent human mdm2 phosphorothioate oligonucleotides.
XX AAZ37471, AAZ37472, AAZ37739, AAZ37740 and AAZ37741 are used in the
XX exemplification of the present invention. The present invention describes
XX novel nucleotide antisense compounds, targeted to the 5' untranslated,
XX translation termination codon, or 3' untranslated region of a nucleic
XX acid encoding human mdm2, that modulates expression of human mdm2. The
XX oligonucleotides mediate their effect by antisense inhibition of
XX hyperproliferative gene expression. The antisense compound is used to
XX treat an animal having a disease or condition associated with mdm2,
XX particularly a hyperproliferative condition, more particularly cancer,
XX especially of the blood, brain, breast, lung or soft tissue, or
XX psoriasis, fibrosis, atherosclerosis or restenosis
XX
SQ Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 644 CCAGGCTGAGTGCAGTGG 662
DB 20 CCAGGCTGAGTGCAGTGG 2

RESULT 667
AAZ37720/C
ID AAZ37720 standard; DNA; 20 BP.
XX
XX AAZ37720;
AC
XX
XX 07-JAN-2000 (first entry)
DT
XX
XX Human mdm2 phosphorothioate oligodeoxynucleotide #250.
DE
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
KW hyperproliferation; blood cancer; brain cancer; breast cancer;
KW lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;
KW restenosis; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9949065-A1.
XX
XX 30-SEP-1999.
XX
XX 26-MAR-1999; 99WO-US006702.
XX
XX 26-MAR-1998; 98US-00048810.
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowseart LM;
XX
XX WPI; 1999-610754/52.
XX
XX New antisense compounds used to treat eg. hyperproliferative conditions.
XX
PS Example 9; Page 54; 157pp; English.
XX

```


CC AA237473-237738 represent human mdm2 phosphorothioate oligonucleotides.
CC AA237471, AA237472, AA237739, AA237740 and AA237741 are used in the
CC exemplification of the present invention. The present invention describes
CC novel nucleotide antisense compounds, targeted to the 5' untranslated,
CC translation termination codon, or 3' untranslated region of a nucleic
CC acid encoding human mdm2, that modulates expression of human mdm2. The
CC oligonucleotides mediate their effect by antisense inhibition of
CC hyperproliferative gene expression. The antisense compound is used to
CC treat an animal having a disease or condition associated with mdm2,
CC particularly a hyperproliferative condition, more particularly cancer,
CC especially of the blood, brain, breast, lung or soft tissue, or
CC psoriasis, fibrosis, atherosclerosis or restenosis
XX

XX Sequence 20 BP; 5 A; 2 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 536 TCCTGCTCAGCTCCCA 554
DB 20 TCCTGCTCAGCTCCCA 2

RESULT 668
AAF0874/c
ID AAF0874 standard; DNA; 20 BP.

AC AAF0874;

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #248.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

XX Homo sapiens;

XX US6184212-B1.

XX 06-FEB-2001.

XX 26-MAR-1999; 99US-00280805.

XX 26-MAR-1998; 98US-00048810.

XX (ISIS-) ISIS PHARM INC.

PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowse LM;

DR WPI; 2001-190948/19.

XX Novel antisense compound 8-30 nucleobases in length targeted to a nucleic
PT acid molecule encoding human mdm-2 useful for modulating the expression
PT of human mdm-2 and reducing hyperproliferation of human cells.

XX Example 9; Col 33; 77pp; English.

XX The present invention relates to an antisense compound 8-30 nucleobases
CC in length targeted to nucleobases 1-308 of the 5' untranslated region,
CC 1776-1806 of the translation termination codon region or 1818-2370 of the
CC 3' untranslated region of a nucleic acid molecule encoding human mdm-2.
CC The invention is useful for reducing hyperproliferation of human cells,
CC modulating the expression of mdm2 in human cells or tissues or in vitro.
CC The hyperproliferative disorder includes cancer or psoriasis
XX

XX Sequence 20 BP; 5 A; 2 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 536 TCCTGCTCAGCTCCCA 554

DB 20 TCCTGCTCAGCTCCCA 2

RESULT 669
AAF0867/c
ID AAF0867 standard; DNA; 20 BP.

AC AAF0867;

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #241.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

XX Homo sapiens.

XX US6184212-B1.

XX 06-FEB-2001.

XX 26-MAR-1999; 99US-00280805.

XX 26-MAR-1998; 98US-00048810.

XX (ISIS-) ISIS PHARM INC.

PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowse LM;

DR WPI; 2001-190948/19.

XX Novel antisense compound 8-30 nucleobases in length targeted to a nucleic
PT acid molecule encoding human mdm-2 useful for modulating the expression
PT of human mdm-2 and reducing hyperproliferation of human cells.

XX Example 9; Col 31; 77pp; English.

XX The present invention relates to an antisense compound 8-30 nucleobases
CC in length targeted to nucleobases 1-308 of the 5' untranslated region,
CC 1776-1806 of the translation termination codon region or 1818-2370 of the
CC 3' untranslated region of a nucleic acid molecule encoding human mdm-2.
CC The invention is useful for reducing hyperproliferation of human cells,
CC modulating the expression of mdm2 in human cells or tissues or in vitro.
CC The hyperproliferative disorder includes cancer or psoriasis
XX

XX Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 644 CCAGGCTGAGTGCACTGG 662
DB 20 CCAGGCTGAGTGCACTGG 2

RESULT 670

ID AAC88720 standard; DNA; 20 BP.

AC AAC88720;

DT 07-MAR-2001 (first entry)

XX Human catenin-binding zinc finger protein PCR primer FVR510F.

XX Catenin-binding zinc finger protein; cancer; neurological disorder;

XX drug screening; PCR primer; ss.

XX Homo sapiens.

XX EP1054059-A1.

```
XX 22-NOV-2000.
PD
XX 17-MAY-1999; 99EP-00201543.
PF
XX 17-MAY-1999; 99EP-00201543.
PR
XX (VLAA-) VLAAWS INTERUNIVERSITAIR INST BIOTECHNOG.
PA
XX Van Roy F, Vanlandeschoot A, Janssens B;
PI
XX WPI; 2001-033776/05.
DR
XX Nucleic acid or its fragments, useful for diagnosing and treating cancer
PT and neurological disorders, corresponds to a catenin-binding protein in
PT signal transduction and gene regulatory pathways.
PS Disclosure; Page 17; 71pp; English.
XX
XX The present invention is related to the coding sequence and protein
CC fragments of a human catenin-binding zinc finger protein. The coding
CC sequence was isolated from a human kidney cDNA library, but is expressed
CC in most human tissue. The sequences provided by the invention can be used
CC in the diagnosis and treatment of cancer and neurological disorders, and
CC in drug screening to identify compounds capable of the same
XX
SQ Sequence 20 BP; 5 A; 3 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 1.9%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 864 GCTGGATTACAGCGCTGA 882
DB 1 GCTGGATTACAGCGCTGA 19
RESULT 671
AADI2635
ID AADI2635 standard; DNA; 20 BP.
XX
AC AADI2635;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human ANC_2H01 cDNA sequencing forward primer, FVR510F.
XX
KW Human; ANC_2H01 protein; catenin-binding protein; signal transduction;
KW gene regulation; zinc finger protein; alphan-catenin; drug screening;
KW therapy; cancer; neurological disorder; cytostatic; neuroprotective;
KW primer; ss.
XX
OS Homo sapiens.
XX
PN WO200147954-A2.
XX
PD 05-JUL-2001.
XX
PF 18-MAY-2000; 2000WO-EP004535.
XX
PR 23-DEC-1999; 99EP-00204512.
XX
PA (VLAA-) VLAAWS INTERUNIVERSITAIR INST BIOTECHNOG.
PI Van Roy F, Vanlandeschoot A, Janssens B;
XX
DR WPI; 2001-418220/44.
XX
PT Novel recombinant nucleic acids useful for diagnosing, prognosing and/or
PT treating cancer and neurological disorders, corresponds to a protein
PT binding to alpha-catenin protein and with signal transduction function.
PS Disclosure; Page 66; 160pp; English.
```

```
XX The invention relates to human catenin-binding proteins and their
CC corresponding cDNA molecules which functions in signal transduction and
CC gene regulatory pathways. The invention also provides an isolated and/or
CC recombinant nucleic acid or its functional fragment, homologue or
CC derivative, corresponding to a alpha-catenin binding protein. The
CC invention also relates to a novel human zinc finger protein binding with
CC a member of the a-cattulin/vinculin family, preferably with a human
CC isoform of alpha N-catenin (neural form). The invention also relates to
CC the field of drug discovery, diagnosis, prognosis and treatment of cancer
CC and neurological disorders. The present sequence is a primer which is
CC used for sequencing human ANC_2H01 cDNA
XX
SQ Sequence 20 BP; 5 A; 3 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 1.9%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 864 GCTGGATTACAGCGCTGA 882
DB 1 GCTGGATTACAGCGCTGA 19
RESULT 672
AAS29482/C
ID AAS29482 standard; DNA; 20 BP.
XX
AC AAS29482;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31620.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW anti arteriosclerotic; vasotropic; antisense; phosphorothioate; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag=a
FT /mod_base= OTHER
FT /note="OTHER= All phosphorothioate linkages,
FT additionally bases 1-6 and bases 15-20 are 2'-O-
FT methoxyethyl bases, and bases 7-14 are deoxynucleotides"
XX
PN US2001016575-A1.
XX
PD 23-AUG-2001.
XX
PF 02-JAN-2001; 2001US-00752983.
XX
PR 26-MAR-1998; 98US-00048810.
XX
PR 26-MAR-1999; 99US-00280805.
XX
PA (MIRA/) MIRAGLIA L J.
PA (NERO/) NERO P.
PA (GRAH/) GRAHAM M J.
PA (MONI/) MONIA B P.
PA (COWS/) COWSERT L M.
PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowert LM;
XX
DR WPI; 2001-535565/59.
XX
PT An antisense compound, useful for treating e.g. cancer, comprises
PT nucleobases targeted a region (e.g. translation termination codon region)
PT of a nucleic acid encoding human mdm2.
XX
PS Example 9; Page 18; 81pp; English.
```

CC The present invention relates to antisense compounds, 8-30 nucleobases in
CC length targeted to the 5' untranslated region, translation termination
CC codon region, 3' untranslated region, coding region or translation start
CC site of a nucleic acid encoding human mdm2, where the antisense compound
CC modulates the expression of human mdm2. The antisense oligonucleotides of
CC the invention are useful for encoding human mdm2 and for inhibiting the
CC expression of human mdm2. They may be used for creating an animal having
CC a disease or condition associated with amplification of mdm2 gene or
CC overexpression of mdm2 e.g. a hyperproliferative disorder such as cancer
CC (blood, brain, breast, lung, or a soft tissue cancer) and psoriasis,
CC fibrosis, atherosclerosis or restenosis, tumours, colorectal carcinoma
CC and chronic myelogenous leukemia. The antisense compound may be
CC administered with a chemotherapeutic agent to overcome drug resistance.
CC The antisense compound reduces hyperproliferation of human cells. The
CC method, which involves the use of the antisense compound, is also useful
CC for detecting the role of mdm2 expression in various cell functions and
CC physiological processes and useful in both clinical research and
CC diagnostic tools. AAS29242-AAS29507 represent the human mdm2 antisense
CC oligonucleotides of the present invention
CC
SQ Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 1.9%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 644 CCAGCTGAGTGCAGTGG 662
DB 20 CCAGCTGAGTGCAGTGG 2
RESULT 673
AAS29489/c
ID AAS29489 standard; DNA; 20 BP.
AC AAS29489;
XX
XX 21-NOV-2001 (first entry)
DT
XX
DE Human mdm2 antisense oligonucleotide 31784.
XX
XX Human mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KM anti arteriosclerotic; vasotropic; antisense; phosphorothioate; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= All phosphorothioate linkages,
FT additional bases 1-6 and bases 15-20 are 2'-O-
FT methoxyethyl bases, and bases 7-14 are deoxynucleotides"
XX
XX US2001016575-A1.
PN
XX
PD 23-AUG-2001.
XX
XX 02-JAN-2001; 2001US-00752983.
XX
XX 26-MAR-1998; 98US-00048810.
PR 26-MAR-1999; 99US-00280805.
XX
XX (MIRA/) MIRAGLIA L J.
PA (NERO/) NERO P.
PA (GRAH/) GRAHAM M J.
PA (MONI/) MONIA B P.
PA (COMS/) COMSERT L M.
XX
PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsert LM;
XX
XX WPI; 2001-535565/59.

XX An antisense compound, useful for treating e.g. cancer, comprises
PT nucleobases targeted a region (e.g. translation termination codon region)
PT of a nucleic acid encoding human mdm2.
PS
XX Example 9; Page 18; 81pp; English.
XX
CC The present invention relates to antisense compounds, 8-30 nucleobases in
CC length targeted to the 5' untranslated region, translation termination
CC codon region, 3' untranslated region, coding region or translation start
CC site of a nucleic acid encoding human mdm2, where the antisense compound
CC modulates the expression of human mdm2. The antisense oligonucleotides of
CC the invention are useful for encoding human mdm2 and for inhibiting the
CC expression of human mdm2. They may be used for treating an animal having
CC a disease or condition associated with amplification of mdm2 gene or
CC overexpression of mdm2 e.g. a hyperproliferative disorder such as cancer
CC (blood, brain, breast, lung, or a soft tissue cancer) and psoriasis,
CC fibrosis, atherosclerosis or restenosis, tumours, colorectal carcinoma
CC and chronic myelogenous leukemia. The antisense compound may be
CC administered with a chemotherapeutic agent to overcome drug resistance.
CC The antisense compound reduces hyperproliferation of human cells. The
CC method, which involves the use of the antisense compound, is also useful
CC for detecting the role of mdm2 expression in various cell functions and
CC physiological processes and useful in both clinical research and
CC diagnostic tools. AAS29242-AAS29507 represent the human mdm2 antisense
CC oligonucleotides of the present invention
CC
SQ Sequence 20 BP; 5 A; 2 C; 10 G; 3 T; 0 U; 0 Other;
Query Match 1.9%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 536 TCCTGCTCAGCTCCCAA 554
DB 20 TCCTGCTCAGCTCCCAA 2
RESULT 674
AAD12408/c
ID AAD12408 standard; DNA; 20 BP.
AC AAD12408;
XX
XX 25-SEP-2001 (first entry)
DT
XX
DE Human caspase 8 mRNA antisense compound ISIS 107686.
XX
XX Caspase 8; infection; inflammation; tumour; research reagent; cytostatic;
KW gene therapy; antisense; human; phosphorothioate; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 2
FT /*tag= d
FT /mod_base= m5c
FT modified_base 4
FT /*tag= e
FT /mod_base= m5c
FT modified_base 5
FT /*tag= f
FT /mod_base= m5c
FT modified_base 7

KM	Human; inhibitor-kappa B- β ; I-kappaB; IKK β ; I-kappa-B-related; NFKB1L2;
KW	Ikappab r; antitense; immune response; infection; inflammation; therapy;
KN	tumour; prophylaxis; phosphorothioate; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
FH	
FT	Key
FT	modified_base
FT	1..20
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "Phosphorothioate backbone; All cytidine residues
FT	are 5-methylcytidines"
FT	1..5
FT	modified_base
FT	/tag= b
FT	/mod_base= OTHER
FT	/note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT	16..20
FT	/tag= c
FT	/mod_base= OTHER
FT	/note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX	
PN	WO2003042360-A2.
PD	
PD	22-MAY-2003.
XX	
PF	05-NOV-2002; 2002WO-US035597.
XX	
PR	13-NOV-2001; 2001US-00993731.
PA	(ISIS-) ISIS PHARM INC.
XX	
PI	Monia BP, Watt AT;
XX	
DR	WPI, 2003-468635/44.
XX	
PT	New antisense oligonucleotides targeted to nucleic acids encoding
PT	inhibitor-kappa B-R, useful for diagnosing or treating diseases
PT	associated with expression of inhibitor-kappa B-R, e.g., a heightened
PT	immune response or infection.
XX	
PS	Claim 3; Page 74; 108pp; English.
CC	The invention relates to antisense compounds targetted to a nucleic acid
CC	molecule encoding human inhibitor-kappa B-R (also known as I-kappaB α ,
CC	IKK α , I-kappa-B-related, ikappab r, nuclear factor of kappa light
CC	polypeptides gene enhancer in B-cells inhibitor-like 2 and NFkBIL2) to
CC	inhibit its expression. Antisense compounds of the invention are useful
CC	for treating diseases or conditions associated with the expression of
CC	inhibitor-kappa B-R such as a heightened immune response involving
CC	increased cytokine expression, or a result of infection (e.g. bacterial,
CC	viral or parasitic). They are useful for diagnostics, therapeutics,
CC	prophylaxis e.g. to prevent or delay infection, inflammation or tumour
CC	formation, as research reagents and kits and in distinguishing between
CC	functions of various members of a biological pathway. They are also
CC	useful in antisense therapy. The present sequence is an oligonucleotide
CC	targeted to human inhibitor-kappa B-R DNA
XX	
SQ	Sequence 20 BP; 4 A; 4 C; 9 G; 3 T; 0 U; 0 Other;
Query Match	1.9%; Score 19; DB 1; Length 20;
Best Local Similarity	100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	64S CAGCGTGGAGTGCACTGCGC 663
DB	1 CAGCGTGGAGTGCACTGCGC 19
RESULT 676	
ID ADC65799 standard; DNA; 20 BP.	
XX	

AC	AD65799;
XX	
DT	18-DEC-2003 (first entry)
XX	
DE	Human TGF-beta receptor II targeted antisense oligonucleotide #76.
XX	
KM	human; antisense oligonucleotide;
KM	transforming growth factor beta receptor II; TGF-beta receptor II;
KM	hyperproliferative disorder; breast cancer; autoimmune disorder;
KM	rheumatoid arthritis; 2'-O-methoxyethyl gapper;
XX	phosphorothioate backbone; ss.
OS	Homo sapiens.
XX	
PN	WO200300656-A2.
XX	
PD	03-JAN-2003.
XX	
XX	19-JUN-2002; 2002WO-US019665.
PF	
XX	
PR	21-JUN-2001; 2001US-00888361.
XX	
PA	(ISIS-) ISIS PHARM INC.
XX	
PI	Murray SF, Wyatt JR;
XX	
DR	WPI; 2003-175279/17.
XX	
PT	New compound having a sequence targeted to a nucleic acid encoding
PT	transforming growth factor beta receptor II, useful for preparing a
PT	composition for treating hyperproliferative disorder e.g., lung, liver,
PT	colon or gastric cancer.
XX	
PS	Example 15; SEQ ID NO 95; 141bp; English.
XX	
CC	The invention comprises antisense oligonucleotides that are targeted to
CC	the nucleic acid encoding transforming growth factor beta (TGF-beta)
CC	receptor II. The antisense oligonucleotides of the invention are useful
CC	for treating: hyperproliferative disorders (e.g. breast cancer), or an
CC	autoimmune disorder (e.g. rheumatoid arthritis). The present DNA sequence
CC	represents a 2'-O-methoxyethyl gapper oligonucleotide with a
CC	phosphorothioate backbone that is targeted to human TGF-beta receptor II.
XX	
SQ	Sequence 20 BP; 5 A; 9 C; 3 G; 3 T; 0 U; 0 Other;
XX	
Query Match	1.9%; Score 19; DB 1; Length 20;
Best Local Similarity	100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	541 CCTCAGCCTCCCAAGTAGC 559
DB	2 CCTCAGCCTCCCAAGTAGC 20
XX	
RESULT 77	
ID	ADD21685/c
XX	
AC	ADD21685 standard; DNA; 20 BP.
XX	
AD	ADD21685;
XX	
DT	15-JAN-2004 (first entry)
XX	
DE	Human mdm2 antisense oligonucleotide #248.
XX	
KM	antisense oligonucleotide; human; mdm2; hyperproliferation;
KM	hyperproliferative disorder; cancer; psoriasis; fibrosis;
KM	atherosclerosis; restenosis; apoptosis modulation; p21; ss;
KM	2'-methoxyethoxy-residue; phosphorothioate backbone.
XX	
OS	Homo sapiens.
XX	
PN	WO2003048315-A2.
XX	

```

XX 12-JUN-2003.
PD 12-JUN-2003.
PF 02-DEC-2002; 2002MO-US038281.
PR 02-DEC-2001; 2001US-00005344.
PA (ISIS-) ISIS PHARM INC.
XX Miraglia LJ, Nero PS, Graham MJ, Monia BP, Koller E, Chiang MY;
PI Manoharan M;
XX WPI; 2003-577263/54.
DR
XX
XX Novel antisense compound targeted to 5' untranslated region, coding
PT region, or intron:exon junction of nucleic acid molecule encoding mdm2,
PT useful for treating e.g. cancer, psoriasis or restenosis by inhibiting
PT mdm2 expression.
XX
XX Example 9; SEQ ID NO 250; 289pp; English.
XX
XX The invention comprises antisense oligonucleotides which are targeted to
CC the human mdm2 gene. The antisense oligonucleotides of the invention are
CC useful for reducing hyperproliferation of human cells. The antisense
CC oligonucleotides are also useful for treating: hyperproliferative
CC disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or
CC restenosis. The antisense oligonucleotides are also useful for modulating
CC apoptosis, and for increasing expression of p21. The present DNA sequence
CC represents a human mdm2 gene antisense oligonucleotide of the invention.
CC The present sequence contains 2'-methoxyethoxy-residues and has a
CC phosphorochioate backbone.
XX
XX Sequence 20 BP; 5 A; 2 C; 10 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.9%; Score 19; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+03;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX
XX 536 TCCTGCTCAGCCTCCCA 554
DB 20 TCCTGCTCAGCCTCCCA 2
XX
XX RESULT 678
XX ADD21678/C
XX ID ADD21678 standard; DNA; 20 BP.
XX
XX ADD21678;
XX AC
XX
XX 15-JAN-2004 (first entry)
XX
XX Human mdm2 antisense oligonucleotide #241.
XX
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW atherosclerosis; restenosis; apoptosis modulation; p21; se;
KW 2'-methoxyethoxy-residue; phosphorochioate backbone.
XX
XX Homo sapiens.
XX
XX WO2003048315-A2.
XX
XX 12-JUN-2003.
XX
XX 02-DEC-2002; 2002MO-US038281.
XX
XX 04-DEC-2001; 2001US-00005344.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Miraglia LJ, Nero PS, Graham MJ, Monia BP, Koller E, Chiang MY;
PI Manoharan M;
XX WPI; 2003-577263/54.
XX

```

XX Novel antisense compound targeted to 5' untranslated region, coding
PT region, or intron: exon junction of nucleic acid molecule encoding mdm2,
PT useful for treating e.g. cancer, psoriasis or restenosis by inhibiting
PT mdm2 expression.

PS Claim 4; SEQ ID NO 243; 289pp; English.

XX The invention comprises antisense oligonucleotides which are targeted to
CC the human mdm2 gene. The antisense oligonucleotides of the invention are
CC useful for reducing hyperproliferation of human cells. The antisense
CC oligonucleotides are also useful for treating: hyperproliferative
CC disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or
CC restenosis. The antisense oligonucleotides are also useful for modulating
CC apoptosis, and for increasing expression of p21. The present DNA sequence
CC represents a human mdm2 gene antisense oligonucleotide of the invention.
CC The present sequence contains 2'-methoxyethoxy-residues and has a
CC phosphorothioate backbone.

SQ Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 644 CCAGCTGAGTGCAGTGG 662
DB 20 CCAGCTGAGTGCAGTGG 2

RESULT 679
ADD25037/C
ID ADD25037 standard; DNA; 20 BP.

AC ADD25037;
XX 15-JAN-2004 (first entry)
DT
XX
XX Human caspase-8 antisense oligonucleotide ISIS 107686.
DE
XX
XX Caspase-8; cytostatic; immunosuppressant; anti-HIV; SBI;
KW antisense gene therapy; apoptosis; hyperproliferative disorder;
KW haematopoietic disorder; autoimmune disorder; viral infection; AIDS;
KW neurological disorder; Alzheimer's disease; Parkinson's disease;
KW amyotrophic lateral sclerosis; retinitis pigmentosa; blood cell disorder;
KW cancer; human.
XX
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 1. 20
FT modified_base /tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methylcytidines"
FT 1..5
FT modified_base /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
XX
XX US2003083296-A1.
PN
XX
XX 01-MAY-2003.
PD
XX
XX 12-JUL-2002; 2002US-00181177.
PF
XX 19-JAN-2000; 2000US-00487445.
PR
XX 11-JAN-2001; 2001WO-US000955.
XX

PA (ZHANG/) ZHANG H.
PA (COMS/) COMSERT L M.
XX
XX Zhang H, Cowseert LM;
PI WPI; 2003-810793/76.
DR
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding caspase 8, useful for treating a disease/condition
PT associated with caspase 8, such as hyperproliferative or autoimmune
PT disorders.

PS Example 15; SEQ ID NO 94; 59pp; English.

XX The invention relates to a compound 8-30 nucleobases in length targeted
CC to, and which specifically hybridises with a nucleic acid molecule
CC encoding caspase 8 (a protein involved in apoptosis) and inhibits the
CC expression of caspase 8, i.e. an antisense oligonucleotide. Also included
CC are a compound 8-30 nucleobases in length that specifically hybridises
CC with at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding caspase 8, a composition comprising the compound and a
CC carrier or diluent, inhibiting the expression of caspase 8 in cells or
CC tissues (by contacting the cells or tissues with the compound so that
CC expression of caspase 8 is inhibited) and treating an animal having a
CC disease or condition associated with caspase 8 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of caspase 8 is inhibited. The compound, composition and
CC methods are useful for treating a disease or condition associated with
CC caspase 8, such as hyperproliferative, haematopoietic or autoimmune
CC disorder, viral infection such as AIDS, neurological disorders (e.g.
CC Alzheimer's disease), Parkinson's disease, amyotrophic lateral sclerosis,
CC retinitis pigmentosa, blood cell disorders and cancer. They are also
CC useful in research and diagnostics for modulating the expression of
CC interleukin 8. The present sequence is a caspase-8 targeting antisense
CC oligonucleotide of the invention.

SQ Sequence 20 BP; 4 A; 10 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 646 AGGCTGAGTGCAGTGGCG 664
DB 20 AGGCTGAGTGCAGTGGCG 2

RESULT 680
AB297910
ID AB297910 standard; DNA; 20 BP.
XX
XX AB297910;
AC
XX
XX 17-OCT-2003 (first entry)
DT
XX
XX Human RANTES oligonucleotide sequence.
DE
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX
XX Homo sapiens.
OS
XX
XX WO200285308-A2.
PN
XX
XX 31-OCT-2002.
PD
XX
XX 23-APR-2002; 2002WO-US013135.
PF
XX 24-APR-2001; 2001US-0286137P.
PR
XX

XX 24-APR-2001; 2001US-0286036P.
PR
XX (EPIC-) EPIGENESIS PHARM INC.
PA
XX Nyce JW, Li Y, Sandraseagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shanabuddin S;
XX WPI; 2003-093058/08.
DR
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 13244; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 3 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 638 TGTCAACCCAGGCTGAGTG 656
2 TGTCAACCCAGGCTGAGTG 20
DB
RESULT 683
ABD30941
ID ABD30941 standard; DNA; 20 BP.
XX
AC ABD30941;
XX
DT 29-JUL-2004 (first entry)
XX
XX Human RANTES-derived oligonucleotide SEQ ID 13152.
DB
XX Human, antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
XX analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW

KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
XX WO200285309-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013143.
XX
XX 24-APR-2001; 2001US-0286036P.
XX
XX (EPIC-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandraseagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shanabuddin S;
XX WPI; 2003-093058/08.
DR
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 13152; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 728 GAGTAGCTGGAGCTACAG 746
2 GAGTAGCTGGAGCTACAG 20
DB
RESULT 684
ADU59867

ID ADJ59867 standard; DNA; 20 BP.
XX
AC ADJ59867;
XX
DT 06-MAY-2004 (first entry)
XX
DE Oligonucleotide associated to RANTES #116.
XX
XX Interleukin; IL-4 receptor; IL-5 receptor; lung disease;
KM airway inflammation; allergy; asthma; impeded respiration;
KM cystic fibrosis; acute respiratory distress syndrome;
KM pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
ss.
XX
OS Homo sapiens.
XX
PN MO2004011613-A2.
XX
PD 05-FEB-2004.
XX
PF 25-JUL-2003; 2003WO-US023509.
XX
PR 29-JUL-2002; 2002US-0399076P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Nlyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;
PI Shababuddin S, Lu H, Cong H;
DR WPI; 2004-203534/19.
XX
XX Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codons and introns of respiratory disease-relevant genes e.g.,
PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
PT disease e.g., asthma.
XX
PS Claim 2; SEQ ID NO 723; 85bp; English.
XX
XX The present invention relates to an oligonucleotide anti-sense to e.g.,
CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
CC end of nucleic acid target comprising gene(s) chosen from e.g.
CC Interleukin (IL)-4 receptor, IL-5 receptor or salts of the
CC oligonucleotide and optionally surfactant operatively linked to the
CC oligonucleotide. The method is useful for preventing or treating a
CC respiratory or lung disease, which involves administering to the airways
CC of a subject an effective amount of an inhibitor. The oligonucleotide is
CC useful for production of a medicament for the prevention and/or treatment
CC of a respiratory or lung disease. The respiratory or lung disease is
CC chosen from airway inflammation, allergy(ies), asthma, impeded
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
CC obstruction. The present sequence represents an oligonucleotide of the
CC invention.
XX
SQ Sequence 20 BP; 3 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 638 TGTCAACGAGCTGAGTG 656
DB 2 TGTCAACGAGCTGAGTG 20
XX
XX RESULT 685
ADJ59775
ID ADJ59775 standard; DNA; 20 BP.
XX
AC ADJ59775;
XX
DT 06-MAY-2004 (first entry)

XX
DE Oligonucleotide associated to RANTES #24.
XX
KM Interleukin; IL-4 receptor; IL-5 receptor; lung disease;
KM airway inflammation; allergy; asthma; impeded respiration;
KM cystic fibrosis; acute respiratory distress syndrome;
KM pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
ss.
XX
OS Homo sapiens.
XX
PN MO2004011613-A2.
XX
PD 05-FEB-2004.
XX
PF 25-JUL-2003; 2003WO-US023509.
XX
PR 29-JUL-2002; 2002US-0399076P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Nlyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;
PI Shababuddin S, Lu H, Cong H;
DR WPI; 2004-203534/19.
XX
XX Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codons and introns of respiratory disease-relevant genes e.g.,
PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
PT disease e.g., asthma.
XX
PS Claim 2; SEQ ID NO 631; 85bp; English.
XX
XX The present invention relates to an oligonucleotide anti-sense to e.g.,
CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
CC end of nucleic acid target comprising gene(s) chosen from e.g.
CC Interleukin (IL)-4 receptor, IL-5 receptor or salts of the
CC oligonucleotide and optionally surfactant operatively linked to the
CC oligonucleotide. The method is useful for preventing or treating a
CC respiratory or lung disease, which involves administering to the airways
CC of a subject an effective amount of an inhibitor. The oligonucleotide is
CC useful for production of a medicament for the prevention and/or treatment
CC of a respiratory or lung disease. The respiratory or lung disease is
CC chosen from airway inflammation, allergy(ies), asthma, impeded
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
CC obstruction. The present sequence represents an oligonucleotide of the
CC invention.
XX
SQ Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 728 GAGTAGCTGGAGCTACAGG 746
DB 2 GAGTAGCTGGAGCTACAGG 20
XX
XX RESULT 686
ADM14845/C
ID ADM14845 standard; DNA; 20 BP.
XX
AC ADM14845;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:1032.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
KM microsome1 prostaglandin B2 synthase; mPGEs-1; mPGEs-1 inhibitor;

KM microsome1 prostaglandin E2 synthase inhibitor; cyostatic; antidiabetic;
KM immunomodulator; cardiant; neuroprotective; antiinflammatory;
KM neuroprotective; nocotropic; antiarthritic; vasotropic; ophthalmological;
KM immunomodulatory; cardiovascular; gene therapy; inflammation;
KM Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KM reperfusion injury; ophthalmic disorder; immunological disorder;
KM cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX MPI; 2004-305094/28.
XX
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGEs-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
XX
XX Claim 4; SEQ ID NO 1032; 132bp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsome1 prostaglandin E2 synthase (mPGEs-1). The
CC human mPGEs-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGEs-1, which specifically hybridise with the nucleic acid mPGEs-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGEs-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGEs-1. mPGEs-1 chimeric
CC antisense oligonucleotides and antisense compounds have cyostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nocotropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGEs-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGEs-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 3 A; 6 C; 8 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.9%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No.12e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 846 GCCTCGGCTCCCAAGTG 864

Db 19 GCCTCGGCTCCCAAGTG 1
|||||
RESULT 687
ADM14508/C
ID ADM14508 standard; DNA; 20 BP.
XX
XX ADM14508;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:695.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsome1 prostaglandin E2 synthase inhibitor; mPGEs-1 inhibitor;
XX immunomodulator; cardiant; neuroprotective; antiinflammatory;
XX microsome1 prostaglandin E2 synthase inhibitor; cyostatic; antidiabetic;
XX neuroprotective; nocotropic; antiarthritic; vasotropic; ophthalmological;
XX immunomodulatory; cardiovascular; gene therapy; inflammation;
XX Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
XX reperfusion injury; ophthalmic disorder; immunological disorder;
XX cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX MPI; 2004-305094/28.
XX
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGEs-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
XX
XX Claim 4; SEQ ID NO 695; 132bp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsome1 prostaglandin E2 synthase (mPGEs-1). The
CC human mPGEs-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGEs-1, which specifically hybridise with the nucleic acid mPGEs-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGEs-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGEs-1. mPGEs-1 chimeric
CC antisense oligonucleotides and antisense compounds have cyostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nocotropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGEs-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGEs-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.

PT	encoding mpGS-1, useful for preparing a composition for treating e.g.,
PT	inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT	ischemia.
PS	Claim 4; SEQ ID NO 1543; 132dp; English.
XX	
CC	The present sequence represents a chimeric antisense oligonucleotide
CC	targeted to human microsomal prostaglandin E2 synthase (mpGS-1). The
CC	human mpGS-1 gene is located on chromosome 9, more specifically to
CC	9q34.3. The present invention also describes: (1) antisense compounds;
CC	having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC	mpGS-1, which specifically hybridize with the nucleic acid mpGS-1 and
CC	inhibits its expression; (2) a method of inhibiting the expression of
CC	mpGS-1 in cells or tissues; and (3) a method of treating an animal
CC	having a disease or condition associated with mpGS-1. mpGS-1 chimeric
CC	antisense oligonucleotides and antisense compounds have cytostatic,
CC	antidiabetic, immunomodulator, cardiac, neuroprotective,
CC	antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC	ophthalmological, immunomodulatory and in gene therapy. The antisense compound
CC	can be used for preparing a composition for treating a disease or
CC	condition associated with mpGS-1 e.g., inflammation, Alzheimer's
CC	disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
CC	ophthalmic, immunological, cardiovascular or neurological disorder.
XX	
XX	Sequence 20 BP; 5 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
QY	
DB	719 CAGCCTCTGTAGTACCTGG 737
	19 CAGCCTCTGTAGTACCTGG 1
RESULT 689	
ADMI5012/C	
ID	ADMI5012 standard; DNA; 20 BP.
XX	
AC	ADMI5012;
XX	
DT	01-JUL-2004 (first entry)
XX	
DE	Human mpGS-1 chimeric antisense oligonucleotide SEQ ID NO:1199.
XX	
KW	chimeric; antisense oligonucleotide; phosphorothioate; human;
KW	microsomal prostaglandin E2 synthase; mpGS-1; mpGS-1 inhibitor;
KW	microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW	immunomodulator; cardiac; neuroprotective; antiinflammatory;
KW	neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW	immunomodulatory; cardiovascular; gene therapy; inflammation;
KW	Alzheimer's disease; arthritis; diabetes; cancer; ischemia;
KW	reperfusion injury; ophthalmic disorder; immunological disorder;
KW	cardiovascular disorder; neurological disorder; ss.
OS	Homo sapiens.
OS	Synthetic.
XX	
PH	Key
FT	Location/Qualifiers
FT	1..20
FT	/*tag= b
FT	/mod_base= OTHER
FT	residues are 5-methylcytidines"
FT	1..5
FT	/*tag= a
FT	/mod_base= OTHER
FT	/note= "2'-O-methoxyethyls"
FT	16..20
FT	/*tag= C
FT	/mod_base= OTHER
FT	/note= "2'-O-methoxyethyls"

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XX XX WO2004028458-A2.
XX PN
XX XX 08-APR-2004.
XX PD
XX XX 25-SEP-2003; 2003WO-US030374.
XX PF
XX XX 25-SEP-2002; 2002US-0413549P.
XX PR
XX XX (PHAA ) PHARMACIA CORP.
XX PA
XX XX Gierse JK;
XX PT
XX DR WPI; 2004-305094/28.
XX XX
XX PT New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX PT ischemia.
XX XX
XX PS Claim 4; SEQ ID NO 1199; 132pp; English.
XX XX
XX CC The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulatory, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX CC
XX SQ Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 19; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+03;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 721 GCTCTCTGAGTAGCTGGGA 739
XX |||||
XX DB 20 GCCTCTCTGAGTAGCTGGGA 2
XX
XX RESULT 690
XX ADM15357/C
XX ID ADM15357 standard; DNA; 20 BP.
XX XX
XX AC ADM15357;
XX XX
XX DT 01-JUL-2004 (first entry)
XX XX
XX DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1544.
XX XX
XX XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microosomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
XX microosomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
XX immunomodulatory; cardiant; neuroprotective; antiinflammatory;
XX neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
XX immunomodulatory; cardiovascular; gene therapy; inflammation;
XX Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
XX reperfusion injury; ophthalmic disorder; immunological disorder;
XX cardiovascular disorder; neurological disorder; ss.
XX KW
XX OS Homo sapiens.

```

```

OS Synthetic.
XX XX Location/Qualifiers
XX PH Key modified_base 1..20
XX FT modified_base 1..20
XX FT
XX FT /tag= b
XX FT /mod_base= OTHER
XX FT /note= "phosphorothioate linkages and all cytidine
XX FT residues are 5-methylcytidines"
XX FT modified_base 1..5
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "2'-O-methoxyethyls"
XX FT modified_base 16..20
XX FT /tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-O-methoxyethyls"
XX XX
XX PN WO2004028458-A2.
XX XX
XX PD 08-APR-2004.
XX XX
XX PF 25-SEP-2003; 2003WO-US030374.
XX XX
XX PR 25-SEP-2002; 2002US-0413549P.
XX XX
XX PA (PHAA ) PHARMACIA CORP.
XX XX
XX PT Gierse JK;
XX PT
XX DR WPI; 2004-305094/28.
XX XX
XX PT New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX PT ischemia.
XX XX
XX PS Claim 4; SEQ ID NO 1544; 132pp; English.
XX XX
XX CC The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulatory, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX CC
XX SQ Sequence 20 BP; 12 A; 3 C; 0 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 19; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+03;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 769 TTTTGTATTTTGTAGTACA 787
XX |||||
XX DB 19 TTTTGTATTTTGTAGTACA 1
XX
XX RESULT 691
XX ADM15184/C
XX ID ADM15184 standard; DNA; 20 BP.
XX XX
XX AC ADM15184;

```

XX 01-JUL-2004 (first entry)
 DT Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:1371.
 DE
 XX chimeric; antisense oligonucleotide; phosphorothioate; human;
 KM microsome prostaglandin E2 synthase; mPGEs-1; mPGEs-1 inhibitor;
 KM microsome prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
 KM immunomodulator; cardiant; neuroprotective; antiinflammatory;
 KM neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;
 KM immunomodulatory; cardiovascular; gene therapy; inflammation;
 KM Alzheimer's disease; arthritis; diabetes; cancer; ischemia;
 KM reperfusion injury; ophthalmic disorder; immunological disorder;
 KM cardiovascular disorder; neurological disorder; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= b
 FT /note= "phosphorothioate linkages and all cytidine
 FT residues are 5-methylcytidines"
 FT modified_base 1..5
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyls"
 FT modified_base 15..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyls"
 XX
 XX WO2004028458-A2.
 XX
 XX 08-APR-2004.
 XX
 XX 25-SEP-2003; 2003WO-US030374.
 XX
 XX 25-SEP-2002; 2002US-0413549P.
 XX
 XX (PHAA) PHARMACIA CORP.
 XX
 XX Gierse JK;
 XX WPI; 2004-305094/28.
 XX
 XX New antisense compound, having a sequence targeted to a nucleic acid
 PT encoding mPGEs-1, useful for preparing a composition for treating e.g.,
 PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
 PT ischemia.
 XX
 XX Claim 4; SEQ ID NO 1371; 132PP; English.
 XX
 XX The present sequence represents a chimeric antisense oligonucleotide
 CC targeted to human microsome prostaglandin E2 synthase (mPGEs-1). The
 CC human mPGEs-1 gene is located on chromosome 9, more specifically to
 CC 9p34.3. The present invention also describes: (1) antisense compounds,
 CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
 CC mPGEs-1, which specifically hybridize with the nucleic acid mPGEs-1 and
 CC inhibits its expression; (2) a method of inhibiting the expression of
 CC mPGEs-1 in cells or tissues; and (3) a method of treating an animal
 CC having a disease or condition associated with mPGEs-1. mPGEs-1 chimeric
 CC antisense oligonucleotides and antisense compounds have cytosolic,
 CC antidiabetic, immunomodulator, cardiant, neuroprotective,
 CC antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,
 CC ophthalmological, immunomodulatory and cardiovascular activities, and can
 CC be used as mPGEs-1 inhibitors and in gene therapy. The antisense compound
 CC can be used for preparing a composition for treating a disease or
 CC condition associated with mPGEs-1 e.g., inflammation, Alzheimer's
 CC disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
 CC ophthalmic, immunological, cardiovascular or neurological disorder.
 CC

Sequence 20 BP; 10 A; 4 C; 1 G; 5 T; 0 U; 0 Other;
 Query Match 1.9%; Score 19; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 771 TTTGATTTTTGTAGTACAGA 789
 Db 20 TTTGATTTTTGTAGTACAGA 2
 RESULT 692
 ID ADO45265
 AC ADO45265 standard; DNA; 20 BP.
 XX
 XX ADO45265;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 XX Human oligonucleotide #631.
 DE
 XX Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
 KM CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
 KM tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
 KM lung disease; hyper-responsiveness; adenosis; adenosis A receptor;
 KM asthma; lung allergy; inflammation; inflammatory disease; cystic fibrosis; CF;
 KM airway inflammation; allergy; impeded respiration; allergic rhinitis;
 KM chronic obstructive pulmonary disease; COPD; allergic rhinitis;
 KM acute respiratory distress syndrome; pulmonary hypertension;
 KM lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
 XX
 XX Homo sapiens.
 OS
 OS US2004049022-A1.
 XX
 XX 11-MAR-2004.
 XX
 XX 25-JUL-2003; 2003US-00627930.
 XX
 XX 23-APR-2002; 2002WO-US013135.
 XX
 XX 23-APR-2002; 2002WO-US013143.
 XX
 XX (NYCE/) NYCE J W.
 XX (SAND/) SANDRASAGRA A.
 XX (TANG/) TANG L.
 XX (AGUI/) AGUILAR D.
 XX (MILL/) MILLER S.
 XX (SHAH/) SHAHABUDDIN S.
 XX (LUHH/) LU H.
 XX (CONG/) CONG H.
 XX
 XX Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S,
 PI Shahabuddin S, Lu H, Cong H;
 XX WPI; 2004-293804/27.
 XX
 XX Novel single or multiple target oligonucleotide anti-sense to e.g.
 PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
 PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
 PT asthma.
 XX
 XX Claim 2; SEQ ID NO 631; 174PP; English.
 XX
 XX The invention relates to oligonucleotides anti-sense to an initiation
 CC codon, coding region, 5' or 3' intron-exon junction, intron or region
 CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
 CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
 CC -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
 CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
 CC also relates to a method of screening a candidate compound that binds to
 CC one or more nucleic acid target(s) or expressed product(s), for the
 CC prevention and/or treatment of a respiratory or lung disease. The
 CC oligonucleotides are useful for reducing or inhibiting expression of a

CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
 CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
 CC tryptase b, PDB4 A, PDB4 B, PDB4 C, or PDB4 D. The oligonucleotides are
 CC useful for preventing or treating a respiratory or lung disease. The
 CC receptor or lung disease is associated with hyper-responsiveness to
 CC and/or increased levels of, adenosine and/or levels of adenosine A
 CC receptor(s), and/or asthma and/or lung allergies associated with
 CC inflammation or an inflammatory disease. The respiratory or lung disease
 CC is chosen from allergy inflammation, allergy, asthma, impeded respiration,
 CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
 CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
 CC hypertension, lung inflammation, bronchitis, airway obstruction or
 CC bronchoconstriction. This sequence represents an oligonucleotide of the
 CC invention.

CC Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

CC Query Match 1.9%; Score 19; DB 1; Length 20;

CC Best Local Similarity 100.0%; Pred. No. 1.2e+03;

CC Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Db 728 GAGTAGCTGGGACTACAGG 746

2 GAGTAGCTGGGACTACAGG 20

CC RESULT 693

CC ADO45357

CC ID ADO45357 standard; DNA; 20 BP.

CC AC ADO45357;

CC DT 15-JUL-2004 (first entry)

CC DE Human oligonucleotide #723.

XX Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
 XX CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
 XX tryptase b; PDB4 A; PDB4 B; PDB4 C; PDB4 D; respiratory disease;
 XX lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
 XX asthma; lung allergy; inflammation; inflammatory disease;
 XX airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
 XX chronic obstructive pulmonary disease; COPD; allergic rhinitis;
 XX acute respiratory distress syndrome; pulmonary hypertension;
 XX lung inflammation; bronchitis; airway obstruction; bronchoconstriction.

XX Homo sapiens.

XX OS US2004049022-A1.

XX PN 11-MAR-2004.

XX PD 25-JUL-2003; 2003US-00627930.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 23-APR-2002; 2002WO-US013143.

XX PA (NYCE/) NYCE J W.

XX PA (SAND/) SANDRASAGRA A.

XX PA (TANG/) TANG L.

XX PA (AGUI/) AGUILAR D.

XX PA (MILL/) MILLER S.

XX PA (SHAH/) SHAHABUDDIN S.

XX PA (LUHR/) LU H.

XX PA (CONG/) CONG H.

XX PI NYCE JW, Sandrasagra A, Tang L, Aguilar D, Miller S;

XX PI Shahabuddin S, Lu H, Cong H;

XX DR WPI; 2004-293804/27.

XX PT Novel single or multiple target oligonucleotide anti-sense to e.g.

PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,

PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.

PT asthma.

PS Claim 2; SEQ ID NO 723; 174bp; English.

XX The invention relates to oligonucleotides anti-sense to an initiation
 CC codon, coding region, 5' or 3' intron-exon junction, intron or region
 CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
 CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)-
 CC 5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
 CC tryptase a, tryptase b, PDB4 A, PDB4 B, PDB4 C or PDB4 D. The invention
 CC also relates to a method of screening a candidate compound that binds to
 CC one or more nucleic acid target(s) or expressed product(s), for the
 CC prevention and/or treatment of a respiratory or lung disease. The
 CC oligonucleotides are useful for reducing or inhibiting expression of a
 CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
 CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
 CC tryptase b, PDB4 A, PDB4 B, PDB4 C, or PDB4 D. The oligonucleotides are
 CC useful for preventing or treating a respiratory or lung disease. The
 CC receptor or lung disease is associated with hyper-responsiveness to
 CC and/or increased levels of, adenosine and/or levels of adenosine A
 CC receptor(s), and/or asthma and/or lung allergies associated with
 CC inflammation or an inflammatory disease. The respiratory or lung disease
 CC is chosen from allergy inflammation, allergy, asthma, impeded respiration,
 CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
 CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
 CC hypertension, lung inflammation, bronchitis, airway obstruction or
 CC bronchoconstriction. This sequence represents an oligonucleotide of the
 CC invention.

CC Sequence 20 BP; 3 A; 5 C; 7 G; 5 T; 0 U; 0 Other;

CC Query Match 1.9%; Score 19; DB 1; Length 20;

CC Best Local Similarity 100.0%; Pred. No. 1.2e+03;

CC Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Db 638 TGTACCCAGCGCTGAGTG 656

2 TGTACCCAGCGCTGAGTG 20

CC RESULT 694

CC ADO45357

CC ID ADO45357 standard; DNA; 20 BP.

CC AC ADO45357;

CC DT 26-AUG-2004 (first entry)

CC DE Extend primer 53 used to genotype human glycoprotein VI polymorphism.

XX breast cancer; cytotoxic; gene therapy; human; platelet glycoprotein VI;

XX G6; GPIV; GPIV; chromosome 19q13.4; ss; PCR; primer; SNP;

XX single nucleotide polymorphism.

XX Homo sapiens.

XX OS WO2004047767-A2.

XX PN 10-JUN-2004.

XX PD 25-NOV-2003; 2003WO-US037966.

XX PF 25-NOV-2002; 2002US-0429136P.

XX PR 24-JUL-2003; 2003US-0490234P.

XX PA (SEOU-) SEQUENOM INC.

XX PA Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;

XX DR WPI; 2004-441082/41.

XX PT Identifying a subject at risk of breast cancer by detecting the presence

PT or absence of one or more nucleotide polymorphic variations, useful for
PT diagnosing, preventing and/or treating breast cancer.
XX
XX
PS Example 3; Page 83; 286pp; English.
XX
CC The invention relates to a novel method for identifying a subject at risk
CC of breast cancer which comprises detecting the presence or absence of one
CC or more polymorphic variations associated with breast cancer in a nucleic
CC acid sample from a subject. The method of the invention has cytostatic
CC applications and may be useful for identifying a risk of breast cancer,
CC as well as therapeutic and prophylactic treatments that specifically
CC target breast cancer, such as gene therapy. The current sequence is that
CC of an extend primer of the invention which was used to genotype single
CC nucleotide polymorphisms within human glycoprotein VI (platelet) (GPI;
CC GPIV/GPIIb) DNA which is located at chromosomal position 19q13.4.
XX
XX
SQ Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 719 CAGCCTCCGAGTACCTGG 737
DB 2 CAGCCTCCGAGTACCTGG 20

RESULT 695
ADG30202/C
ID ADG30202 standard; RNA; 21 BP.
XX
AC ADG30202;
XX
DT 26-FEB-2004 (first entry)
XX
DE PKR-targeted siNA DNA-RNA hybrid - SEQ ID 768.
XX
XX double-stranded short interfering nucleic acid; siNA;
KM antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KM anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KM Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KM amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; PKR.
XX
OS Unidentified.
OS Synthetic.
XX
XX WO2003074654-A2.
XX
XX 12-SEP-2003.
XX
XX 20-FEB-2003; 2003WO-US005028.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 06-JUN-2002; 2002US-036782P.
XX 29-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409293P.
XX 15-JAN-2003; 2003US-0440129P.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX McSwiggen J, Beigelman L, Chowrira B, Pavco P, Fonaugh K;
PI Jamison S, Usman N, Thompson J;
XX
XX WPI; 2003-731676/69.
XX
XX New double-stranded short interfering nucleic acid molecule, useful for
XX down-regulating the expression of an endogenous mammalian target gene or
XX for treating diseases that respond to modulation of gene expression or
XX activity.
XX
XX Example 24; SEQ ID NO 768; 593pp; English.
PS

XX
CC The invention relates to a double-stranded short interfering nucleic acid
CC (siNA) molecule that down-regulates expression of an endogenous mammalian
CC target gene comprising one or more chemical modifications and each strand
CC of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC the invention demonstrates antiarteriosclerotic, neuroprotective,
CC nootropic, antiparkinsonian and anticonvulsant activities and may be
CC useful for down-regulating the expression of an endogenous mammalian
CC target gene and therefore in the treatment of any disease or condition
CC that responds to modulation of gene expression or activity in a cell.
CC tissue or organism. The disease or condition may include pulmonary
CC diseases such as restenosis, atherosclerosis, Alzheimer's disease, or
CC Parkinson's disease, epilepsy, dementia, huntington's disease or
CC amyotrophic lateral sclerosis. Furthermore, the siNA may be utilized for
CC gene therapy applications. The current sequence is that of the siNA DNA-
CC RNA hybrid of the invention.
XX
XX
SQ Sequence 21 BP; 5 A; 3 C; 7 G; 2 T; 4 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1117 GGTCTCAACTCCTGACCT 1135
DB 19 GGTCTCAACTCCTGACCT 1

RESULT 696
ADL25334/C
ID ADL25334 standard; DNA; 21 BP.
XX
XX ADL25334;
XX
XX 20-MAY-2004 (first entry)
XX
XX Intestinal epithelium/peyer's patch M cell-associated PCR primer #479.
XX
XX Intestinal epithelium cell development; peyer's patch M cell development;
KM inflammatory bowel disease; glutenenteropathy; infectious disease;
KM autoimmune disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;
KM Grave's disease; multiple sclerosis; allergy; asthma; diabetic mellitus;
KM immune system disorder; hypersensitivity; anaphylaxis;
KM blood group incompatibility; ss; PCR; primer.
XX
XX Macaca fascicularis.
XX
XX WO200280852-A2.
XX
XX 17-OCT-2002.
XX
XX 04-APR-2002; 2002WO-US010873.
XX
XX 04-APR-2001; 2001US-028146P.
XX
XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
XX Brayden DJ, Byrne D, O'mahony DJ, Evans CF, Mah SP, Lo DD;
PI WPI; 2003-075470/07.
XX
XX Novel isolated or purified polypeptide encoded by genes associated with
XX intestinal epithelium or M cell development, differentiation or function,
XX useful for treating autoimmune diseases and infectious diseases.
XX
XX Disclosure; SEQ ID NO 844; 152pp; English.
XX
XX The invention comprises DNA sequences which are associated with
XX intestinal epithelium and peyer's patch M cells. The DNA sequences of the
XX invention are useful for assessing, modifying, modulating or regulating
XX intestinal epithelium or M cell development. The DNA sequences of the
XX invention are also useful in the treatment of: inflammatory bowel
XX disease, glutenenteropathy, infectious diseases, autoimmune diseases
XX

CC (e.g. haemolytic anaemia, rheumatoid arthritis, dermatitis, Grave's
 CC disease, multiple sclerosis, allergy, asthma and diabetic mellitus),
 CC diseases or disorders of the immune system, hypersensitivity,
 CC anaphylaxis, and blood group incompatibility. The present DNA sequence
 CC represents a PCR primer that was used to amplify an intestinal
 CC epithelium/peyer's patch M cell-associated DNA sequence of the invention.

Query Match	1.9%	Score 19	DB 1	Length 21
Best Local Similarity	100.0%	Pred. No.	1.3e+03	
Matches 19, Conservative	0	Mismatches	0	Gaps 0

QY 1008 TTCTCCTGTCAGCCTCC 1026
|||||
Db 21 TTCTCCTGTCAGCCTCC 3

RESULT 697
AAZ25166
ID AAZ25166 standard; DNA; 22 BP.

AC	AAZ25166;
XX	
DT	13-DEC-1999 (first entry)

DE Human short interspersed repetitive element PCR primer #24.

KM Human, short interspersed repetitive element; SINE; PCR; primer;
KM Oncorhynchus; restriction primer; short interspersed repeated sequence;
KW eukaryote; restricted polymerase chain reaction fingerprinting;
KM identification; DNA specimen; discrimination; ss.

OS Synthetic.
OS Homo sapiens.

PN JP2913035-B1.

PD 28-JUN-1999.

PF 10-JUL-1998; 98JP-00195692.

PR 10-JUL-1998; 98JP-00195692.

PA (NORQ) NORINSUISANSHO SUI SANCHO YOSHOKU KENKYUSHOCHO .

DR WPI; 1999-583348/50.

PT Restriction primer for distinguishing individuals with short interspersed
PT repeated sequence of eukaryotes by restricted polymerase chain reaction
PT fingerprinting.

PS Claim 6; Page 4; 17pp; Japanese.

The present invention describes a restriction primer for eukaryotic short interspersed repeated sequences (SINE), which has one or more additional bases that are a mismatch to, or are unrelated to, the 3'-terminal end of the SINE. The annealing temperature of the primer to the DNA sequence is kept higher than the fusion temperature of the primer during polymerase chain reaction (PCR). The PCR fragments obtained are subjected to electrophoresis to obtain a fingerprint. By comparing the polymorphs from the electrophoresis band pattern, eukaryotic individuals are distinguished. The primer is used for amplifying a eukaryotic deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by polymerase chain reaction (PCR) fingerprinting. In particular it may be used individual identification of humans for medical and legal applications and ecological studies. DNA specimens in traces (approximately 10 ng in mass) can be used for individual discrimination of eukaryotes using the primer in a polymerase chain reaction (PCR). AA255143 to AA255191 represent specifically claimed examples of primers from the present invention

Sequence 22 BP; 5 A; 6 C; 8 G; 3 T; 0 U; 0 Other;

Query Match	1.9%	Score 19	DB 1	Length 22
Similarity	100.0%	Pred. No.	1.3e+03	
Best Local				
Matches 19	0	Mismatches	0	Indels 0
Conservative				Gaps 0

QY 869 GATTACAGGCGTGAGCCAC 887
|||
Db 1 GATTACAGGCGTGAGCCAC 19

RESULT 698
AAZ25157
ID AAZ25157 standard; DNA; 22 BP.

AC AA225157;

DT	13-DEC-1999 (first entry)
XX	
DE	Human short interspersed repetitive element PCR primer #15.

KM Human, short interspersed repetitive element; SINE, PCR, primer;
 KM Oenochrychus; restriction primer; short interspersed repeated sequence;
 KM eukaryote; restricted polymerase chain reaction fingerprinting;
 KM identification; DNA specimen; discrimination; ss.

OS Synthetic.
OS Homo sapiens.

PN JP2913035-B1.

PD 28-JUN-1999

PF 10-JUL-1998; 98JP-00195692.

PR 10-JUL-1998; 98JP-00195692.

PA (NORQ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO

DR WPT; 1999-583348/50.

PT Restriction primer for distinguishing individuals with short interspersed repeated sequence of eukaryotes by restricted polymerase chain reaction fingerprinting.

PS Claim 6; Page 3; 17pp; Japanese.

The present invention describes a restriction primer for eukaryotic short interspersed repeated sequences (SINE), which has one or more additional bases that are a mismatch to, or are unrelated to, the 3'-terminal end of the SINE. The annealing temperature of the primer to the DNA sequence is kept higher than the fusion temperature of the primer during polymerase chain reaction (PCR). The PCR fragments obtained are subjected to electrophoresis to obtain a fingerprint. By comparing the polymorphs from the electrophoresis band pattern, eukaryotic individuals are distinguished. The primer is used for amplifying a eukaryotic deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by polymerase chain reaction (PCR) fingerprinting. In particular it may be used for individual identification of humans for medical and legal applications and ecological studies. DNA specimens in traces (approximately 10 ng in mass) can be used for individual discrimination of eukaryotes using the primer in a polymerase chain reaction (PCR). AA251513 to AA251591 represent specifically claimed examples of primers from the present invention

SQ Sequence 22 BP; 7 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match	1.9%	Score 19;	DB 1;	Length 22;
Best Lcbal Similarity	100.0%;	Pred. No. 1.3e+03;		
Matches 19, Conservative	0;	Mismatches	0;	Gaps 0

QY 869 GATTACAGGCGTGAGCCAC 887
|||||
Db 1 GATTACAGGCGTGAGCCAC 19


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RESULT 699
AAZ25158
ID AAZ25158 standard; DNA; 22 BP.
XX
XX
AC AAZ25158;
XX
XX 13-DEC-1999 (first entry)
XX
DE Human short interspersed repetitive element PCR primer #16.
XX
XX Human; short interspersed repetitive element; SINE; PCR; primer;
XX Oncohychnus; restriction primer; short interspersed repeated sequence;
XX eukaryote; restricted polymerase chain reaction fingerprinting;
XX identification; DNA specimen; discrimination; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX JP2913035-B1.
XX
XX 28-JUN-1999.
XX
XX 10-JUL-1998; 98JP-00195692.
XX
XX 10-JUL-1998; 98JP-00195692.
XX
XX (NORQ ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.
XX
XX WPI; 1999-583348/50.
XX
XX Restriction primer for distinguishing individuals with short interspersed
XX repeated sequence of eukaryotes by restricted polymerase chain reaction
XX fingerprinting.
XX
XX Claim 6; Page 3; 17pp; Japanese.
XX
XX The present invention describes a restriction primer for eukaryotic short
XX interspersed repeated sequences (SINE), which has one or more additional
XX bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
XX the SINE. The annealing temperature of the primer to the DNA sequence is
XX kept higher than the fusion temperature of the primer during polymerase
XX chain reaction (PCR). The PCR fragments obtained are subjected to
XX electrophoresis to obtain a fingerprint. By comparing the polymorphs from
XX the electrophoresis band pattern, eukaryotic individuals are
XX distinguished. The primer is used for amplifying a eukaryotic
XX deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
XX polymerase chain reaction (PCR) fingerprinting. In particular it may be
XX used individual identification of humans for medical and legal
XX applications and ecological studies. DNA specimens in traces
XX (approximately 10 ng in mass) can be used for individual discrimination
XX of eukaryotes using the primer in a polymerase chain reaction (PCR).
XX AAZ25143 to AAZ25191 represent specifically claimed examples of primers
XX from the present invention
XX
XX Sequence 22 BP; 6 A; 5 C; 7 G; 4 T; 0 U; 0 Other:
XX
Query Match 1.9%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 869 GATTACAGGCGGTGAGCCAC 887
DB 1 GATTACAGGCGGTGAGCCAC 19

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DT 13-DEC-1999 (first entry)
XX
XX Human short interspersed repetitive element PCR primer #28.
XX
XX Human; short interspersed repetitive element; SINE; PCR; primer;
XX Oncohychnus; restriction primer; short interspersed repeated sequence;
XX eukaryote; restricted polymerase chain reaction fingerprinting;
XX identification; DNA specimen; discrimination; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX JP2913035-B1.
XX
XX 28-JUN-1999.
XX
XX 10-JUL-1998; 98JP-00195692.
XX
XX 10-JUL-1998; 98JP-00195692.
XX
XX 10-JUL-1998; 98JP-00195692.
XX
XX (NORQ ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.
XX
XX WPI; 1999-583348/50.
XX
XX Restriction primer for distinguishing individuals with short interspersed
XX repeated sequence of eukaryotes by restricted polymerase chain reaction
XX fingerprinting.
XX
XX Claim 6; Page 4; 17pp; Japanese.
XX
XX The present invention describes a restriction primer for eukaryotic short
XX interspersed repeated sequences (SINE), which has one or more additional
XX bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
XX the SINE. The annealing temperature of the primer to the DNA sequence is
XX kept higher than the fusion temperature of the primer during polymerase
XX chain reaction (PCR). The PCR fragments obtained are subjected to
XX electrophoresis to obtain a fingerprint. By comparing the polymorphs from
XX the electrophoresis band pattern, eukaryotic individuals are
XX distinguished. The primer is used for amplifying a eukaryotic
XX deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
XX polymerase chain reaction (PCR) fingerprinting. In particular it may be
XX used individual identification of humans for medical and legal
XX applications and ecological studies. DNA specimens in traces
XX (approximately 10 ng in mass) can be used for individual discrimination
XX of eukaryotes using the primer in a polymerase chain reaction (PCR).
XX AAZ25143 to AAZ25191 represent specifically claimed examples of primers
XX from the present invention
XX
XX Sequence 22 BP; 5 A; 5 C; 7 G; 5 T; 0 U; 0 Other:
XX
QY 869 GATTACAGGCGGTGAGCCAC 887
DB 1 GATTACAGGCGGTGAGCCAC 19

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RESULT 701
AAZ25172
ID AAZ25172 standard; DNA; 22 BP.
XX
XX
AC AAZ25172;
XX
XX 13-DEC-1999 (first entry)
XX
XX Human short interspersed repetitive element PCR primer #30.
XX
XX Human; short interspersed repetitive element; SINE; PCR; primer;
XX Oncohychnus; restriction primer; short interspersed repeated sequence;
XX eukaryote; restricted polymerase chain reaction fingerprinting;
XX identification; DNA specimen; discrimination; ss.

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XX OS Synthetic.
XX OS Homo sapiens.
XX XX JP2913035-B1.
XX XX 28-JUN-1999.
XX XX 10-JUL-1998; 98JP-00195692.
XX PF 10-JUL-1998; 98JP-00195692.
XX PR 10-JUL-1998; 98JP-00195692.
XX PA (NORO ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.
XX XX WPI; 1999-583348/50.
XX DR Restriction primer for distinguishing individuals with short interspersed
XX PT repeated sequence of eukaryotes by restricted polymerase chain reaction
XX PT fingerprinting.
XX PS Claim 6; Page 4; 17pp; Japanese.
XX XX The present invention describes a restriction primer for eukaryotic short
XX CC interspersed repeated sequences (SINE), which has one or more additional
XX CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
XX CC the SINE. The annealing temperature of the primer to the DNA sequence is
XX CC kept higher than the fusion temperature of the primer during polymerase
XX CC chain reaction (PCR). The PCR fragments obtained are subjected to
XX CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from
XX CC the electrophoresis band pattern, eukaryotic individuals are
XX CC distinguished. The primer is used for amplifying a eukaryotic
XX CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
XX CC polymerase chain reaction (PCR) fingerprinting. In particular it may be
XX CC used individual identification of humans for medical and legal
XX CC applications and ecological studies. DNA specimens in traces
XX CC (approximately 10 ng in mass) can be used for individual discrimination
XX CC of eukaryotes using the primer in a polymerase chain reaction (PCR).
XX CC AA25143 to AA25191 represent specifically claimed examples of primers
XX CC from the present invention
XX SQ Sequence 22 BP; 6 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 869 GATTACAGCGGTGAGCCAC 887
DB 1 GATTACAGCGGTGAGCCAC 19

RESULT 702
AA25159
ID AA25159 standard; DNA; 22 BP.
XX AC AA25159;
XX AC
XX DT 13-DEC-1999 (first entry)
XX DE Human short interspersed repetitive element PCR primer #17.
XX XX Human; short interspersed repetitive element; SINE; PCR; primer;
XX KW Oncorhynchus; restriction primer; short interspersed repeated sequence;
XX KW eukaryote; restricted polymerase chain reaction fingerprinting;
XX KW identification; DNA specimen; discrimination; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN JP2913035-B1.
XX PD 28-JUN-1999.
XX DR
XX XX

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PF 10-JUL-1998; 98JP-00195692.
XX XX 10-JUL-1998; 98JP-00195692.
XX PR (NORO ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.
XX XX WPI; 1999-583348/50.
XX DR Restriction primer for distinguishing individuals with short interspersed
XX PT repeated sequence of eukaryotes by restricted polymerase chain reaction
XX PT fingerprinting.
XX PS Claim 6; Page 3; 17pp; Japanese.
XX XX The present invention describes a restriction primer for eukaryotic short
XX CC interspersed repeated sequences (SINE), which has one or more additional
XX CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
XX CC the SINE. The annealing temperature of the primer to the DNA sequence is
XX CC kept higher than the fusion temperature of the primer during polymerase
XX CC chain reaction (PCR). The PCR fragments obtained are subjected to
XX CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from
XX CC the electrophoresis band pattern, eukaryotic individuals are
XX CC distinguished. The primer is used for amplifying a eukaryotic
XX CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
XX CC polymerase chain reaction (PCR) fingerprinting. In particular it may be
XX CC used individual identification of humans for medical and legal
XX CC applications and ecological studies. DNA specimens in traces
XX CC (approximately 10 ng in mass) can be used for individual discrimination
XX CC of eukaryotes using the primer in a polymerase chain reaction (PCR).
XX CC AA25143 to AA25191 represent specifically claimed examples of primers
XX CC from the present invention
XX SQ Sequence 22 BP; 7 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 869 GATTACAGCGGTGAGCCAC 887
DB 1 GATTACAGCGGTGAGCCAC 19

RESULT 703
AA25163
ID AA25163 standard; DNA; 22 BP.
XX AC AA25163;
XX AC
XX DT 13-DEC-1999 (first entry)
XX DE Human short interspersed repetitive element PCR primer #21.
XX XX Human; short interspersed repetitive element; SINE; PCR; primer;
XX KW Oncorhynchus; restriction primer; short interspersed repeated sequence;
XX KW eukaryote; restricted polymerase chain reaction fingerprinting;
XX KW identification; DNA specimen; discrimination; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN JP2913035-B1.
XX PD 28-JUN-1999.
XX PF 10-JUL-1998; 98JP-00195692.
XX PR 10-JUL-1998; 98JP-00195692.
XX PA (NORO ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.
XX XX WPI; 1999-583348/50.
XX DR
XX XX

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PT Restriction primer for distinguishing individuals with short interspersed
PT repeated sequence of eukaryotes by restricted polymerase chain reaction
PT fingerprinting.
XX
XX
PS Claim 6; Page 3; 17pp; Japanese.
XX
XX The present invention describes a restriction primer for eukaryotic short
CC interspersed repeated sequences (SINE), which has one or more additional
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
CC the SINE. The annealing temperature of the primer to the DNA sequence is
CC kept higher than the fusion temperature of the primer during polymerase
CC chain reaction (PCR). The PCR fragments obtained are subjected to
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from
CC the electrophoresis band pattern, eukaryotic individuals are
CC distinguished. The primer is used for amplifying a eukaryotic
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be
CC used for individual identification of humans for medical and legal
CC applications and ecological studies. DNA specimens in traces
CC (approximately 10 ng in mass) can be used for individual discrimination
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).
CC AA25143 to AA25191 represent specifically claimed examples of primers
CC from the present invention
XX
XX
SQ Sequence 22 BP; 6 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 869 GATTACAGCGGTGAGCCAC 887
Db 1 GATTACAGCGGTGAGCCAC 19
|||||
AA25169
AA25169 standard; DNA; 22 BP.
XX
XX AA25169;
XX
XX 13-DEC-1999 (first entry)
XX
XX Human short interspersed repetitive element PCR primer #27.
XX
XX Human; short interspersed repetitive element; SINE; PCR; primer;
KW Oncohychnus; restriction primer; short interspersed repeated sequence;
KW eukaryote; restricted polymerase chain reaction fingerprinting;
XX identification; DNA specimen; discrimination; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX JP2913035-B1.
XX
XX 28-JUN-1999.
XX
XX 10-JUL-1998; 98BP-00195692.
XX
XX 10-JUL-1998; 98BP-00195692.
XX
XX (NORQ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.
XX
XX WPI; 1999-583348/50.
XX
XX Restriction primer for distinguishing individuals with short interspersed
PT repeated sequence of eukaryotes by restricted polymerase chain reaction
PT fingerprinting.
XX
XX Claim 6; Page 4; 17pp; Japanese.
XX
XX The present invention describes a restriction primer for eukaryotic short
CC interspersed repeated sequences (SINE), which has one or more additional
CC

CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
CC the SINE. The annealing temperature of the primer to the DNA sequence is
CC kept higher than the fusion temperature of the primer during polymerase
CC chain reaction (PCR). The PCR fragments obtained are subjected to
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from
CC the electrophoresis band pattern, eukaryotic individuals are
CC distinguished. The primer is used for amplifying a eukaryotic
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be
CC used for individual identification of humans for medical and legal
CC applications and ecological studies. DNA specimens in traces
CC (approximately 10 ng in mass) can be used for individual discrimination
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).
CC AA25143 to AA25191 represent specifically claimed examples of primers
CC from the present invention
XX
XX
SQ Sequence 22 BP; 6 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 869 GATTACAGCGGTGAGCCAC 887
Db 1 GATTACAGCGGTGAGCCAC 19
|||||
AA25171
AA25171 standard; DNA; 22 BP.
XX
XX AA25171;
XX
XX 13-DEC-1999 (first entry)
XX
XX Human short interspersed repetitive element PCR primer #29.
XX
XX Human; short interspersed repetitive element; SINE; PCR; primer;
KW Oncohychnus; restriction primer; short interspersed repeated sequence;
KW eukaryote; restricted polymerase chain reaction fingerprinting;
XX identification; DNA specimen; discrimination; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX JP2913035-B1.
XX
XX 28-JUN-1999.
XX
XX 10-JUL-1998; 98BP-00195692.
XX
XX 10-JUL-1998; 98BP-00195692.
XX
XX (NORQ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.
XX
XX WPI; 1999-583348/50.
XX
XX Restriction primer for distinguishing individuals with short interspersed
PT repeated sequence of eukaryotes by restricted polymerase chain reaction
PT fingerprinting.
XX
XX Claim 6; Page 4; 17pp; Japanese.
XX
XX The present invention describes a restriction primer for eukaryotic short
CC interspersed repeated sequences (SINE), which has one or more additional
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
CC the SINE. The annealing temperature of the primer to the DNA sequence is
CC kept higher than the fusion temperature of the primer during polymerase
CC chain reaction (PCR). The PCR fragments obtained are subjected to
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from
CC the electrophoresis band pattern, eukaryotic individuals are
CC distinguished. The primer is used for amplifying a eukaryotic
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by

DB 1 GATTACAGCGGTGAGCCAC 19

RESULT 708

AAZ25165
ID AAZ25165 standard; DNA; 22 BP.

AC AAZ25165;

DT 13-DEC-1999 (first entry)

DE Human short interspersed repetitive element PCR primer #23.

XX Human; short interspersed repetitive element; SINE; PCR; primer;

KW Oncohyunchus; restriction primer; short interspersed repeated sequence;

KM eukaryote; restriction polymerase chain reaction fingerprinting;

KW Identification; DNA specimen; discrimination; ss.

OS Synthetic.

OS Homo sapiens.

XX JP2913035-B1.

XX 28-JUN-1999.

XX 10-JUL-1998; 98JP-00195692.

XX 10-JUL-1998; 98JP-00195692.

XX (NORQ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.

XX WPI; 1999-583348/50.

XX Restriction primer for distinguishing individuals with short interspersed

PT repeated sequence of eukaryotes by restricted polymerase chain reaction

PT fingerprinting.

XX Claim 6; Page 4; 17pp; Japanese.

XX The present invention describes a restriction primer for eukaryotic short

CC interspersed repeated sequences (SINE), which has one or more additional

CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of

CC the SINE. The annealing temperature of the primer to the DNA sequence is

CC kept higher than the fusion temperature of the primer during polymerase

CC chain reaction (PCR). The PCR fragments obtained are subjected to

CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from

CC the electrophoresis band pattern, eukaryotic individuals are

CC distinguished. The primer is used for amplifying a eukaryotic

CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by

CC polymerase chain reaction (PCR) fingerprinting. In particular it may be

CC used, individual identification of humans for medical and legal

CC applications and ecological studies. DNA specimens in traces

CC (approximately 10 ng in mass) can be used for individual discrimination

CC of eukaryotes using the primer in a polymerase chain reaction (PCR).

CC AAZ25143 to AAZ25191 represent specifically claimed examples of primers

CC from the present invention

XX Sequence 22 BP; 6 A; 6 C; 7 G; 3 T; 0 U; 0 Other;

XX Query Match 1.9%; Score 19; DB 1; Length 22;

XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 869 GATTACAGCGGTGAGCCAC 887

XX 1 GATTACAGCGGTGAGCCAC 19

XX DB

XX RESULT 709

XX ADG30198

XX ID ADG30198 standard; RNA; 23 BP.

XX XX

XX ADG30198;

XX 26-FEB-2004 (first entry)

XX PKR-targeted siNA DNA-RNA hybrid - SEQ ID 764.

XX double-stranded short interfering nucleic acid; siNA;

KW antiarteriosclerotic; neuroprotective; neurotropic; antiparkinsonian;

KW anticonvulsant; pulmonary disease; restenosis; atherosclerosis;

KW Alzheimer's; Parkinson's; epilepsy; dementia; Huntington's;

KW amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; PKR.

XX Unidentified.

OS Synthetic.

XX WO2003074654-A2.

XX 12-SEP-2003.

XX 20-FEB-2003; 2003WO-US005028.

XX 20-FEB-2002; 2002US-0358580P.

XX 11-MAR-2002; 2002US-0363124P.

XX 06-JUN-2002; 2002US-0386782P.

XX 29-AUG-2002; 2002US-0406784P.

XX 05-SEP-2002; 2002US-0408378P.

XX 09-SEP-2002; 2002US-0409293P.

XX 15-JAN-2003; 2003US-0440129P.

XX (SIRN-) SIRNA THERAPEUTICS INC.

XX Mcswiggen J, Beigelman L, Chowitra B, Payco P, Fossnaugh K,

XX Jamison S, Ueman N, Thompson J;

XX WPI; 2003-731676/69.

XX New double-stranded short interfering nucleic acid molecule, useful for

PT down-regulating the expression of an endogenous mammalian target gene or

PT for treating diseases that respond to modulation of gene expression or

PT activity.

XX Example 24; SEQ ID NO 764; 593pp; English.

XX The invention relates to a double-stranded short interfering nucleic acid

CC (siNA) molecule that down-regulates expression of an endogenous mammalian

CC target gene comprising one or more chemical modifications and each strand

CC of the double-stranded siNA comprises about 21 nucleotides. The siNA of

CC the invention demonstrates antiarteriosclerotic, neuroprotective,

CC neurotropic, antiparkinsonian and anticonvulsant activities and may be

CC useful for down-regulating the expression of any disease or condition

CC target gene and therefore in the treatment of any disease or condition

CC that responds to modulation of gene expression or activity in a cell,

CC tissue or organism. The disease or condition may include pulmonary

CC diseases such as restenosis, atherosclerosis, Huntington's disease or

CC Parkinson's disease, epilepsy, dementia, Huntington's disease or

CC amyotrophic lateral sclerosis. Furthermore, the siNA may be utilized for

CC gene therapy applications. The current sequence is that of the siNA DNA-

CC RNA hybrid of the invention.

XX Sequence 23 BP; 4 A; 7 C; 3 G; 2 T; 5 U; 2 Other;

XX Query Match 1.9%; Score 19; DB 1; Length 23;

XX Best Local Similarity 73.7%; Pred. No. 1.4e+03;

XX Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

XX QY 1117 GGTCGAACCTCGACCT 1135

XX 2 GGTCGAACCTCGACCT 20

XX DB

XX RESULT 710

XX AAT39493

XX ID AAT39493 standard; DNA; 22 BP.

XX XX

AC AAT39493;
XX
DT 21-MAY-1997 (first entry)
XX
DE Steroidogenesis acute regulatory protein exon 4 PCR primer EX4S.
XX
KW Human; steroidogenesis; acute regulatory protein; hSTAR; analysis;
KW mutation; detection; prenatal; genetic defect; congenital; protein;
KW lipid adrenal hyperplasia; treatment; prevention; gene;
KW replacement therapy; hypercholesterolemia; primer; PCR;
KW polymerase chain reaction; exon 4; ss.
XX
OS Synthetic.
XX
PN WO9629338-A1.
XX
PD 26-SEP-1996.
XX
PF 22-MAR-1996; 96WO-US003896.
XX
PR 23-MAR-1995; 95US-00410540.
XX
PA (RBCG) UNIV CALIFORNIA.
XX (UTPE-) UNIV PENNSYLVANIA.
XX
PI Miller WL, Ian D, Strause JF;
XX
DR WPI; 1996-44330/44.
XX
PT Isolated human steroidogenesis acute regulatory protein gene - used for
PT detection of mutation(s) of this gene that cause congenital lipid
PT adrenal hyperplasia.
XX
PS Disclosure; Page 36; 89pp; English.
XX
CC The present sequence is a PCR primer for exon 4 of the human
CC steroidogenesis acute regulatory protein (hSTAR) gene. The hSTAR gene can
CC be analysed for mutations to detect (e.g. prenatally) genetic defects
CC associated with congenital lipid adrenal hyperplasia (CAH), or its
CC transmission to children. CAH can be treated by protein or gene
CC replacement therapy, which can also be used to prevent or treat
CC hypercholesterolemia. A human adrenal cortex cDNA library was screened
CC with a mouse STAR probe to isolate a 1.6 kb insert, including an ORF for
CC a 285 residue protein. When it was cloned into pSPORT and expressed in
CC COS-1 cells cotransfected with pPA50sec abd pADX, it increased the level
CC of pregnenolone synthesis from cholesterol or 20-alpha-hydroxycholesterol
XX
SQ Sequence 22 BP; 5 A; 3 C; 8 G; 6 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 863 TGCTGGATTACAGCGGTGAGC 884
DB 1 TGCTGGATTATAGCGGTGAAC 22
RESULT 711
AAX83018
ID AAX83018 standard; DNA; 22 BP.
XX
AC AAX83018;
XX
DT 31-AUG-1999 (first entry)
XX
DE Primer K to isolate human WRN gene 5' exons.
XX
KW Human; WRN; Werner's syndrome; detection; diagnosis; autosomal;
KW recessive disorder; phenotype; primer; RT-PCR; amplification; ss.
XX
OS Synthetic.
OS Homo sapiens.

XX
PN WO9724435-A1.
XX
PD 10-JUL-1997.
XX
PF 30-DEC-1996; 96WO-US020785.
XX
PR 29-DEC-1995; 95US-0009409P.
XX
PR 29-DEC-1995; 95US-00580539.
XX
PR 30-JAN-1996; 96US-0010835P.
XX
PR 30-JAN-1996; 96US-00594242.
XX
PR 12-APR-1996; 96US-00632175.
XX
PA (DARW-) DARWIN MOLECULAR CORP.
XX
PI Oshima J, Fu Y, Yu C, Mulligan J, Schellenberg GD;
XX
DR WPI; 1997-363671/33.
XX
PT Isolated nucleic acid molecule encoding the WRN gene product - useful for
PT detection and treatment of Werner's syndrome, and related diseases.
XX
PS Example 2; Page 41; 153pp; English.
XX
CC Primers AAX83008-X83064 were used to RT-PCR amplify exons from the 5' and
CC 3' ends of the human WRN gene (AAX83003) which encodes a protein related
CC to Werner's syndrome. The products can be used for the detection and
CC treatment of Werner's syndrome (WS), an autosomal recessive disorder with
CC a complex phenotype, as well as related diseases
XX
SQ Sequence 22 BP; 5 A; 4 C; 7 G; 6 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 479 AGTGCAGTGTGTGATCAGC 500
DB 1 AGTGCAGTGTGTATCATATAGC 22
RESULT 712
AAC69375/C
ID AAC69375 standard; DNA; 22 BP.
XX
AC AAC69375;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human ABC1 BAC contig polymorphic site, SEQ ID NO:274.
XX
KW Human ABC1 cholesterol transporter; chromosome 9q31;
KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
KW cardiovascular disease; coronary artery disease; coronary restenosis;
KW cerebrovascular disease; peripheral vascular disease;
KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
KW prognosis; prophylaxis; drug screening; transgenic animal; ds.
XX
OS Homo sapiens.
XX
PN WO200055318-A2.
XX
PD 21-SEP-2000.
XX
PF 15-MAR-2000; 2000WO-IB000532.
XX
PR 15-MAR-1999; 99US-0124702P.
XX
PR 08-JUN-1999; 99US-0138048P.
XX
PR 17-JUN-1999; 99US-0139600P.
XX
PR 01-SEP-1999; 99US-0151977P.
XX


```

RESULT 714
AAAF84349/c
ID   AAAF84349 standard; DNA; 22 BP.
XX
AC   AAAF84349;
XX
DT   20-JUN-2001 (first entry)
DE
XX   Human CYP2C181 PCR primer #5.
XX
KW   Gene polymorphism; drug-metabolising enzyme; PCR primer; CYP2C181; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001017185-A.
XX
PD   23-JAN-2001.
XX
PF   10-DEC-1999; 99JP-00351610.
PR   19-MAR-1999; 99JP-00076592.
RR   06-MAY-1999; 99JP-00125918.
PA   (SAKA ) OTSUKA PHARM CO LTD.
XX
DR   WPI; 2001-285409/30.
XX
PT   Detection of gene polymorphism of drug-metabolizing enzymes useful for
FT   diagnosis and testing comprising carrying out polymerase chain reaction.
XX
PS   Example 1; Page 13; 27pp; Japanese.
XX
CC   The present invention relates to a kit and method for the detection of
CC   gene polymorphisms of drug-metabolizing enzyme genes. The kit contains a
CC   polymerase chain reaction (PCR) buffer solution containing DNA polymerase
CC   and NTP, a normal forward primer, a mutated forward primer, a reverse
CC   primer and a fluorescence-labelling probe. The method involves carrying
CC   out PCR on sample DNA, containing a drug-metabolising enzyme gene,
CC   together with PCR buffer, the normal forward primer, the reverse primer
CC   and the fluorescence-labelling probe (step A); and carrying out PCR on
CC   the sample DNA together with PCR buffer, the mutated forward primer, the
CC   reverse primer and the fluorescence-labelling probe (step B), and a step
CC   of comparing the result of step A with that of step B. The present
CC   sequence is a primer for human CYP2C181, which was used to illustrate the
CC   present invention
XX
SQ   Sequence 22 BP; 5 A; 7 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 1.9%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred.No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0
DY      861 AGTCTGGGATTACAGCGCTGA 882
Db      22 AATGCTGGGATTACAGCATGA 1
          ||| ||||| ||||| ||||| |||
RESULT 715
AAAF29797/c
ID   AAFA29797 standard; DNA; 22 BP.
XX
AC   AAFA29797;
XX
DT   09-APR-2001 (first entry)
DE
XX   Presentiline-1 gene promoter PCR primer Prom22R.
XX
KW   Human; PSEN1; Alzheimer's disease; polymorphism; diagnosis;
XX   presentiline-1; chromosome 14; PCR primer; ss.
XX
OS   Homo sapiens.
XX
```

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PN WO200079000-A1.
PD 28-DEC-2000.
XX
XX 22-JUN-2000; 2000WO-EP005942.
PF
XX 22-JUN-1999; 99EP-00201991.
PR
XX (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
PA
XX Theuns J, Cruts M, Van Broeckhoven C;
XX
XX MPI; 2001-071402/08.
DR
XX
XX Determining whether a human subject has or is at risk of developing (early
PT onset) Alzheimer's disease comprises detecting the presence/absence of a
PR genetic lesion in the presenilin-1 gene.
XX
XX Example 1; Page 45; 56pp; English.
PS
XX The present invention describes a method for determining the presence of
CC or susceptibility to Alzheimer's disease in humans, involving detecting a
CC genetic lesion in the presenilin-1 (PSEN1) gene, found on chromosome 14.
CC The genetic lesion is a polymorphism in the promoter or upstream
CC regulatory region of the gene. The invention also describes transgenic
CC animals which can be used to identify compounds useful in treating
CC Alzheimer's disease
XX
XX Sequence 22 BP; 9 A; 7 C; 2 G; 4 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.9%; Score 18.8; DB 1; Length 22;
XX Best Local Similarity 90.9%; Pred. No. 1.3e+03;
XX Matches 20; Conservatively 0; Mismatches 2; Indels 0; Gaps 0;
OY 174 TTTTACTAGACATGAGATTTC 195
XX |||||||
XX 22 TTTTACTAGACGCGGTTTC 1
XX
XX RESULT 716
XX AAD31453/C
XX ID AAD31453 standard; DNA; 22 BP.
XX
XX AAD31453;
XX
XX 31-MAY-2002 (first entry)
XX
XX Human chromosome 17 92kb gene fragment amplifying PCR primer, wt1R.
XX
XX Human; Van Buchem's disease; genomic deletion; craniofacial dysmaturity;
XX autosomal recessive disorder; chromosome 17; chromosome 17q21;
XX bone dysplasia; 92Kb gene fragment; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200210455-A2.
XX
XX 07-FEB-2002.
XX
XX 30-JUL-2001; 2001WO-US023968.
XX
XX 28-JUL-2000; 2000US-0221855P.
XX 06-JUL-2001; 2001US-0303386P.
XX
XX (CELL-) CELLTECH R & D INC.
XX (STRA/) STRAHLING HAMPTON K.
XX
XX Brunkow ME, Proll S, Paepel B;
XX
XX MPI; 2002-227089/28.
XX
XX Methods for identifying subjects who are afflicted with or carriers of
PT diseases associated with genomic deletion(s), e.g. Van Buchem's disease,

```


PT by determining the presence of a deletion in the 92 kb region of human
PT chromosome 17 at 17q21.
XX
PS Example 3; Page 26; 109pp; English.
XX
CC The present invention relates to methods for distinguishing between
CC individuals homozygous for and therefore afflicted with Van Buchem's
CC disease, individuals heterozygous for and therefore carriers of Van
CC Buchem's disease and individuals who are not afflicted with Van Buchem's
CC disease comprise identifying a large genomic deletion in chromosome 17 at
CC 17q21. The method is useful for identifying individuals who are afflicted
CC with or carriers of diseases associated with one or more genomic
CC deletion, particularly Van Buchem's disease, which is a rare autosomal
CC recessive disorder that results in a bone dysplasia referred to a
CC craniotubular hypertosis. The present sequence is a PCR primer used to
CC amplify 92Kb gene fragment in human chromosome 17 at 17q21
XX
SQ Sequence 22 BP; 7 A; 2 C; 10 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 532 ATCCTCTGCTCAGCTCCCA 553
DB 22 ATTCTCTTGCTCAGCTCCCA 1
XX
RESULT 717
AAD31457/c
ID AAD31457 standard; DNA; 22 BP.
XX
AC AAD31457;
XX
DT 31-MAY-2002 (first entry)
XX
DE Human chromosome 17 92Kb gene fragment amplifying PCR primer, wt3r.
XX
KM Human; Van Buchem's disease; genomic deletion; craniotubular hypertosis;
KM autosomal recessive disorder; chromosome 17; chromosome 17q21;
KM bone dysplasia; 92Kb gene fragment; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200210455-A2.
XX
PD 07-FEB-2002.
XX
PF 30-JUL-2001; 2001WO-US023368.
XX
PR 28-JUL-2000; 2000US-0221855P.
PR 06-JUL-2001; 2001US-0303386P.
XX
PA (CELL-) CELLTech R & D INC.
PA (STRA/) STRAHLING HAMPTON K.
XX
PI Brunkow ME, Proll S, Paepfer B;
XX
DR WPI; 2002-227089/28.
XX
PT Methods for identifying subjects who are afflicted with or carriers of
PT diseases associated with genomic deletion(s), e.g. Van Buchem's disease,
PT by determining the presence of a deletion in the 92 kb region of human
PT chromosome 17 at 17q21.
XX
PS Example 3; Page 26; 109pp; English.
XX
CC The present invention relates to methods for distinguishing between
CC individuals homozygous for and therefore afflicted with Van Buchem's
CC disease, individuals heterozygous for and therefore carriers of Van
CC Buchem's disease and individuals who are not afflicted with Van Buchem's
CC disease comprise identifying a large genomic deletion in chromosome 17 at
CC 17q21. The method is useful for identifying individuals who are afflicted

CC with or carriers of diseases associated with one or more genomic
CC deletion, particularly Van Buchem's disease, which is a rare autosomal
CC recessive disorder that results in a bone dysplasia referred to a
CC craniotubular hypertosis. The present sequence is a PCR primer used to
CC amplify 92Kb gene fragment in human chromosome 17 at 17q21
XX
SQ Sequence 22 BP; 7 A; 2 C; 10 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 532 ATCCTCTGCTCAGCTCCCA 553
DB 22 ATTCTCTTGCTCAGCTCCCA 1
XX
RESULT 718
ADL66998/c
ID ADL66998 standard; DNA; 22 BP.
XX
AC ADL66998;
XX
DT 03-JUN-2004 (first entry)
XX
DE Multiplex PCR primer #2.
XX
KM DNA polymerase; anti-DNAp antibody; reverse transcriptase;
KM anti-RT antibody; single strand binding protein; SSB; ss; primer.
XX
OS Synthetic.
XX
PN WO2004022770-A2.
XX
PD 18-MAR-2004.
XX
PF 05-SEP-2003; 2003WO-US027705.
XX
PR 05-SEP-2002; 2002US-0408609P.
PR 19-NOV-2002; 2002US-0427867P.
XX
PA (INVT-) INVTROGEN CORP.
XX
PI Park K;
XX
DR WPI; 2004-248479/23.
XX
PT New compositions comprising one or more anti-reverse transcriptase
PT antibodies, anti-DNA polymerases or single strand binding proteins,
PT useful for synthesizing nucleic acids.
XX
PS Example 4; Page 89; 201pp; English.
XX
CC The invention relates to a new composition which comprises at least one
CC anti-DNA polymerases (anti-DNAp) antibody and/or at least one anti-
CC reverse transcriptase (anti-RT) antibody, and at least one single strand
CC binding protein (SSB) or at least two different SSBs. The compositions
CC are useful for nucleic acid synthesis reactions or are generated during
CC nucleic acid synthesis reactions. The methods are useful for synthesizing
CC one or more nucleic acid molecules. The compositions and methods are also
CC be used in amplifying nucleic acid molecules, in reverse transcription of
CC nucleic acid molecules and in coupled or uncoupled reverse
CC transcription/amplification. The present sequence is used in the
CC exemplification of the present invention.
XX
SQ Sequence 22 BP; 7 A; 5 C; 8 G; 2 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 670 TTGGCTCAGTCAACCTGTGCC 691
XX

DB 22 TTGGCTCACTGAGCCTGCCC 1
RESULT 719
AAA37708
ID AAA37708 standard; DNA; 23 BP.
XX
XX
AC AAA37708;
XX
XX
DT 22-NOV-2000 (first entry)
XX
XX
DE Human Rad51 antisense inhibitor AS8.
XX
XX
KW Antisense inhibitor; human; Rad51; cell proliferation; cancer survival;
XX radiation sensitivity; therapy; AS8; ss.
XX
OS Homo sapiens.
XX
XX WO200047231-A2.
XX
XX 17-AUG-2000.
XX
XX 03-FEB-2000; 2000WO-US002881.
XX
XX 10-FEB-1999; 99US-0119578P.
XX 06-DEC-1999; 99US-00454495.
XX
XX (PANG-) PANGENE CORP.
XX
XX Reddy G;
XX
XX WPI; 2000-506091/45.
XX
XX Inhibiting cell proliferation useful for cancer therapy, comprises
XX administering Rad51 inhibitor in vivo.
XX
XX Claim 8; Page 26; 42pp; English.
XX
XX This sequence represents an antisense inhibitor of human Rad51,
XX designated AS8 (also referred to as R51AS8). The antisense inhibitors can
XX be used in a method of the invention, for inhibiting cell proliferation.
XX They can also be used in methods for inducing sensitivity to radiation
XX and DNA damaging chemotherapeutics in an individual and in a method for
XX prolonging survival in an individual with cancer. The methods and
XX antisense molecules are useful for inhibiting cell proliferation,
XX especially cancerous cell proliferation, for inducing sensitivity to
XX radiation and DNA damaging chemotherapeutics in individuals and for
XX prolonging survival in an individual with cancer. Kits for carrying out
XX the methods may be used to diagnose and/or treat cancer and for
XX adjunctive therapy
XX
SQ Sequence 23 BP; 2 A; 13 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 1.9%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 1.4e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 837 GATCGCCTGCGCCTGCC 858
DB 2 GATCCACCTGCTCGGCTGCC 23
RESULT 720
AAS01201
ID AAS01201 standard; cDNA; 23 BP.
XX
XX AAS01201;
XX
XX 04-JUL-2001 (first entry)
XX
XX Human RAD51 antisense oligonucleotide, AS8.
XX
XX Human; Rad51; antisense; drug screening; cancer; autoimmune disease;

KW arthritis; graft rejection; inflammatory bowel disease; surgery;
XX angioplasty; ss.
XX
XX Homo sapiens.
XX
XX WO200119397-A1.
XX
XX 22-MAR-2001.
XX
XX 18-SEP-2000; 2000WO-US025838.
XX
XX 17-SEP-1999; 99US-0154616P.
XX 06-DEC-1999; 99US-00455300.
XX
XX (PANG-) PANGENE CORP.
XX
XX Reddy G;
XX
XX WPI; 2001-244704/25.
XX
XX Inhibiting cell proliferation for treating arthritis, graft rejection,
XX inflammatory bowel disease, cancer, proliferation induced after medical
XX procedure, involves administering Rad51 antibody or its fragment to cell.
XX
XX Example 6; Fig 16C; 102pp; English.
XX
XX The sequence represents the human Rad51 antisense oligonucleotide, AS8.
XX The antisense oligonucleotide is used to study down-regulation of Rad51
XX protein in human brain, breast and prostate cells. Rad51 protein is
XX defective in repair of damaged DNA, genetic recombination and the
XX cancer. Inhibiting cell proliferation involves administering to a cell a
XX Rad51 antibody or its fragment. The Rad51 antibody or its fragment is
XX useful for inhibiting cell proliferation, for treating disease states
XX such as cancer, autoimmune disease, arthritis, graft rejection,
XX inflammatory bowel disease, proliferation induced after medical
XX procedures such as surgery, angioplasty etc. in humans and animals
XX
SQ Sequence 23 BP; 2 A; 13 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 1.9%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 1.4e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 837 GATCGCCTGCGCCTGCC 858
DB 2 GATCCACCTGCTCGGCTGCC 23
RESULT 721
AAD43247
ID AAD43247 standard; DNA; 23 BP.
XX
XX AAD43247;
XX
XX 14-NOV-2002 (first entry)
XX
XX Antisense oligonucleotide R51AS8.
XX
XX Tumour cell proliferation; Rad51 inhibitor; p53 protein; premature aging;
XX hyperproliferative disorder; Hodgkin's disease; squamous cell carcinoma;
XX leukaemia; autoimmune disease; cancer; graft rejection; angioplasty;
XX inflammatory bowel disease; immunosuppressive; gene therapy; arthritis;
XX antisense; phosphorothioate backbone; ss.
XX
XX Unidentified.
XX
XX
XX Key Location/Qualifiers
XX modified_base 1..23
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone"

CC base -1569. They are used in a method for detecting cytochrome P4501A2
CC gene polymorphism, in partic. for detecting a base substitution at
CC position -1569 and may be used with primers for the detection of a T to G
CC base substitution at position 2064 and a C to A substitution at position
CC 2640. The method is easy, convenient and has a high degree of sensitivity
CC and accuracy. Polymorphisms in the P4501A2 gene can lead to a
CC modification of metabolism which may be beneficial or deleterious
XX
SQ Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 721 GCCTCCTGAGTAGCTGGAC 740
DB 20 GCGTCTGAGTAGCTGGAC 1

RESULT 724

AAT66010
ID AAT66010 standard; DNA; 20 BP.

AC AAT66010;

DT 25-MAR-2003 (revised)
DT 18-JUN-1997 (first entry)

DE Primer #1 to amplify repeat sequence marker Mfd107.

XX Polymorphism; repeat sequence; genetic marker; primer; amplification;
KM PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
KM linkage analysis; genetic disease; animal; plant; breeding; locus;
XX hybridisation; chromosome; ds.

OS Synthetic.

XX US5582979-A.

PD 10-DEC-1996.

XX 04-APR-1994; 94US-00222177.

XX 21-APR-1989; 89US-00341562.

PR 05-SEP-1991; 91US-00754351.

XX (MARS-) MARSHFIELD CLINIC.

XX Weber JL;

DR WPI; 1997-042299/04.

PT Detection of polymorphic genetic markers of the form (dc-da)n(dg-dt)n -
PT using novel nucleic acid mols. as primers.

XX Claim 7; Col 13-14; 186pp; English.

XX The invention relates to the isolation of polymorphic repeat sequences
CC having the sequence (dc-da)n.(dg-dt)n which can be used as genetic
CC markers. Primers based on these sequences can be used to detect these
CC repeats, especially for use in e.g. paternity or maternity testing, human
CC genetic analysis such as linkage analysis of genetic disease, commercial
CC animal or plant breeding or pedigree analysis. Clones containing the
CC repeat sequences were isolated by hybridisation of chromosome-specific
CC phase libraries with a synthetic poly(dg-dt) probe. Over 100
CC repeat blocks were isolated. The primers AAT65798-T66047 were used to PCR
CC amplify the inserts from the isolated clones containing the repeat
CC sequences. The primers AAT66010-1 were used to amplify the repeat
CC sequence marker clone Mfd107 (AAT65778). (Updated on 25-MAR-2003 to
CC correct PF field.)
XX
SQ Sequence 20 BP; 7 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 386 CCCAAGTCTGGATTACA 405
DB 1 CCCAAGTCTGGATTACA 20

RESULT 725

AAT66017/c
ID AAT66017 standard; DNA; 20 BP.

AC AAT66017;

DT 25-MAR-2003 (revised)
DT 18-JUN-1997 (first entry)

DE Primer #2 to amplify repeat sequence marker Mfd110.

XX Polymorphism; repeat sequence; genetic marker; primer; amplification;
KM PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
KM linkage analysis; genetic disease; animal; plant; breeding; locus;
XX hybridisation; chromosome; ds.

OS Synthetic.

XX US5582979-A.

PD 10-DEC-1996.

XX 04-APR-1994; 94US-00222177.

XX 21-APR-1989; 89US-00341562.

PR 05-SEP-1991; 91US-00754351.

XX (MARS-) MARSHFIELD CLINIC.

XX Weber JL;

DR WPI; 1997-042299/04.

PT Detection of polymorphic genetic markers of the form (dc-da)n(dg-dt)n -
PT using novel nucleic acid mols. as primers.

XX Claim 7; Col 13-14; 186pp; English.

XX The invention relates to the isolation of polymorphic repeat sequences
CC having the sequence (dc-da)n.(dg-dt)n which can be used as genetic
CC markers. Primers based on these sequences can be used to detect these
CC repeats, especially for use in e.g. paternity or maternity testing, human
CC genetic analysis such as linkage analysis of genetic disease, commercial
CC animal or plant breeding or pedigree analysis. Clones containing the
CC repeat sequences were isolated by hybridisation of chromosome-specific
CC phase libraries with a synthetic poly(dg-dt) probe. Over 100
CC repeat blocks were isolated. The primers AAT65798-T66047 were used to PCR
CC amplify the inserts from the isolated clones containing the repeat
CC sequences. The primers AAT66016-7 were used to amplify the repeat
CC sequence marker clone Mfd110 (AAT65781). (Updated on 25-MAR-2003 to
CC correct PF field.)
XX
SQ Sequence 20 BP; 4 A; 2 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 577 ACCACTACCTGGCTAATT 596
DB 20 ACCACACACCTGGCTAATT 1

RESULT 726

```

AA794341
ID   AA794341 standard; DNA; 20 BP.
XX
XX   AA794341:
XX
XX   04-MAR-1998 (first entry)
XX
XX   Human DPC4 sequence tagged site sense primer p0960-F5.
XX
XX   DPC4; pancreatic cancer; deleted; locus 4; diagnosis; human;
XX   tumour suppressor gene; proliferative disease; bile duct; bladder;
XX   colorectal; cancer; Crohn's disease; colitis; PCR primer;
XX   sequence tagged site; STS; ss.
XX
XX   Synthetic.
XX   Homo sapiens.
XX
XX   MO9766271-A1.
XX
XX   24-JUL-1997.
XX
XX   17-JAN-1997; 97MO-US0000827.
XX
XX   19-JAN-1996; 96US-00588821.
XX
XX   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
XX   Kern SE, Hahn SA;
XX
XX   WPI; 1997-385290/35.
XX
XX   Deleted in Pancreatic Cancer locus 4 polypeptide - and related nucleic
XX   acids; used in diagnosis and treatment of proliferative diseases, e.g.
XX   cancer of pancreas or other organs.
XX
XX   Example 2; Page 56; 104pp; English.
XX
XX   The present sequence represents a sequence tagged site (STS) primer used
XX   in the isolation of cosmids from the DPC4 (deleted in pancreatic cancer,
XX   locus 4) region, and gene identification. DPC4 is a tumour suppressor
XX   gene. Detection of truncated DPC4 protein, or of homozygous deletions or
XX   intergenic mutations in the nucleic acid encoding it, is used to diagnose
XX   (in vivo or in vitro) proliferative diseases, especially pancreatic
XX   carcinoma, bile duct, bladder or colorectal cancer, Crohn's disease,
XX   colitis-associated neoplasia or chronic ulcerative colitis. These
XX   conditions, where associated with a homozygous deletion, can be treated
XX   by administering an agent that: (a) modulates DPC4 expression,
XX   specifically a sense DPC4 sequence (particularly in the form of a vector,
XX   i.e. by gene therapy), but also an antisense sequence where DPC4 protein
XX   is over expressed or (b) mimics the activity of DPC4. DPC4 nucleic acid
XX   is also used as hybridisation probes for detecting presence/absence of
XX   human chromosome 18q21.1 fragments. When a homozygous deletion is
XX   detected in this region, an agent can be administered that accumulates
XX   within, or kills, only cells which contain such a deletion. This agent
XX   exploits the absence of an enzyme (or other protein) encoded by a
XX   neighbouring gene and lost by the deletion, i.e. it has a highly
XX   selective action
XX
XX   Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
SQ
Query Match      1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      385 TCCCAAGTCTGGGATTAC 404
DB      1 TCCCAAGTCTGGGATTTC 20

```

```

AC   AAV85762;
XX
XX   10-FEB-1999 (first entry)
XX
XX   LRP5 exon primer 57-4 1r.
XX
XX   LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis;
XX   insulin dependent diabetes mellitus; autoimmune disease;
XX   glomerulonephritis; inflammation; viral infection; osteoporosis;
XX   hypercholesterolemia; Alzheimer's disease; low density lipoprotein;
XX   PCR primer; ss.
XX
XX   Synthetic.
XX   Homo sapiens.
XX
XX   WO9846743-A1.
XX
XX   22-OCT-1998.
XX
XX   15-APR-1998; 98MO-GB001102.
XX
XX   15-APR-1997; 97US-0043553P.
XX
XX   05-JUN-1997; 97US-0048740P.
XX
XX   (WELL ) WELLCOME TRUST LTD.
XX   (MERI ) MERCK & CO INC.
XX
XX   Todd JA, Hess JW, Caskey CT, Cox RD, Gerhold D, Hammond H;
XX   Hey P, Kawaguchi Y, Merriman TR, Metzker ML, Nakagawa Y;
XX   Phillips MS, Twells RCJ;
XX
XX   WPI; 1998-594573/50.
XX
XX   New isolated LDL-receptor related protein - used to develop products for
XX   treating, e.g. elevated triglyceride levels, diabetes, autoimmune
XX   disorders, inflammation or Alzheimer's disease.
XX
XX   Claim 12; Page 105; 200pp; English.
XX
XX   The present invention describes LRP5 (low density lipoprotein (LDL)
XX   receptor related protein, previously designated LRP-3). AAV85587 to
XX   AAV85822 represent exon primers used for obtaining LRP5 cDNA. Nucleic
XX   acid molecules (NAVs) encoding LRP5 can be used for determining if an
XX   individual is susceptible to insulin dependent diabetes mellitus (IDDM).
XX   The NAVs or proteins can be used for reducing triglyceride levels in the
XX   serum of an individual. Therapies that affect LRP5 may also be useful in
XX   the treatment of autoimmune diseases such as glomerulonephritis, diseases
XX   and disorders involving disruption of endocytosis and/or antigen
XX   presentation, cytokine clearance and/or inflammation, viral infection,
XX   pathogenic bacterial toxin contamination, elevation of free fatty acids
XX   or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's
XX   disease and cardiovascular disease. Products from the present invention
XX   can also be used for detection, diagnosis and drug screening
XX
XX   Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;
SQ
Query Match      1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      391 AGTCTGGGATTACAGCGT 410
DB      20 AGTCTGGGATTACAGCGAT 1

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RESULT 727
AAV85762/C
ID   AAV85762 standard; DNA; 20 BP.
XX

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RESULT 728
AAV85840/C
ID   AAV85840 standard; DNA; 20 BP.
XX
XX   AAV85840;
XX
XX   10-FEB-1999 (first entry)
XX

```


OS Synthetic.
 OS Homo sapiens.
 XX MO9846743-A1.
 XX 22-OCT-1998.
 PD
 XX 15-APR-1998; 98WO-GB001102.
 PF
 XX 15-APR-1997; 97US-0043553P.
 PR 05-JUN-1997; 97US-0048740P.
 XX
 XX (WELL) WELLCOME TRUST LTD.
 PA (MERCK) MERCK & CO INC.
 XX
 XX Todd JA, Hess JW, Caskey CT, Cox RD, Gerhold D, Hammond H;
 PI Hey P, Kawaguchi Y, Merriman TR, Metzker ML, Nakagawa Y;
 PI Phillips MS, Twells RCU;
 XX
 DR WPI; 1998-594573/50.
 XX
 PT New isolated LDL-receptor related protein - used to develop products for
 PT treating, e.g. elevated triglyceride levels, diabetes, autoimmune
 PT disorders, inflammation or Alzheimer's disease.
 PS
 XX Claim 12; Page 111; 200pp; English.
 CC The present invention describes LRP5 (low density lipoprotein (LDL)
 CC receptor related protein, previously designated LRP-3). AAY85823 to
 CC AAY85900 represent SNP primers used for obtaining LRP5 cDNA. Nucleic acid
 CC molecules (NAMS) encoding LRP5 can be used for determining if an
 CC individual is susceptible to insulin dependent diabetes mellitus (IDDM).
 CC The NAMS or proteins can be used for reducing triglyceride levels in the
 CC serum of an individual. Therapies that affect LRP5 may also be useful in
 CC the treatment of autoimmune diseases such as glomerulonephritis, diseases
 CC and disorders involving disruption of endocytosis and/or antigen
 CC presentation, cytokine clearance and/or inflammation, viral infection,
 CC pathogenic bacterial toxin contamination, elevation of free fatty acids
 CC or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's
 CC disease and cardiovascular disease. Products from the present invention
 CC can also be used for detection, diagnosis and drug screening
 CC
 XX Sequence 20 BP; 3 A; 8 C; 3 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 1.9%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 673 GCTCAGTCAACCTCTGCCT 692
 DB 1 GTTCAGTCAACCTCTGCCT 20
 RESULT 731
 AAX90795/c
 ID AAX90795 standard; DNA; 20 BP.
 AC AAX90795;
 XX
 DT 13-JAN-2000 (first entry)
 XX
 DE Human 7SL RNA specific PCR primer-1.
 KM PCR primer; human 7SL RNA; amplify; human staufen cDNA; hStau;
 KM synthesised; random hexamer primer; Superscript II reverse transcriptase;
 KM ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX MO9951255-A1.
 FN
 PD 14-OCT-1999.

XX
 PF 06-APR-1999; 99WO-US007533.
 XX
 PR 06-APR-1998; 98US-0080783P.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 PA
 XX Greider CW, Le S;
 PI
 DR WPI; 1999-620168/53.
 XX
 XX Human staufen polypeptide useful in methods for identifying telomerase
 XX inhibitors.
 PT
 PS Example 1; Page 25; 50pp; English.
 XX
 XX The present sequence is a PCR primer specific to human 7SL RNA. It is
 CC used to amplify human staufen (hStau) cDNA synthesised using random
 CC hexamer primers and Superscript II reverse transcriptase
 CC
 XX Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 1.9%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 730 GTAGCTGGGACTACAGGCGC 749
 DB 20 GTAGCTGGGACTACAGGCGC 1
 RESULT 732
 AAX86546
 ID AAX86546 standard; DNA; 20 BP.
 AC AAX86546;
 XX
 DT 04-OCT-1999 (first entry)
 XX
 DE Primer rec617 used for amplification and sequencing of Rhd gene exons.
 XX
 KW Allele; Rheus D antigen; Rhd; weak D phenotype; blood transfusion;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX MO9937763-A2.
 PD 29-JUL-1999.
 XX
 PF 18-DEC-1998; 98WO-EP008319.
 PR 23-JAN-1998; 98EP-00101203.
 XX
 XX (DRKB-) DRK BLUTSPENDEDIENST BADEN WUERTTEMBERG.
 PA Flegel WA, Wagner FF;
 XX
 DR WPI; 1999-469127/39.
 XX
 XX Nucleic acid sequences correlated with Rheus weak D phenotype, useful
 PT for screening blood from donors and recipients for transfusion methods.
 XX
 PS Example; Page 33; 64pp; English.
 XX
 XX PCR primers AAX86523-62 were used for amplification and sequencing of
 CC exons of the Rheus D (Rhd) antigen gene. The specification describes a
 CC Rhd contributing to or indicative of the weak D phenotype, where the Rhd
 CC polynucleotide carries at least one missense mutation as compared to the
 CC wild-type Rhd, in its transmembrane and/or intracellular regions,
 CC especially in amino acid positions 2-16, 114-149, 179-225 or/and 267-397,
 CC with the proviso that the D antigen does not carry a single missense

CC mutation leading to a F233V or T283I substitution. The probes and
CC antibodies are useful in the methods for detection of weak D phenotypes.
CC Red blood cells, from probands, are useful for the assessment of the
CC affinity, avidity and/or reactivity of monoclonal anti-D antibodies.
CC polyclonal anti-D antisera or of anti-globulin or anti-human-globulin
CC antisera. Detecting the presence of the Rhd associated with weak D
CC phenotype is useful for determining that a patient in need of a blood
CC transfusion is to be transfused with Rhd negative blood from a donor.
CC Alternatively, testing for weak D phenotype Rhd in the blood of a donor
CC is useful for determining whether the donor blood should be excluded for
CC transfusion to patients having wild type Rhd or weak D types, other than
CC that of the donor weak D type
XX
SQ Sequence 20 BP; 4 A; 9 C; 2 G; 5 T; 0 U; 0 Other;
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 968 TCTCGGCTCAGTCGCAACCTC 987
DB 1 TCTCAGCTCAGTCGCAACCTC 20
RESULT 733
AAZ37738/C
ID AAZ37738 standard; DNA; 20 BP.
XX
AC AAZ37738;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #268.
XX
KM Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KM antisense; modulation; oligonucleotide; expression; inhibition;
KM hyperproliferation; blood cancer; brain cancer; breast cancer;
KM lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;
KM restenosis; ss.
XX
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9949065-A1.
XX
PD 30-SEP-1999.
XX
PF 26-MAR-1999; 99WO-US006702.
XX
PR 26-MAR-1998; 98US-00048810.
XX
PA (ISIS-) ISIS PHARM INC.
PI Miragila LJ, Nero P, Graham MJ, Monia BP, Cowseert LM;
PI WPI; 1999-610754/52.
DR
XX New antisense compounds used to treat eg. hyperproliferative conditions.
XX
PS Example 9; Page 55; 157pp; English.
XX
CC AAZ37473-237738 represent human mdm2 phosphorothioate oligonucleotides.
CC AAZ37471, AAZ37472, AAZ37739, AAZ37740 and AAZ37741 are used in the
CC exemplification of the present invention. The present invention describes
CC novel nucleotide antisense compounds, targeted to the 5' untranslated,
CC translation termination codon, or 3' untranslated region of a nucleic
CC acid encoding human mdm2, that modulates expression of human mdm2. The
CC oligonucleotides mediate their effect by antisense inhibition of
CC hyperproliferative gene expression. The antisense compound is used to
CC treat an animal having a disease or condition associated with mdm2,
CC particularly a hyperproliferative condition, more particularly cancer,
CC especially of the blood, brain, breast, lung or soft tissue, or
CC psoriasis, fibrosis, atherosclerosis or restenosis

XX
SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 868 GGATTACAGCGGTGAGCCAC 887
DB 20 GGATTACAGCGGTGAGCCAC 1
RESULT 734
AAZ37716/C
ID AAZ37716 standard; DNA; 20 BP.
XX
AC AAZ37716;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #246.
XX
KM Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KM antisense; modulation; oligonucleotide; expression; inhibition;
KM hyperproliferation; blood cancer; brain cancer; breast cancer;
KM lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;
KM restenosis; ss.
XX
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9949065-A1.
XX
PD 30-SEP-1999.
XX
PF 26-MAR-1999; 99WO-US006702.
XX
PR 26-MAR-1998; 98US-00048810.
XX
PA (ISIS-) ISIS PHARM INC.
PI Miragila LJ, Nero P, Graham MJ, Monia BP, Cowseert LM;
PI WPI; 1999-610754/52.
DR
XX New antisense compounds used to treat eg. hyperproliferative conditions.
XX
PS Claim 4; Page 54; 157pp; English.
XX
CC AAZ37473-237738 represent human mdm2 phosphorothioate oligonucleotides.
CC AAZ37471, AAZ37472, AAZ37739, AAZ37740 and AAZ37741 are used in the
CC exemplification of the present invention. The present invention describes
CC novel nucleotide antisense compounds, targeted to the 5' untranslated,
CC translation termination codon, or 3' untranslated region of a nucleic
CC acid encoding human mdm2, that modulates expression of human mdm2. The
CC oligonucleotides mediate their effect by antisense inhibition of
CC hyperproliferative gene expression. The antisense compound is used to
CC treat an animal having a disease or condition associated with mdm2,
CC particularly a hyperproliferative condition, more particularly cancer,
CC especially of the blood, brain, breast, lung or soft tissue, or
CC psoriasis, fibrosis, atherosclerosis or restenosis
XX
SQ Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 668 TCTTGCTCAGTCGCAACCTC 687
DB 20 TCTTGCTCAGTCGCAACCTC 1


```
RESULT 735
AAA18013
ID AAA18013 standard; DNA; 20 BP.
XX
AC AAA18013;
XX
DT 29-AUG-2000 (first entry)
XX
DE Uncoupling protein isoform UCP5S1 nucleotide sequence PCR primer.
XX
KM Uncoupling protein 5; UCP5; metabolism; chromosome 10q23-25; H+ leak;
XX metabolic rate; obesity; stroke; trauma; burn trauma; sepsis; infection;
XX human; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN MO200032624-A2.
XX
PD 08-JUN-2000.
XX
PF 03-NOV-1999; 99WO-US025947.
XX
PR 30-NOV-1998; 98US-0110286P.
XX 16-APR-1999; 99US-0129583P.
XX 15-JUL-1999; 99US-0143886P.
XX
PA (GENTH ) GEMENTECH INC.
XX
PI Adams S, Pan J;
XX
DR WPI; 2000-412284/35.
XX
PT Isolated nucleic acid encodes human uncoupling protein 5 useful in
XX diagnostic assays and treatment of obesity, stroke, trauma, sepsis and
XX infection.
XX
PS Example 2; Page 37; 90p; English.
XX
CC This sequence represents a PCR primer specific for the human uncoupling
XX protein 5 isoform hUCP5S1 encoding DNA sequence. UCP5 is involved in
XX metabolism, and it may be involved in catalysing H+ leak, and therefore
XX be involved in energetic inefficiency in vivo. The present invention
XX relates to human and murine UCP5 nucleotide and protein sequences. There
XX are three isoforms of human UCP5, hUCP5L, hUCP5S, and two
XX isoforms of murine UCP5, mUCP5L and mUCP5S. The human UCP5 gene is
XX located on chromosome 10q23-25. The nucleic acid encoding UCP5 can be
XX used as hybridization probes, in chromosome and gene mapping, for the
XX generation of antisense RNA and DNA and in the preparation of recombinant
XX UCP5 proteins. UCP5 nucleic acids can be used in gene therapy for
XX regulation of metabolic conditions. Upregulating or downregulating UCP5
XX activity in a mammal is used for modulating metabolic rate in the mammal,
XX in particular upregulation of UCP5 activity stimulates an increase in
XX metabolic rate in an obese mammal. Other therapeutic applications
XX associated with modulating UCP5 activity are treating symptoms associated
XX with stroke, trauma (e.g. burn trauma), sepsis and infection. Detecting
XX UCP5 activity can be used to assist predictions concerning metabolic
XX conditions or risk for onset of obesity and as UCP5 may control the
XX generation of reactive oxygen to diagnose impaired neural activity or
XX neural degeneration. Anti-UCP5 antibodies can be used in diagnostic
XX assays and for the affinity purification of UCP5 from recombinant cell
XX culture or natural sources
XX
SQ Sequence 20 BP; 5 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
RESULT 736
AAA11943
ID AAA11943 standard; DNA; 20 BP.
XX
AC AAA11943;
XX
DT 16-AUG-2000 (first entry)
XX
DE Human MDMX antisense oligonucleotide #31223.
XX
KM MDMX; human; antisense; inhibitor; anticarcinogen; antiinflammatory;
XX antineoplastic; modulation; treatment; disease; diagnosis; primer; ss.
XX
OS Homo sapiens.
XX
PN US6046320-A.
XX
PD 04-APR-2000.
XX
PF 09-APR-1999; 99US-00289267.
XX
PR 09-APR-1999; 99US-00289267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monica BP, Cowseert LM;
XX
DR WPI; 2000-282710/24.
XX
PT New antisense oligonucleotides targeting nucleic acids encoding human
XX MDMX useful for inhibiting MDMX expression and for treating diseases
XX associated with MDMX expression e.g. tumor formation, inflammation.
XX
PS Example 15; Col 97-98; 51p; English.
XX
CC This invention describes a novel antisense compound (I), 8-30 nucleobases
XX in length, targeted to a nucleic acid encoding a human MDMX. (I)
XX specifically hybridizes with and inhibits the expression of human MDMX.
XX The products of the invention have anticarcinogen, antiinflammatory and
XX antineoplastic activity. Synthesized chimeric oligonucleotides targeted
XX to human MDMX, 20 nucleotides in length, composed of a central gap region
XX consisting of ten 2'-deoxynucleotides flanked on both sides by 5-
XX nucleotide wings were tested for antisense inhibition of MDMX expression.
XX Results of real-time quantitative polymerase chain reaction (PCR) showed
XX 71 out of the 159, 20 base pair sequences, all fully defined in the
XX CC specification, demonstrated at least 30% inhibition of MDMX expression.
XX The antisense oligonucleotides are useful for effective and specific
XX modulation, particularly inhibition of MDMX expression, and may be used
XX in treating humans or animals suspected of having or being prone to a
XX disease or condition associated with expression of MDMX. The antisense
XX oligonucleotides may also be used as research reagents or kits, and as
XX diagnostics, e.g. to elucidate the function of a particular gene or to
XX distinguish between functions of various members of a biological pathway,
XX and as prophylaxis, e.g. to prevent or delay infection, inflammation or
XX tumor formation. AAA11781-A11945 represent antisense oligonucleotides
XX described in the method of the invention
XX
SQ Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
RESULT 737
AAZ52253
ID AAZ52253 standard; DNA; 20 BP.
XX
AC AAZ52253;
XX
```

XX 18-JUL-2000 (first entry)
DT
XX
DE Primer ZC12502 for sequencing human stomach protein zsig28 cDNA.
XX
XX Human; stomach; zsig28 protein; chromosome 3q22.1-3q22.2; gene therapy;
XX claudin; oligodendrocyte-specific protein; OSP; apoptosis; RVP.1;
XX rat androgen-withdrawal apoptosis protein; growth factor receptor;
XX cell signalling molecule; cytoskeletal; antibacterial; food poisoning;
XX Botulism; diarrhoea; inflammation; cramping; cancer; gastric ulcer;
XX diagnosis; prevention; treatment; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200015659-A2.
XX
XX 23-MAR-2000.
XX
XX 14-SEP-1999; 99WO-US021023.
XX
XX 16-SEP-1999; 98US-00154444.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Sheppard PO, Foley KP;
XX
XX MPI; 2000-271379/23.
XX
XX New isolated polynucleotide encoding a stomach zsig28 polypeptide used
XX for diagnosis, prevention and treatment of stomach disorders caused by
XX bacteria, gastric ulcers or cancer.
XX
XX Example 1; Page 121; 121pp; English.
XX
XX The present sequence is a primer ZC12502 used for sequencing a cDNA
XX corresponding to an expressed sequence tag identified in a human lung
XX library, to obtain full length clone of polynucleotide encoding stomach
XX protein zsig28. The zsig28 gene is located at 3q22.1-3q22.2 region of
XX human chromosome 3. The zsig28 protein shows homology to a diverse family
XX of receptor proteins containing e.g. human claudin 1 and 2, human and
XX murine oligodendrocyte-specific protein (OSP) and rat androgen-withdrawal
XX apoptosis protein RVP.1. It is thought to be a cell-cell signalling
XX molecule, a growth factor receptor or extracellular matrix associated
XX protein with growth factor hormone activity and may be involved in an
XX apoptotic cellular pathway. The protein may act as an anti-microbial
XX agent and may bind toxins produced by bacteria which cause food
XX poisoning, Botulism, severe diarrhoea, inflammation and cramping. zsig28
XX agonists are useful for promoting apoptosis in cells over-expressing
XX zsig28 e.g. in cancer cells. They are also useful for stimulating cell
XX growth or differentiation. Altered levels of zsig28 protein in a test
XX sample such as saliva, serum, sweat or biopsy can be monitored as an
XX indication of digestive function, gastric ulcer or cancer. zsig28
XX expression can be used as a differentiation marker to determine the stage
XX of tumour or cell maturity, particularly in epithelial cells.
XX Polynucleotides encoding zsig28 can be used in gene therapy applications
XX to increase or inhibit zsig28 activity
XX
XX Sequence 20 BP; 5 A; 3 C; 8 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX 10-APR-2001 (first entry)
DT
XX
DE Human RANK antisense oligonucleotide, SEQ ID NO: 80.
XX
XX Human; cytoskeletal; antiinflammatory; antisense oligonucleotide; cancer;
XX receptor activator of NF-kappaB; RANK; infection; inflammation; ss.
XX
XX Homo sapiens.
XX
XX US6171860-B1.
XX
XX 09-JAN-2001.
XX
XX 05-NOV-1999; 99US-00435296.
XX
XX 05-NOV-1999; 99US-00435296.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Baker BF, Cowsett LM;
XX
XX MPI; 2001-136876/14.
XX
XX Novel antisense compounds capable of modulating expression of human
XX receptor activator of NF-kappaB useful for diagnosis, prophylaxis and
XX treatment of diseases associated with expression of RANK.
XX
XX Claim 14; Col 44; 40pp; English.
XX
XX The present sequence is one of a number of antisense compounds of 8 to 30
XX nucleobases in length that have been designed to target a 5' untranslated
XX region, start codon, coding region or 3' untranslated region of the human
XX receptor activator of NF-kappaB (RANK). The antisense compounds
XX specifically hybridise with and inhibit the expression of RANK. The
XX antisense oligonucleotides are useful for inhibiting the expression of
XX human RANK in human cells or tissues. They can be utilised for
XX diagnostics, therapeutics for the treatment of diseases associated with
XX the expression of RANK, prophylaxis e.g. to prevent or delay infection,
XX inflammation or tumour formation, and as research reagent. The antisense
XX compounds are safely and effectively administered to humans
XX
XX Sequence 20 BP; 2 A; 4 C; 10 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 843 CCTGCTCGGCTCCCAAG 862
DB 20 CCAGCTCGGCTCCCAAG 1

RESULT 738
AAF31823/C
ID AAF31823 standard; DNA; 20 BP.
XX
AC AAF31823;
XX
XX 10-APR-2001 (first entry)
XX
XX Human RANK antisense oligonucleotide, SEQ ID NO: 81.
XX
XX Human; cytoskeletal; antiinflammatory; antisense oligonucleotide; cancer;
XX receptor activator of NF-kappaB; RANK; infection; inflammation; ss.
XX
XX Homo sapiens.
XX
XX US6171860-B1.
XX
XX 09-JAN-2001.
XX
XX 05-NOV-1999; 99US-00435296.
XX
XX

```
XX 05-NOV-1999; 99US-00435296.
XX (ISIS-) ISIS PHARM INC.
XX Baker BP, Cowsett LM;
XX WPI; 2001-136876/14.
XX
XX Novel antisense compounds capable of modulating expression of human
XX receptor activator of NF-kappaB useful for diagnosis, prophylaxis and
XX treatment of diseases associated with expression of RANK.
XX
XX Claim 14; Col 44; 40pp; English.
XX
XX The present sequence is one of a number of antisense compounds of 8 to 30
XX nucleobases in length that have been designed to target a 5' untranslated
XX region, start codon, coding region or 3' untranslated region of the human
XX receptor activator of NF-kappaB (RANK). The antisense compounds
XX specifically hybridise with and inhibit the expression of RANK. The
XX antisense oligonucleotides are useful for inhibiting the expression of
XX human RANK in human cells or tissues. They can be utilised for
XX diagnostics, therapeutics for the treatment of diseases associated with
XX the expression of RANK, prophylaxis e.g. to prevent or delay infection,
XX inflammation or tumour formation, and as research reagent. The antisense
XX compounds are safely and effectively administered to humans
XX
XX Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 392 GTCGCTGGATTACAGCGGTG 411
XX |||||||||||||||
XX DB 20 GTACTGGATTACAGCGGTG 1
XX
XX RESULT 740
XX AAD14819/C
XX ID AAD14819 standard; DNA; 20 BP.
XX
XX AC AAD14819;
XX
XX DT 01-NOV-2001 (first entry)
XX
XX DE Human glycogen synthase kinase 3 alpha antisense oligo ISIS #116660.
XX
XX KW Human; glycogen synthase kinase 3 alpha; antidiabetic; cytostatic;
XX antisense therapy; diabetes; hyperproliferative disorder; inflammation;
XX neurological disorder; tumour; haematopoietic disorder; infection;
XX hyperproliferative disorder; developmental disorder; antisense;
XX phosphothioate backbone; ss.
XX
XX OS Homo sapiens.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone"
XX FT modified_base 1..5
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "Methoxyethyl residues"
XX FT modified_base 2
XX FT /*tag= d
XX FT /mod_base= m5c
XX FT modified_base 4
XX FT /*tag= e
XX FT /mod_base= m5c
XX FT modified_base 5
XX FT
```

```
FT /*tag= f
FT /mod_base= m5c
FT modified_base 6
FT /*tag= g
FT /mod_base= m5c
FT modified_base 7
FT /*tag= h
FT /mod_base= m5c
FT modified_base 14
FT /*tag= i
FT /mod_base= m5c
FT modified_base 15
FT /*tag= j
FT /mod_base= m5c
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "Methoxyethyl residues"
FT modified_base 16
FT /*tag= k
FT /mod_base= m5c
FT modified_base 19
FT /*tag= l
FT /mod_base= m5c
XX
XX WO200152865-A1.
XX
XX 26-JUL-2001.
XX
XX 16-JAN-2001; 2001WO-US001411.
XX
XX 21-JAN-2000; 2000US-00488856.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX PI Monia BP, McKay R, Butler MM, Wyatt JR;
XX
XX WPI; 2001-442247/47.
XX
XX Antisense compound 8 to 30 nucleobases in length comprising a compound
XX that is targeted to a nucleic acid molecule encoding glycogen synthase
XX kinase 3 alpha, useful for the treatment of e.g. diabetes and
XX hyperproliferative disorders.
XX
XX Example 15; Page 84; 115pp; English.
XX
XX CC The invention relates to an antisense compound 8 to 30 nucleobases in
XX length targeted to a nucleic acid encoding glycogen synthase kinase 3
XX alpha. The antisense compound specifically hybridises with and inhibits
XX the expression of glycogen synthase kinase 3 alpha. The antisense
XX compound is useful for the treatment of a diseases associated with
XX glycogen synthase kinase 3 alpha such as diabetes, a neurological
XX disorder, a haematopoietic disorder, a hyperproliferative disorder or a
XX developmental disorder. The antisense compounds may also be used
XX prophylactically to prevent or delay infection, inflammation or tumour
XX formation. The present sequence is a phosphorothioate antisense
XX oligonucleotide targeted to human glycogen synthase kinase 3 alpha
XX genomic DNA
XX
XX SQ Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 863 TGCTGGATTACAGCGGTGA 882
XX |||||||||||||||
XX DB 20 TGCTGGATTACAGCGGTGA 1
XX
XX RESULT 741
XX AAD14817/C
XX ID AAD14817 standard; DNA; 20 BP.
```

XX AAD14817;
AC
XX 01-NOV-2001 (first entry)
DT
XX Human glycogen synthase kinase 3 alpha antisense oligo ISIS #116658.
DE
XX Human; glycogen synthase kinase 3 alpha; antidiabetic; cytostatic;
XX antisense therapy; diabetes; hyperproliferative disorder; inflammation;
KW neurological disorder; tumour; haematopoietic disorder; infection;
KM hyperproliferative disorder; developmental disorder; antisense;
KM phosphorothioate backbone; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base
FT 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "Methoxyethyl residues"
FT modified_base
FT 8
FT /tag= d
FT /mod_base= m5c
FT modified_base
FT 14
FT /tag= e
FT /mod_base= m5c
FT modified_base
FT 15
FT /tag= f
FT /mod_base= m5c
FT modified_base
FT 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "Methoxyethyl residues"
FT modified_base
FT 16
FT /tag= g
FT /mod_base= m5c
FT
FT
PN WO200152865-A1.
XX
XX 26-JUL-2001.
PD
XX 16-JAN-2001; 2001WO-US001411.
PF
XX 21-JAN-2000; 2000US-0048856.
PR
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, McKay R, Butler MM, Wyatt JR;
PI
DR WPI; 2001-442247/47.
XX
XX Antisense compound 8 to 30 nucleobases in length comprising a compound
PT that is targeted to a nucleic acid molecule encoding glycogen synthase
PT kinase 3 alpha, useful for the treatment of e.g. diabetes and
PT hyperproliferative disorders.
XX
XX Example 15; Page 83; 115pp; English.
XX
XX The invention relates to an antisense compound 8 to 30 nucleobases in
CC length targeted to a nucleic acid encoding glycogen synthase kinase 3
CC alpha. The antisense compound specifically hybridises with and inhibits
CC the expression of glycogen synthase kinase 3 alpha. The antisense
CC compound is useful for the treatment of a disease associated with
CC glycogen synthase kinase 3 alpha such as diabetes, a neurological
CC disorder, a haematopoietic disorder, a hyperproliferative disorder or a
CC developmental disorder. The antisense compounds may also be used
CC prophylactically to prevent or delay infection, inflammation or tumour
CC formation. The present sequence is a phosphorothioate antisense

CC oligonucleotide targeted to human glycogen synthase kinase 3 alpha
CC genomic DNA
XX
XX Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 968 TCTGGGCTACTGCACTC 987
DB 20 TCTGGGCTACTGCACTC 1
RESULT 742
AAK95122/C
ID AAK95122 standard; DNA; 20 BP.
XX
XX AAK95122;
AC
XX 06-NOV-2001 (first entry)
DT
XX
XX Human cDNA clone-specific primer, SEQ ID NO: 4367.
DE
XX Human, full length cDNA; cDNA synthesis; oligo-capping; PCR primer; ss.
XX Homo sapiens.
OS
XX EP130094-A2.
PN
XX 05-SEP-2001.
PD
XX 07-JUL-2000; 2000EP-00114089.
PF
XX 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183765.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Nishikawa T, Isogai T, Hayaishi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
PI WPI; 2001-524255/58.
DR
XX 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
PT
XX Example 18; Page 131; 1380pp + Sequence Listing; English.
XX
XX The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesizing the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a primer used to amplify a human cDNA
CC clone provided in the invention
XX
XX Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
SQ
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 725 CCTGAGTAGCTGGGACTACA 744
DB 20 CCTGAGTAGCTGGGACTACA 1
RESULT 743

```
AAH02356
ID AAH02356 standard; DNA; 20 BP.
XX
AC AAH02356;
XX
DT 12-JUN-2001 (first entry)
XX
DE Human AKAP10 coding sequence PCR primer SEQ ID NO: 53.
XX
KM Database; polymorphism; SNP; human; genetic marker; disease; infection;
XX drug response; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200127857-A2.
XX
PD 19-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028413.
XX
PR 13-OCT-1999; 99US-0159176P.
PR 10-JUL-2000; 2000US-0217251P.
PR 10-JUL-2000; 2000US-0217658P.
PR 19-SEP-2000; 2000US-00663968.
XX
XX (SEQ-) SEQUENOM INC.
PA
PI Braun A, Koeser H, Van Den Boom D, Ping Y, Rodi C, He L;
PI Chiu N, Jurinke C;
PI WPI; 2001-273865/28.
XX
DR Producing a database for identifying polymorphic genetic markers,
PT comprises obtaining data relating to members of a healthy population and
PT entering the information into a database.
XX
PS Example 3; Page 293; 304pp; English.
XX
CC The present invention provides a database of human samples obtained from
CC healthy individuals which can be used to identify polymorphic genetic
CC markers. Data obtained for the database can be used to sort the samples
CC by parameters such as age, sex and ethnicity. This is useful in linking
CC markers with diseases, susceptibility to infection and drug responses.
CC The present primer was used in an assay to demonstrate the uses of the
CC database of the invention
XX
SQ Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 385 TCCCAAAAGTCTGGGATTAC 404
Db 1 TCCCAAAAGTCTGGGATTAC 20
XX
RESULT 744
AAF92892/c
ID AAF92892 standard; DNA; 20 BP.
XX
AC AAF92892;
XX
DT 17-MAY-2001 (first entry)
XX
DE Human ABC1 transcription factor binding site #53.
XX
KM High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.
XX
OS Homo sapiens.
XX
PN WO200115676-A2.
XX
```

```
PD 08-MAR-2001.
XX
XX 01-SEP-2000; 2000WO-IB001492.
XX
PF 01-SEP-1999; 99US-0151977P.
XX
PR 15-MAR-2000; 2000US-00526193.
PR 23-JUN-2000; 2000US-0213958P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
PA
PA (XENO-) XENON GENETICS INC.
XX
PI Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;
XX
XX WPI; 2001-244356/25.
XX
DR WPI; 2001-244356/25.
XX
PT Treating a lower than normal high density lipoprotein-cholesterol (HDL-C)
PT level, a higher than normal triglyceride level, or a cardiovascular
PT disease, by administering a compound that modulates LXR- or RXR-mediated
PT transcriptional activity.
XX
XX Disclosure; Fig 3; 317pp; English.
XX
PS The present invention relates to a method for treating a patient
XX diagnosed as having a lower than normal high density lipoprotein-
XX cholesterol (HDL-C) level, a higher than normal triglyceride level, or a
XX cardiovascular disease, involving administering a compound that modulates
XX LXR- or RXR-mediated transcriptional activity or ABC1 expression or
XX activity. The LXR gene product may be used in an assay to identify
XX compounds useful for the treatment of a disease or condition selected a
XX lower than normal HDL cholesterol level, a higher than normal
XX triglyceride level, and a cardiovascular disease
XX
SQ Sequence 20 BP; 6 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 485 GTGGTGATCTCAGCTCAC 504
Db 20 GTGGTGATCTCAGCTCAC 1
XX
RESULT 745
AAH28044
ID AAH28044 standard; DNA; 20 BP.
XX
AC AAH28044;
XX
DT 05-SEP-2001 (first entry)
XX
DE PCR primer for a minimal deletion in FRA16D oxidoreductase gene.
XX
KM Cancer associated protein; FOR gene; FRA16D; fragile site; aphidicolin;
KM chromosomal rearrangement; cancer; splice variant; DNA instability;
KM FRA16D oxidoreductase; neoplasia; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200144466-A1.
XX
PN WO200144466-A1.
XX
PD 21-JUN-2001.
XX
PF 15-DEC-2000; 2000WO-AU001539.
XX
PR 16-DEC-1999; 99AU-00004711.
PR 19-APR-2000; 2000AU-00007025.
XX
XX (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
PA
PI Richards R, Ried K, Finnis M, Hobson L, Mangelsdorf M, Dayan S;
PI Nancarrow J, Woollatt E, Baker E;
```


XX 14-AUG-2001 (first entry)
DT SNP specific lower PCR primer SEQ ID 1398.
XX
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX MO200129262-A2.
PN
XX 26-APR-2001.
PD
XX 13-OCT-2000; 2000MO-US028436.
PF
XX 15-OCT-1999; 99US-0160096P.
PR
XX (ORCH-) ORCHID BIOSCIENCES INC.
PA
XX Picoult-Newburg L, Pohl M;
PI
XX WPI; 2001-290930/30.
DR
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
XX
PS Claim 1; Page 57; 83pp; English.
XX
XX Sequences AAH37205 - AAH0944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence
XX
SQ Sequence 20 BP; 6 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 869 GATTACAGCGCTGAGCCACC 888
DB 1 GATTACAGCGCTGAGCCACC 20
XX
RESULT 749
AAH37610/C
ID AAH37610 standard; DNA; 20 BP.
XX

AC AAH37610;
XX 14-AUG-2001 (first entry)
DT SNP specific lower PCR primer SEQ ID 406.
XX
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX MO200129262-A2.
PN
XX 26-APR-2001.
PD
XX 13-OCT-2000; 2000MO-US028436.
PF
XX 15-OCT-1999; 99US-0160096P.
PR
XX (ORCH-) ORCHID BIOSCIENCES INC.
PA
XX Picoult-Newburg L, Pohl M;
PI
XX WPI; 2001-290930/30.
DR
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
XX
PS Claim 1; Page 52; 83pp; English.
XX
XX Sequences AAH37205 - AAH0944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence
XX
SQ Sequence 20 BP; 8 A; 7 C; 4 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 188 GGAGTTTCGATGTGTC 207
DB 20 GGAGTTTCGATGTGTC 1
XX
RESULT 750
AAH40090
ID AAH40090 standard; DNA; 20 BP.
XX

KW inflammation; cancer; autoimmune disease; graft rejection; amplify;
 KW graft versus host disease; systemic lupus erythematosus;
 KW polymerase chain reaction; ss.
 OS Synthetic.
 XX WO200146260-A2.
 XX PN 28-JUN-2001.
 XX PD 22-DEC-2000; 2000MO-US034963.
 XX PF 23-DEC-1999; 99US-0172025P.
 XX PR (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX PA Starling GC, Finger J;
 XX PI WPI; 2001-418044/44.
 XX DR Novel Antigen Presenting cell expression protein useful for treating
 PT asthma, arteriosclerosis, autoimmune diseases, AIDS, cirrhosis, Crohn's
 PT disease and atopic dermatitis.
 XX PS Claim 50; Page 83; 112P; English.
 XX CC The sequences given in AAC86117-42 are primers which were used to isolate
 CC the cDNA sequences which encode antigen presenting cell expression (APEX)
 CC -1, APEX-2 and APEX-3 proteins. APEX-1 and APEX-2 comprise an
 CC extracellular domain having one immunoglobulin (Ig)-like structure and N-
 CC glycosylation site, a transmembrane domain, and a cytoplasmic domain
 CC having at least one SH2-binding motif. APEX proteins and antibodies are
 CC useful in the study, diagnosis, prevention and treatment of disease
 CC associated with the presence of an APEX protein e.g., asthma,
 CC arteriosclerosis, AIDS, cirrhosis, Crohn's disease, atopic dermatitis,
 CC autoimmune anaemia, buritis, cholecystitis, diabetes mellitus,
 CC emphysema, atrophic gastritis, inflammatory bowel disease, multiple
 CC sclerosis, myasthenia gravis, myocardial or pericardial inflammation,
 CC osteoarthritis, osteoporosis, psoriasis, Reiter's syndrome, rheumatoid
 CC arthritis, inflammation, cancer, immune disorders, autoimmune diseases,
 CC graft rejections, graft versus host reaction and systemic lupus
 CC erythematosus. APEX proteins are useful as diagnostic and/or prognostic
 CC markers on APCs or APEX expressing cells, the ability to elicit the
 CC generation of antibodies and as targets for various therapeutic
 CC modalities. APEX proteins are also useful for identifying and isolating
 CC ligand that bind APEX
 XX CC
 XX Sequence 20 BP; 4 A; 8 C; 3 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 1.9%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 867 GGGATTACAGCGGTGAGCCA 886
 |||||
 DB 20 GGGATTACAGGTGAGCCA 1

RESULT 753
 AAH20704/C
 ID AAH20704 standard; DNA; 20 BP.
 XX
 AC AAH20704;
 XX
 DT 13-AUG-2001 (first entry)
 XX
 DE Human telomeric repeat binding factor 2 oligonucleotide 111432.
 XX
 KW Antisense; phosphorothioate; human; telomeric repeat binding factor 2;
 KW inhibitor; premature aging; hyperproliferative disorder; cancer;
 KW cytoskeletal; ss.
 XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Modified_base 1..20
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "phosphorothioate backbone"
 FT modified_base 1..3
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2-O-methoxyethyl"
 FT modified_base 13..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2-O-methoxyethyl"
 XX
 XX WO200143752-A1.
 XX PN 21-JUN-2001.
 XX PD 14-DEC-2000; 2000MO-US033954.
 XX PF 17-DEC-1999; 99US-00467642.
 XX PR (ISIS-) ISIS PHARM INC.
 XX PA Monia BP, Cowseart LM;
 XX PI WPI; 2001-398071/42.
 XX DR Antisense compounds targeted to nucleic acid encoding telomeric repeat
 PT binding factor 2 useful for treating conditions such as premature aging
 PT and diseases such as cancer.
 XX PS Claim 3; Page 81; 108pp; English.
 XX CC This invention describes a novel antisense compound (I) 8-30 nucleobases
 CC in length targeted to a polynucleotide encoding human telomeric repeat
 CC binding factor 2 (II) which specifically hybridizes with, and inhibits
 CC the expression of (II). (I) is useful for treating a human having a
 CC disease or condition associated with (II) such as premature aging or a
 CC hyperproliferative disorder especially cancer. (I) is useful for
 CC expression of (II) in human cells or tissues. (I) is useful for
 CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
 CC The products of the invention have cytostatic activity. This sequence
 CC represents an antisense oligonucleotide used to illustrate the method of
 CC the invention
 XX CC
 XX Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 1.9%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 863 TGCTGGATTACAGCGCTGA 882
 |||||
 DB 20 TGCTGGATTACAGCGATGA 1

RESULT 754
 AAH20699/C
 ID AAH20699 standard; DNA; 20 BP.
 XX
 AC AAH20699;
 XX
 DT 13-AUG-2001 (first entry)
 XX
 DE Human telomeric repeat binding factor 2 oligonucleotide 111427.
 XX
 KW Antisense; phosphorothioate; human; telomeric repeat binding factor 2;
 KW inhibitor; premature aging; hyperproliferative disorder; cancer;
 KW cytoskeletal; ss.
 XX
 OS Homo sapiens.

DE Human mdm2 antisense oligonucleotide 31468.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW anti arteriosclerotic; vasotropic; antisense; phosphorothioate; ss.
XX
XX Homo sapiens.
XX
XX
FH Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "OTHER= All phosphorothioate linkages,
FT additionally bases 1-6 and bases 15-20 are 2'-O-
FT methoxyethyl bases, and bases 7-14 are deoxynucleotides"
XX
XX US2001016575-A1.
XX
XX
XX 23-AUG-2001.
XX
XX 02-JAN-2001; 2001US-00752983.
XX
XX 26-MAR-1998; 98US-00048810.
XX 26-MAR-1999; 99US-00280805.
XX
XX (MIRA/) MIRAGLIA L J.
XX (NERO/) NERO P.
XX (GRAH/) GRAHAM M J.
XX (MONT/) MONTA B P.
XX (COMS/) COMSERT L M.
XX
XX
XX Miraglia LJ, Nero P, Graham MJ, Montia BP, Comsert LM;
XX WPI; 2001-535565/59.
XX
XX An antisense compound, useful for treating e.g. cancer, comprises
XX nucleobases targeted a region (e.g. translation termination codon region)
XX of a nucleic acid encoding human mdm2.
XX
XX
XX Claim 4; Page 18; 81pp; English.
XX
XX The present invention relates to antisense compounds, 8-30 nucleobases in
XX length targeted to the 5' untranslated region, translation termination
XX codon region, 3' untranslated region, coding region or translation start
XX site of a nucleic acid encoding human mdm2, where the antisense compound
XX modulates the expression of human mdm2. The antisense oligonucleotides of
XX the invention are useful for encoding human mdm2 and for inhibiting the
XX expression of human mdm2. They may be used for treating an animal having
XX a disease or condition associated with amplification of mdm2 gene or
XX overexpression of mdm2 e.g. a hyperproliferative disorder such as cancer
XX (blood, brain, breast, lung, or a soft tissue cancer) and psoriasis,
XX fibrosis, atherosclerosis or restenosis, tumours, colorectal carcinoma
XX and chronic myelogenous leukemia. The antisense compound may be
XX administered with a chemotherapeutic agent to overcome drug resistance.
XX The antisense compound reduces hyperproliferation of human cells. The
XX method, which involves the use of the antisense compound, is also useful
XX for detecting the role of mdm2 expression in various cell functions and
XX physiological processes and useful in both clinical research and
XX diagnostic tools. AAS2242-AAS29507 represent the human mdm2 antisense
XX oligonucleotides of the present invention
XX
XX Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 668 TCTTGCTCCTCACTGCAACCTC 687
XX |||||||
XX 20 TCTTGCTCCTCACTGCAACCTC 1
XX
XX
XX RESULT 757

AAD28754
ID AAD28754 standard; DNA; 20 BP.
XX
XX AAD28754;
AC
XX
XX 07-MAY-2002 (first entry)
XX
XX
XX Target specific PCR primer #2 to amplify human AKAP10-1 target sequence.
XX
XX Human; polymorphic A-Kinase anchor protein; AKAP; disorder; neurological;
XX bipolar; cardiovascular; cardiac; proliferative; neurodegenerative;
XX cardiomyopathy; peripheral retinopathy; obesity; signal transduction;
XX left ventricular function; Alzheimer's disease; retinitis pigmentosa;
XX diabetes; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX
XX WO200204489-A2.
XX
XX 17-JAN-2002.
XX
XX 05-JUL-2001; 2001WO-US021308.
XX
XX 10-JUL-2000; 2000US-0217251P.
XX 13-OCT-2000; 2000US-0240335P.
XX 12-APR-2001; 2001US-00834700.
XX
XX (SEQU-) SEQUENOM INC.
XX
XX Braun A;
XX
XX WPI; 2002-154919/20.
XX
XX
XX New polynucleotide encoding polymorphic A-Kinase anchor proteins for
XX detecting an allelic variant of the human gene which is indicative of an
XX alteration in signal transduction, and is related to a disorder e.g.
XX Alzheimer's disease.
XX
XX
XX Example 3; Page 90; 290pp; English.
XX
XX
XX The present invention relates to a polynucleotide encoding polymorphic A-
XX Kinase anchor protein (AKAP), with isoleucine residue at position 646
XX replaced with valine, leucine or phenylalanine. AKAP is useful for
XX detecting an allelic variant of a human AKAP10 gene which is indicative
XX of an alteration in signal transduction, where the alteration is related
XX to a disorder selected from cardiovascular, cardiac, proliferative,
XX neurological, neurodegenerative disorders, obesity, diabetes and
XX peripheral retinopathies, especially the disorders including Alzheimer's
XX disease, altered left ventricular function, cardiomyopathies, bipolar
XX disorder and retinitis pigmentosa. The method of the invention is useful
XX for indicating susceptibility to morbidity and/or increased or early
XX mortality of a subject, where the predominant allele comprises A at
XX position corresponding to 2073 of AKAP, or a polymorphic region of AKAP10
XX comprises a nucleotide other than A at position T corresponding to
XX position 2073 of AKAP, or other than T of the complement of AKAP, and the
XX detecting step is performed by allele specific hybridisation, primer
XX specific extension, oligonucleotide ligation assay, restriction enzyme
XX site analysis and single-stranded conformation polymorphism analysis, or
XX the detection is by detecting a signal group from radioisotopes, enzymes,
XX antigens, antibodies, spectrophotometric reagents, chemiluminescent
XX reagents, fluorescent reagents and other light producing reagents. The
XX present sequence is a target specific PCR primer used to amplify human
XX AKAP10-1 target sequence
XX
XX Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 385 TCCCAAGTCTGGGATTAC 404
XX |||||||
XX 1 TCCCAAGTCTGGGATTAC 20
XX
XX
XX RESULT 757

```
RESULT 758
AAL40357
ID AAL40357 standard; DNA; 20 BP.
XX
AC AAL40357;
XX
XX
XX 19-SEP-2002 (first entry)
XX
XX
XX Human caspase 6 antisense inhibition related oligo SEQ ID No 76.
XX
XX Muscular; cytosolic; neurotrophic; neuroprotective; ophthalmological;
XX antilipemic; osteopathic; caspase 6; Rieger's syndrome; bone metabolism;
XX ataxia telangiectasia; hyperproliferative disorder; cholesterol disorder;
XX haematopoietic disorder; cancer; neurological; Alzheimer's disease;
XX apoptotic; human; ds.
XX
XX Homo sapiens.
XX
XX WO200229066-A1.
XX
XX 11-APR-2002.
XX
XX 03-OCT-2001; 2001WO-US030871.
XX
XX 04-OCT-2000; 2000US-00679299.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Brown-Driver VL, Zhang H, Watt AT;
XX
XX WPI; 2002-471315/50.
XX
XX An antisense oligonucleotide of 8 to 50 nucleotides in length that
XX inhibits caspase 6, is useful for treating Rieger's syndrome.
XX
XX Claim 3; Page 89; 141pp; English.
XX
XX The invention relates to an antisense oligonucleotide compound of 8 to 50
XX nucleotides in length that is targeted to a nucleic acid molecule
XX encoding caspase 6, where the oligonucleotide specifically hybridises
XX with and inhibits the expression of caspase 6. The oligonucleotide of the
XX invention specifically hybridises to and inhibits expression of caspase 6
XX in cells or tissues. The oligonucleotides can be administered
XX therapeutically or prophylactically to treat an animal having a disease
XX or condition associated with caspase 6, such as Rieger's syndrome or
XX ataxia telangiectasia, hyperproliferative disorder, a haematopoietic
XX disorder, a bone metabolism or cholesterol disorder, various types of
XX cancer, neurological conditions such as Alzheimer's disease and other de-
XX regulated apoptotic pathological conditions. This polynucleotide sequence
XX represents a human caspase 6 oligonucleotide relating to the invention.
XX NOTE: This phosphorothioate oligonucleotide sequence has 2'-MOE wings and
XX a deoxy gap
XX
XX SQ Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
XX
XX Human phosphorylase kinase beta antisense oligonucleotide #52.
XX
XX Human; phosphorylase kinase beta; metabolic disorder; diabetes;
XX infection; inflammation; tumour formation; antidiabetic;
XX antiinflammatory; cytosolic; phosphorothioate; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX
XX /*tag= a
XX /mod_base= OTHER
XX /note= "OTHER= phosphorothioate internucleotide linkages,
XX optionally bases 1-5 and 16-20 are 2'-methoxyethoxy (2'-
XX MOE) bases, where the 2'-MOE cytidines are also
XX 5'-methylcytidines"
XX
XX WO200222637-A1.
XX
XX 21-MAR-2002.
XX
XX 12-SEP-2001; 2001WO-US028586.
XX
XX 14-SEP-2000; 2000US-00662250.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Wyatt JR;
XX
XX WPI; 2002-351873/38.
XX
XX Novel antisense oligonucleotide which inhibits expression of
XX phosphorylase kinase beta, useful for treating metabolic disorder e.g.
XX diabetes, prevent or delay infection, inflammation or tumor formation.
XX
XX Claim 3; Page 83; 132pp; English.
XX
XX The present invention relates to antisense compounds and methods for
XX modulating the expression of human phosphorylase kinase beta. The
XX antisense compounds, particularly antisense oligonucleotides, target and
XX inhibit the expression of human phosphorylase kinase beta. The antisense
XX compounds are useful for inhibiting the expression of human phosphorylase
XX kinase beta in human cells or tissues and for treating an animal,
XX particularly a human suspected of having or being prone to a disease or
XX condition associated with expression of phosphorylase kinase beta such as
XX a metabolic disorder e.g. diabetes. The compounds are useful for
XX diagnosis, therapeutics and as research reagent, e.g. prophylactically
XX to prevent or delay infection, inflammation or tumour formation. The
XX antisense compounds are useful in the preparation of a pharmaceutical
XX formulation. They are highly specific, have an enhanced affinity for the
XX nucleic acid target, and are safely and effectively administered to
XX humans. ABK68888-ABK6895 represent human phosphorylase kinase beta
XX antisense oligonucleotides which comprise a phosphorothioate backbone
XX
XX SQ Sequence 20 BP; 2 A; 6 C; 6 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
RESULT 759
ABK68939
ID ABK68939 standard; DNA; 20 BP.
XX
XX ABK68939;
XX
XX 02-JUL-2002 (first entry).
```

```
RESULT 760
AAL38181/C
ID AAL38181 standard; DNA; 20 BP.
XX
XX AAL38181;
XX
XX 29-AUG-2003 (revised)
```

PT		15-AUG-2002	(first entry)
XX			
DE	Human BH3 interacting domain death mRNA agonist inhibitor SEQ ID 24.		
XX			
KW	Hepatocellular; immunomodulatory; cytostatic; antiinflammatory; hepatitis;		
KM	haematoxic; BH3 interacting domain death agonist; liver disease;		
KX	haematopoietic disorder; developmental disorder; immunological disorder;		
KV	hyperproliferative disorder; apoptosis; human; chimeric; 2'-methoxyethyl;		
XX	2'-MOE; phosphorothioate backbone; ds.		
OS	Homo sapiens.		
XX			
OS	Chimeric.		
XX			
PN	WO200220547-AI.		
PD	14-MAR-2002.		
PF	31-AUG-2001; 2001WO-US027316.		
XX			
XX	07-SEP-2000; 2000US-00657346.		
PR	07-MAR-2001; 2001US-00800631.		
PA	(ISIS-) ISIS PHARM INC.		
PI	Zhang H, Wyatt JR;		
DR	WPI; 2002-393838/42.		
PT	Novel antisense compound targeted to nucleic acid molecule encoding the		
PT	BH3 interacting domain death agonist, useful for treating animals with		
PT	diseases associated with BH3 interacting domain death agonist, e.g.		
PT	hepatitis.		
PS	Claim 3; Page 86; 171pp; English.		
XX			
CC	The invention relates to a compound 8 to 50 nucleotides in length		
CC	targeted to a nucleic acid molecule encoding a BH3 interacting domain		
CC	death agonist, where the compound specifically hybridises with and		
CC	inhibits the expression of the BH3 interacting domain death agonist. The		
CC	compound of the invention is useful for inhibiting the expression of the		
CC	BH3 interacting domain death agonist in cells or tissues. The compound is		
CC	also useful for treating an animal having a disease or condition		
CC	associated with the BH3 interacting domain death agonist, e.g.		
CC	haematopoietic disorder, hyperproliferative disorder, a developmental		
CC	disorder, immunological disorder, or a disease or condition of the liver		
CC	e.g., hepatitis, or a condition associated with apoptosis. The compound		
CC	is useful for diagnostics, therapeutics, prophylaxis and as research		
CC	reagents and kits. This polynucleotide sequence represents an antisense		
CC	oligonucleotide inhibitor of the DNA from human BH3 interacting domain		
CC	death agonist RNA of the invention. NOTE: This sequence is a chimeric		
CC	oligonucleotide 20 nucleotides in length, which is flanked on both sides		
CC	by five-nucleotide 'wings'. The wings are composed of 2'-methoxyethyl (2'		
CC	-MOE) nucleotides. The internucleoside (backbone) linkages are		
CC	phosphorothioate (P=S) throughout the oligonucleotide. (Updated on 29-AUG		
CC	-2003 to standardise OS field)		
SQ	Sequence 20 BP; 4 A; 4 C; 9 G; 3 T; 0 U; 0 Other;		
Query Match	1.9%; Score 18.4; DB 1; Length 20;		
Best Local Similarity	95.0%; Pred. No. 1.3e+03;		
Matches 19; Conservative	0; Mismatches 1; Indels 0; Gaps 0		
OY	538 CTGCGCTCAGCGTCCCAAGTA 557		
DG			
20	CTGCCCTCAGGCTTCGCGAGTA 1		
RESULT 761			
AAL38190			
ID	AAL38190 standard; DNA; 20 BP.		
AC	AAL38190;		
XX			

DT	29-AUG-2003	(revised)	
DT	15-AUG-2002	(first entry)	
DE	Human BH3 interacting domain death mRNA agonist inhibitor SEQ ID 33.		
XX	Hepatotropic; immunomodulatory; cytostatic; antiinflammatory; hepatitis;		
KW	hematotoxic; BH3 interacting domain death agonist; liver disease;		
KW	hematopoietic disorder; developmental disorder; immunological disorder;		
KW	hyperproliferative disorder; apoptosis; human; chimeric; 2'-methoxyethyl;		
XX	2'-MOE; phosphorothioate backbone; ds.		
OS	Homo sapiens.		
OS	Chimeric.		
XX	MO200220547-A1.		
PN	14-MAR-2002.		
PD	31-AUG-2001; 2001WO-US027316.		
PE	07-SEP-2000; 2000US-00657346.		
PR	07-MAR-2001; 2001US-00800631.		
XX	(ISIS-) ISIS PHARM INC.		
PA	Zhang H, Wyatt JR;		
PI	WPI; 2002-393838/42.		
DR	Novel antisense compound targeted to nucleic acid molecule encoding the		
PT	BH3 interacting domain death agonist, useful for treating animals with		
PT	diseases associated with BH3 interacting domain death agonist, e.g.		
PT	hepatitis.		
PS	Claim 3; Page 86; 171pp; English.		
CC	The invention relates to a compound 8 to 50 nucleotides in length		
CC	targeted to a nucleic acid molecule encoding a BH3 interacting domain		
CC	death agonist, where the compound specifically hybridises with and		
CC	inhibits the expression of the BH3 interacting domain death agonist. The		
CC	compound of the invention is useful for inhibiting the expression of the		
CC	BH3 interacting domain death agonist in cells or tissues. The compound is		
CC	also useful for treating an animal having a disease or condition		
CC	associated with the BH3 interacting domain death agonist, e.g.		
CC	haematopoietic disorder, hyperproliferative disorder, a developmental		
CC	disorder, immunological disorder, or a disease or condition of the liver		
CC	e.g., hepatitis, or a condition associated with apoptosis. The compound		
CC	is useful for diagnostics, therapeutics, prophylaxis and as research		
CC	reagents and kits. This polynucleotide sequence represents an antisense		
CC	oligonucleotide inhibitor of the DNA from human BH3 interacting domain		
CC	death agonist RNA of the invention. NOTE: This sequence is a chimeric		
CC	oligonucleotide 20 nucleotides in length, which is flanked on both sides		
CC	by five-nucleotide 'wings'. The wings are composed of 2'-methoxyethyl (2'		
CC	-MOE) nucleotides. The internucleoside (backbone) linkages are		
CC	phosphorothioate (p-S) throughout the oligonucleotide. (updated on 29-AUG		
CC	-2003 to standardise OS field)		
XX	Sequence 20 BP; 4 A; 9 C; 2 G; 5 T; 0 U; 0 Other;		
XX	SO		
QY	Query Match 1.9%; Score 18.4; DB 1; Length 20;		
QY	Best Local Similarity 95.0%; Pred. No. 1.3e+03;		
Db	Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0		
QY	968 TCTCGGCTCACTGCAACCTC 987		
Db	1 TCTCGGCTCACTGCAACCTC 20		
RESULT 762			
ABQ74794/C			
ID	ABQ74794 standard; DNA; 20 BP.		
XX	ABQ74794;		
AC			

XX		Human; thrombotic thrombocytopenic purpura; TTP; disintegrin;
KW		metalloproteinase; thrombospondin 1-like domains 13; ADAMTS13;
KM		chromolytic; haemostatic; PCR; primer; RT-PCR; 5' RACE; 3' RACE; ss.
XX		
OS	Homo sapiens.	
XX		
PN	MO2003016492-A2.	
XX		
PD	27-FEB-2003.	
XX		
PF	16-AUG-2002; 2002WO-US026285.	
XX		
PR	16-AUG-2001; 2001US-0312834P.	
FR	16-AUG-2002; 2002US-00312834.	
XX		
PA	(UNMI) UNIV MICHIGAN.	
XX		
PI	Ginsburg D, Levy G, Teal H;	
XX		
DR	WPI; 2003-268316/26.	
XX		
PT	Identifying risk of developing thrombotic thrombocytopenic purpura	
PT	disease, using a novel disintegrin and metalloproteinase containing	
PT	thrombospondin 1-like domains genes and proteases.	
XX		
PS	Example 1, Page 87, 98pp; English.	
XX		
CC	The invention relates to a novel method for identifying subjects at risk	
CC	of developing thrombotic thrombocytopenic purpura (TTP) disease,	
CC	comprising providing nucleic acid having a disintegrin and	
CC	metalloproteinase containing thrombospondin 1-like domains 13 (ADAMTS13)	
CC	gene from a subject, and detecting the presence or absence of one or more	
CC	variations in the ADAMTS13 gene. The method of the invention has	
CC	therapeutic and haemostatic activity. The methods and compositions of	
CC	the present invention are useful for the diagnosis and treatment of,	
CC	and/or analysing risks for thrombotic thrombocytopenic purpura. The	
CC	present sequence is used in the exemplification of the invention	
XX		
SQ	Sequence 20 BP; 5 A; 3 C; 9 G; 3 T; 0 U; 0 Other;	
	Query Match	1.9%; Score 18.4; DB 1; Length 20;
	Best Local Similarity	95.0%; Pred. No. 1.3e+03;
	Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
OY	931 CTCACCTGTATCCAGGCT 950	
DB	20 CTCACCTGTATCCAGGCT 1	
RESULT 764		
ABZ71056/C		
ID	ABZ71056 standard; DNA; 20 BP.	
XX		
AC	ABZ71056;	
XX		
DT	28-APR-2003 (first entry)	
XX		
DE	Human HKR1 phosphorothioate antisense oligonucleotide SEQ ID NO:84.	
XX		
KM	Human; HKR1; cytotoxic; HKR1 inhibitor; hyperproliferative disorder;	
KW	cancer; antisense oligonucleotide; 2'-O-methoxyethyl; 2'-MOE; control;	
KX	phosphorothioate; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	modified_base	1..20
FT		/*tag= a
FT		/mod base= OTHER
FT		/note= "phosphorothioate linkages"
FT	modified_base	1..5
FT		/*tag= b

```
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides"
XX
XX WO2003004513-A1.
XX
XX 16-JAN-2003.
XX
XX 02-JUL-2002; 2002WO-US021090.
XX
XX 03-JUL-2001; 2001US-00898556.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett FC, Freier SM;
XX
XX WPI; 2003-210336/20.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding HKR1, useful for treating a disease/condition
XX associated with HKR1, such as hyperproliferative disorder, e.g. lung,
XX brain or breast cancer.
XX
XX Claim 3; Page 73; 105pp; English.
XX
XX The present invention describes a compound 8-50 nucleobases in length
XX targeted to, and which specifically hybridises with a nucleic acid
XX molecule encoding HKR1, and inhibits the expression of HKR1. Also
XX described: (1) a compound 8-50 nucleobases in length that specifically
XX hybridises with at least an 8-nucleobase portion of an active site on a
XX nucleic acid molecule encoding HKR1; (2) a composition comprising the
XX compound and a carrier or diluent; (3) a method for inhibiting the
XX expression of HKR1 in cells or tissues by contacting the cells or tissues
XX with the compound so that expression of HKR1 is inhibited; and (4) a
XX method of treating an animal having a disease or condition associated
XX with HKR1 by administering to the animal a therapeutic or prophylactic
XX amount of the compound so that expression of HKR1 is inhibited. HKR1
XX antisense oligonucleotides have cytostatic activities and can be used as
XX HKR1 inhibitors. The compound, composition and methods are useful for
XX treating a disease or condition associated with HKR1, such as a
XX hyperproliferative disorder, e.g. lung, brain or breast cancer, by
XX inhibiting the expression of HKR1. They are also useful in research and
XX diagnostics for modulating the expression of HKR1. The present sequence
XX represents a human HKR1 chimeric phosphorothioate oligonucleotide having
XX 2'-O-methoxyethyl (2'-MOE) wings and a deoxy gap, which is an antisense
XX oligonucleotide used in the inhibition of human HKR1 in an example from
XX the present invention
XX
XX Sequence 20 BP; 5 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 967 ATCTGGCTCAGTCGACACT 966
XX ||||||||||||||||
XX 20 ATCTGGCTCAGTCGACACT 1
XX
XX RESULT 765
XX ADA20921/c
XX ID ADA20921 standard; DNA; 20 BP.
XX
XX ADA20921;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human BAX chimeric phosphorothioate oligonucleotide SEQ ID NO:94.
XX
XX BCL2-associated X; BAX; nootropic; neuroprotective; antiparkinsonian;
```

```
KW anticonvulsant; ophthalmological; antidiabetic; vitricide;
KW antisense therapy; BAX antagonist; BAX inhibitor;
KW familial amyotrophic lateral sclerosis; Alzheimer's disease;
KW Parkinson's disease; Hodgkin's disease; cartilage-hair hyperplasia;
KW diabetes-associated ocular disorder; scrapie infection;
KW aberrant apoptosis; human; phosphorothioate; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1. .20
XX /*tag= b
XX /mod_base= OTHER
XX /note= "phosphorothioate linkages, and all cytidine
XX residues are 5-methylcytidines"
XX
XX modified_base 1. .5
XX /*tag= a
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX modified_base 16. .20
XX /*tag= c
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX WO2003008543-A2.
XX
XX 30-JAN-2003.
XX
XX 13-JUL-2002; 2002WO-US022417.
XX
XX 17-JUL-2001; 2001US-00908147.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Zhang H, Watt AT;
XX
XX WPI; 2003-239321/23.
XX
XX New antisense compounds, useful for modulating the expression of BCL2-
XX associated X (BAX) protein or for treating a disease or condition
XX associated with BAX protein, e.g. Parkinson's disease, Hodgkin's disease
XX or Alzheimer's disease.
XX
XX Claim 3; Page 87; 139pp; English.
XX
XX The present invention describes a compound (1) 8-50 nucleobases in length
XX targeted to a nucleic acid molecule encoding BCL2-associated X (BAX)
XX protein, where the compound specifically hybridises with the nucleic acid
XX molecule encoding BAX protein and inhibits the expression of BAX protein.
XX The compound specifically hybridises with at least 8-nucleobase portion
XX of an active site on a nucleic acid molecule encoding BAX protein. Also
XX described: (1) a composition comprising (1) and a pharmaceutical carrier
XX or diluent; (2) inhibiting the expression of BAX protein in cells or
XX tissues comprising contacting the cells or tissues with (1); and (3)
XX treating an animal having a disease or condition associated with BAX
XX protein comprising administering to the animal (1) so that expression of
XX BAX protein is inhibited. (1) has nootropic, neuroprotective,
XX antiparkinsonian, anticonvulsant, ophthalmological, antidiabetic and
XX vitricide activities, and can be used in antisense therapy, and as a BAX
XX antagonist. The antisense compounds (1) are useful for modulating the
XX expression of BAX protein, and for treating a disease or condition
XX associated with BAX protein, e.g. familial amyotrophic lateral
XX sclerosis, Alzheimer's disease, Parkinson's disease, Hodgkin's disease,
XX cartilage-hair hyperplasia, diabetes-associated ocular disorders or
XX scrapie infection, or a condition that arises from aberrant apoptosis.
XX The compounds are useful as research reagents and in diagnostics. The
XX present sequence represents a human BAX chimeric phosphorothioate
XX oligonucleotide, which is used in an example from the present invention.
XX
XX Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
```

Best Local Similarity	95.0%;	Pred. No.	1.3e+03;
Matches	19;	Conservative	0; Mismatches 1; Indels 0; Gaps 0

OY	672	GCGTCACGTGCAACCTTGCC	691
Db	20	GATTCACTGCACAACCTTGCC	1

RESULT 766

XX	ACF39682	standard; DNA; 20 BP.
XX	ACF39682;	
XX	29-SEP-2003	(first entry)
DE	MHC class II transactivator antisense oligonucleotide SEQ ID NO:85.	
XX		
KM	Human; major histocompatibility complex class II transactivator;	
KW	MHC class II transactivator; antisense modulation; immunosuppressive;	
KW	antimicrobial; antidiabetic; antirheumatic; antiarthritic; cytostatic;	
KW	nootropic; neuroprotective; immunostimulant; autoimmune disorder;	
KW	MHC Class II transactivator inhibitor; infection; transplant rejection;	
KM	diabetes; rheumatoid arthritis; cancer; Alzheimer's disease;	
KM	multiple sclerosis; severe combined immunodeficiency disease;	
KM	phosphorochioate; antisense oligonucleotide; ss.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	modified_base	1..20
FT		/tag= a
FT		/mod_base= OTHER
FT		/note= "phosphorochioate linkages; all cytidine residues
FT		are 5-methylcytidines"
FT	modified_base	1..5
FT		/tag= b
FT		/mod_base= OTHER
FT		/note= "2'-O-methoxyethyls"
FT	modified_base	16..20
FT		/tag= c
FT		/mod_base= OTHER
FT		/note= "2'-O-methoxyethyls"
XX		
PN	WO2003050247-A2.	
XX		
PD	19-JUN-2003.	
XX		
PF	04-DEC-2002; 2002MO-US038616.	
XX		
PR	05-DEC-2001; 2001US-0006366.	
XX		
PPA	(ISIS-) ISIS PHARM INC.	
XX		
PI	Bennett FC, Dobie KW;	
XX		
DR	WPI; 2003-577294/54.	
XX		
PT	New antisense oligonucleotides for modulating MHC class II transactivator	
PT	gene expression, particularly useful for treating autoimmune disorders	
PT	such as transplant rejection, Alzheimer's disease, or multiple sclerosis,	
PT	or infection.	
XX		
PS	Example 15; Page 84; 129pp; English.	
XX		
CC	The present invention describes a compound (I) that is 8-50 nucleobases	
CC	in length: (a) targets a nucleic acid molecule encoding major	
CC	histocompatibility complex (MHC) class II transactivator, and	
CC	specifically hybridizes with the nucleic acid encoding the MHC class II	
CC	transactivator, and inhibits the expression of MHC class II	
CC	transactivator; or (b) specifically hybridizes with at least an 8-	
CC	nucleobase portion of an active site on a nucleic acid molecule encoding	

CC MHC class II transactivator. (I) has immunosuppressive, antitubercular,
CC antidiabetic, antirheumatic, antiarthritic, cytoskeletal, noctropic, an MHC
CC neuroprotective and immunostimulant activities, and can be used as an MHC
CC Class II transactivator inhibitor. The MHC class II transactivator
CC antisense oligonucleotides can be used for treating an animal having a
CC disease or condition associated with MHC class II transactivator, e.g.
CC autoimmune disorder or infection. The antisense oligonucleotides can be
CC used for inhibiting the expression of MHC class II transactivator in
CC cells or tissues. In particular, these diseases include transplant
CC rejection, diabetes, rheumatoid arthritis, cancer, Alzheimer's disease,
CC multiple sclerosis, or severe combined immunodeficiency disease. The
CC antisense compounds are useful for diagnostics, prophylaxis, or as
CC research reagents or kits. The present sequence represents a human MHC
CC class II transactivator chimeric phosphorothioate antisense
CC oligonucleotide, which is used in an example from the present invention

SX Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Qy Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Dy 1024 TCCTAAGCAGCTGCGATTAC 1043
|||||
Dd 1 TCCTGAGCAGCTGGGATTAC 20

RESULT 767
ABT44432
ID ABT44432 standard; DNA; 20 BP.

XX ABT44432;
XX
DT 06-NOV-2003 (first entry)

DE Chimeric antisense oligonucleotide ISIS 192407 to inhibit human ESRB.

XX
XX Oestrogen receptor beta; ERSB; steroid hormone; female sexual maturation;
KW bone maintenance; cardiovascular system; ER beta; oestrogen receptor 2;
KW ERS2; Alzheimer's; uterine leiomyoma; cytostatic; kidney neoplasm; ss;
KM cellular proliferation; cancer; human; antisense; chimeric.

XX Chimeric - Homo sapiens.
XS
OS WO2003050133-A1.
PN 19-JUN-2003.
PD 06-DEC-2002; 2002WO-US039200.
PX 07-DEC-2001; 2001US-00005058.
PR (ISIS-) ISIS PHARM INC.
PA
PI Dobie KW, Roach MP, Koller E;
PT MPI; 2003-577284/54.
DR
XX
XX
PT New antisense oligonucleotides for modulating estrogen receptor beta gene
expression, particularly useful for treating cancers, specifically
PT leiomyoma, pancreatic cancer, prostate cancer, breast cancer, bone cancer
or lymphoma.
PT
XX
PS Claim 3; Page 82; 160pp; English.

CC This invention relates to a novel antisense compounds that modulate the
CC expression of oestrogen receptor beta (ERSB). Oestrogen is a steroid
CC hormone that exerts a wide range of effects throughout the human body
CC being primarily involved in female sexual maturation. Additionally,
CC however, oestrogen targets male reproductive tissues, is known to be
CC important in bone maintenance and plays a protective role in the
CC cardiovascular system. This hormone receptor, ERSB (also known as ER
CC beta), oestrogen receptor 2 and ERS2) has been mapped to chromosome 14q22-

CC q24, a region known to be associated with early onset of Alzheimer's
CC disease, uterine leiomyomata and neoplasms of the kidney. Furthermore,
CC ERBB has been localized to metastatic cells indicating an involvement in
CC cellular proliferation. Accordingly, the selective inhibition of ERBB by
CC the cytostatic antisense oligonucleotides of this invention could provide
CC a therapeutic target for the treatment of cancer, as well as other ERBB-
CC related disorders. This oligonucleotide sequence is the chimeric human
CC antisense oligo used to inhibit expression of human ERBB, the aim of the
CC invention. Note that it has two terminal five nucleotide 2'-methoxyethyl
CC (2'-MOE) wings separated by a ten deoxynucleotide gap. The
CC oligonucleotide backbone is phosphorothioate throughout
XX
SQ Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1115 CTGCTCAAACTCTGACC 1134
Db 1 CTGCTTCAAACTCTGACC 20
XX
RESULT 768
ADD21681/c
ID ADD21681 standard; DNA; 20 BP.
XX
AC ADD21681;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #244.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW atherosclerosis; restenosis; apoptosis modulation; p21; ss;
KW 2'-methoxyethoxy-residue; phosphorothioate backbone.
XX
OS Homo sapiens.
XX
PN WO2003048315-A2.
XX
PD 12-JUN-2003.
XX
PT 02-DEC-2002; 2002WO-US038281.
XX
PT useful for treating e.g. cancer, psoriasis or restenosis by inhibiting
XX mdm2 expression.
XX
PR 04-DEC-2001; 2001US-00005344.
XX
PS (ISIS-) ISIS PHARM INC.
XX
PI Miraglia LJ, Nero PS, Graham MJ, Monia BP, Koller E, Chiang MY;
PI Manoharan M;
XX
DR WPI; 2003-577263/54.
XX
PT Novel antisense compound targeted to 5' untranslated region, coding
PT region, or intron:exon junction of nucleic acid molecule encoding mdm2,
PT useful for treating e.g. cancer, psoriasis or restenosis by inhibiting
PT mdm2 expression.
XX
XX
XX Claim 4; SEQ ID NO 246; 289pp; English.
XX
CC The invention comprises antisense oligonucleotides which are targeted to
CC the human mdm2 gene. The antisense oligonucleotides of the invention are
CC useful for reducing hyperproliferation of human cells. The antisense
CC oligonucleotides are also useful for treating: hyperproliferative
CC disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or
CC restenosis. The antisense oligonucleotides are also useful for modulating
CC apoptosis, and for increasing expression of p21. The present DNA sequence
CC represents a human mdm2 gene antisense oligonucleotide of the invention.
CC The present sequence contains 2'-methoxyethoxy-residues and has a
CC phosphorothioate backbone.
XX

SQ Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 668 TCTTGCTCAGCAGCACTC 687
Db 20 TCTTGCTCAGCAGCACTC 1
XX
RESULT 769
ADD21703/c
ID ADD21703 standard; DNA; 20 BP.
XX
AC ADD21703;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #266.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW atherosclerosis; restenosis; apoptosis modulation; p21; ss;
KW 2'-methoxyethoxy-residue; phosphorothioate backbone.
XX
OS Homo sapiens.
XX
PN WO2003048315-A2.
XX
PD 12-JUN-2003.
XX
PT 02-DEC-2002; 2002WO-US038281.
XX
PT useful for treating e.g. cancer, psoriasis or restenosis by inhibiting
XX mdm2 expression.
XX
PR 04-DEC-2001; 2001US-00005344.
XX
PS (ISIS-) ISIS PHARM INC.
XX
PI Miraglia LJ, Nero PS, Graham MJ, Monia BP, Koller E, Chiang MY;
PI Manoharan M;
XX
DR WPI; 2003-577263/54.
XX
PT Novel antisense compound targeted to 5' untranslated region, coding
PT region, or intron:exon junction of nucleic acid molecule encoding mdm2,
PT useful for treating e.g. cancer, psoriasis or restenosis by inhibiting
PT mdm2 expression.
XX
XX
XX Claim 4; SEQ ID NO 268; 289pp; English.
XX
CC The invention comprises antisense oligonucleotides which are targeted to
CC the human mdm2 gene. The antisense oligonucleotides of the invention are
CC useful for reducing hyperproliferation of human cells. The antisense
CC oligonucleotides are also useful for treating: hyperproliferative
CC disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or
CC restenosis. The antisense oligonucleotides are also useful for modulating
CC apoptosis, and for increasing expression of p21. The present DNA sequence
CC represents a human mdm2 gene antisense oligonucleotide of the invention.
CC The present sequence contains 2'-methoxyethoxy-residues and has a
CC phosphorothioate backbone.
XX
SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 868 GGATTACAGCGGTGAGCCAC 867
Db 20 GGATTACAGCGGTGAGCCAC 1
XX
RESULT 770

ADE43606/c
 ID ADE43606 standard; DNA; 20 BP.
 XX
 AC ADE43606;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human KNSL1 sequencing primer, SEQ ID 211.
 XX
 KW Neurodegenerative disease; uPA; SNGG; IDE; KNSL1; LIPA; TNFRSF6;
 KM Alzheimer's disease; neuroprotective; noctropic; gene therapy;
 KM Chromosome 10; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003054143-A2.
 XX
 PD 03-JUL-2003.
 XX
 PF 25-OCT-2002; 2002WO-US034679.
 XX
 PR 25-OCT-2001; 2001US-0339525P.
 XX
 PR 08-NOV-2001; 2001US-0336929P.
 XX
 PR 08-NOV-2001; 2001US-0338010P.
 XX
 PR 09-NOV-2001; 2001US-0338363P.
 XX
 PR 04-DEC-2001; 2001US-0337052P.
 XX
 PR 28-MAR-2002; 2002US-0368919P.
 XX
 PA (NEUR-) NEUROGENETICS INC.
 PA (GERO) GEN HOSPITAL CORP.
 XX
 PI Becker KD, Velicelbi G, Elliott KJ, Wang X, Tanzi RE, Bertram L;
 PI Saunders AJ, Mullin KM, Sampson AJ, Blacker DL;
 XX
 DR MPI; 2003-559131/52.
 XX
 PT Determining a predisposition for or the occurrence of neurodegenerative
 PT disease, e.g. Alzheimer's disease by detecting in a target nucleic acid
 PT the presence or absence of an allelic variant of one or more polymorphic
 PT regions.
 XX
 PS Example 3; Page 287; 848bp; English.
 XX
 CC The present invention relates to a method (M1) for determining a
 CC predisposition for or the occurrence of neurodegenerative disease in a
 CC subject. The method comprises detecting in a target nucleic acid obtained
 CC from the subject the presence or absence of an allelic variant of one or
 CC more polymorphic regions of one or more genes selected from uPA
 CC (Urokinase plasminogen activator), SNGG (gamma-synuclein), IDE (insulin-
 CC degrading enzyme), KNSL1 (Kinesin-like protein 1), LIPA (lysosomal acid
 CC lipase), and TNFRSF6 (Tumour Necrosis Factor Receptor-SF6), where the
 CC presence of at least one of the allelic variant of one or more
 CC polymorphic regions is indicative of a predisposition for or the
 CC occurrence of neurodegenerative disease. The genes are all located on
 CC chromosome 10. M1 is useful for determining a predisposition for or the
 CC occurrence of, and for treating neurodegenerative disease, particularly
 CC Alzheimer's disease. The present sequence is a PCR primer, which was used
 CC in the method of the invention.
 XX
 SQ Sequence 20 BP; 12 A; 2 C; 2 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 1.9%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX
 AC ADE86781;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE GATA primer #1.
 XX
 KW ss; primer; molecular phenotyping; brain; lung; CD31+ cell;
 KM lineage committed cell; survival; proliferation; differentiation;
 KM haematopoietic stem cell; cancer; leukaemia; bone marrow;
 KM transplantation.
 XX
 OS Homo sapiens.
 XX
 PN WO2003089592-A2.
 XX
 PD 30-OCT-2003.
 XX
 PF 15-APR-2003; 2003WO-US011649.
 XX
 PR 16-APR-2002; 2002US-0373127P.
 XX
 PA (UNIV) UNIV OREGON HEALTH SCI.
 XX
 PI Fleming WH, Li B;
 XX
 DR MPI; 2003-854104/79.
 XX
 PT A composition for promoting survival, proliferation and/or
 PT differentiation of hematopoietic stem cells useful in e.g. bone marrow
 PT transplantation, comprises lin cells that express CD31, CD34 and CD105.
 XX
 PS Example 1; Page 27; 54pp; English.
 XX
 CC This sequence represents a primer which was used in the molecular
 CC phenotyping of brain and lung derived CD31+ cells. This primer was used
 CC to isolate cells which are CD31+ CD34+ CD45- CD105+ c-kit- lin-. The
 CC isolated cells were used in the composition of the invention which
 CC comprises fewer than 20% of lineage committed cells. The composition of
 CC the invention is useful for reconstituting haematopoiesis, and therefore
 CC in promoting survival, proliferation and/or differentiation of
 CC haematopoietic stem cells which may be used in treating cancers (e.g.
 CC leukaemia) or in bone marrow transplantation as well as transplantation
 CC of other organs in association with the transplantation of bone marrow.
 XX
 SQ Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 1.9%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 391 AGTGCTGGGATTACAGGCGT 410
 DB 20 AGTGCTGGGATTACAGGCGT 1
 XX
 RESULT 772
 ADI61628
 ID ADI61628 standard; DNA; 20 BP.
 XX
 AC ADI61628;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human SAP-1 gene targeted oligonucleotide ISIS 176450.
 XX
 KW cytostatic; antisense therapy; Serum response factor Accessory Protein;
 KM SAP-1; splice variant; hyperproliferative disorder; cancer; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers

[illegible]

XX	Human; antisense; lung dysfunction; nasal airway dysfunction;
KW	antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW	antiasthmatic; hypotensive; immunosuppressive; cytotoxic; gene therapy;
KW	antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW	lung inflammation; respiratory disease; ds.
XX	
XX	Homo sapiens.
XX	
PN	WO200285308-A2.
PD	
PD	31-OCT-2002.
XX	
PP	23-APR-2002; 2002WO-US013135.
XX	
PR	24-APR-2001; 2001US-0286137P.
XX	
PA	(EPIG-) EPIGENESIS PHARM INC.
XX	
PI	Nyge JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI	Miller S, Yang L, Shahabuddin S;
DR	WPI; 2003-229219/22.
XX	
PT	Pharmaceutical composition for treating ailments associated with impaired
PT	respiration, has oligo(s) antisense to specific gene(s) or its
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT	ubiquinone.
XX	
PS	Disclosure; SEQ ID NO 13207; 872pp; English.
XX	
XX	The invention relates to a novel pharmaceutical composition, which has a
CC	first active agent comprising an oligonucleotide antisense to the
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC	junctions of genes encoding a polypeptide associated with lung and/or
CC	nasal airway dysfunction and a second active agent comprising an
CC	antiinflammatory steroid and ubiquinone. A composition of the invention
CC	has antiinflammatory, cytostatic activity. The composition may have a
CC	immunosuppressive, and antiallergic, antiasthmatic, hypotensive,
CC	use in antisense gene therapy. The composition is useful for treating or
CC	preventing a respiratory, lung or malignant disease or condition, also
CC	for enhancing the prophylactic or therapeutic respiratory effect of an
CC	antiinflammatory steroid in a subject, for reducing or depleting levels
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC	lung inflammation, lung allergies, or a respiratory disease or condition.
CC	Note: The sequence data for this patent is not represented in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences
XX	
XX	Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 U; 0 Other;
QY	
DB	537 CCTGGCTCAGCCTCCCAAGT 556
	1 CCTGGCTCAGCCTCCCAAGT 20
	Query Match 1.9%; Score 18.4; DB 1; Length 20;
	Best Local Similarity 95.0%; Pred. No. 1.3e+03;
	Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
RESULT 774	
ID	AB289864/c
AC	AB289864 standard; DNA; 20 BP.
DT	17-OCT-2003 (first entry)
XX	
XX	Human oligonucleotide sequence.

XX	Human; antisense; lung dysfunction; nasal airway dysfunction;
KW	antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM	antiallergic; hypotensive; immunosuppressive; cytoskeletal; gene therapy;
KW	antisense gene therapy; respiratory; lung; adenosine sensitivity;
KM	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW	lung inflammation; respiratory disease; ds.
XX	
OS	Homo sapiens.
PN	WO200285308-A2.
XX	
PD	31-OCT-2002.
XX	
PF	23-APR-2002; 2002WO-US013135.
XX	
PR	24-APR-2001; 2001US-0286137P.
XX	
PA	(EPIG-) EPIGENESIS PHARM INC.
PI	Nyze JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX	
P1	Miller S, Tang L, Shahabuddin S;
XX	
DR	WPI; 2003-229219/22.
XX	
PT	Pharmaceutical composition for treating ailments associated with impaired
XX	respiration, has oligo(s) antisense to specific gene(s) or its
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX	ubiquinone.
PS	Disclosure; SEQ ID NO 13206; 872pp; English.
XX	
XX	The invention relates to a novel pharmaceutical composition, which has a
CC	first active agent comprising an oligonucleotide antisense to the
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC	junctions of genes encoding a polypeptide associated with lung and/or
CC	nasal airway dysfunction and a second active agent comprising an
CC	antiinflammatory steroid and ubiquinone. A composition of the invention
CC	has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC	immunosuppressive, and cytoskeletal activity. The composition may have a
CC	use in antisense gene therapy. The composition is useful for treating or
CC	preventing a respiratory, lung or malignant disease or condition, also
CC	for enhancing the prophylactic or therapeutic respiratory effect of an
CC	antiinflammatory steroid in a subject, for reducing or depleting levels
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC	lung inflammation, lung allergies, or a respiratory disease or condition.
CC	Note: The sequence data for this patent is not represented in the printed
CC	specification, but was obtained in electronic format directly from WPI
CC	at ftp.wipo.int/pub/published_pct_sequences
XX	
SEQ	Sequence 20 BP; 2 A; 10 C; 2 G; 6 T; 0 U; 0 Other;
XX	
Query Match	1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity	95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	532 ATCGTCGCGCTCAGCTCC 551
DB	1 ATTCCTCGCTCAGCTCC 20
XX	
RESULT 776	
ABZ97909	
ID	ABZ97909 standard; DNA; 20 BP.
XX	
AC	ABZ97909;
XX	
DT	17-OCT-2003 (first entry)
XX	
DE	Human RANTES oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiallergic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX Homo sapiens.
 OS
 XX WO200285308-A2.
 PN
 XX 31-OCT-2002.
 PD
 XX 23-APR-2002; 2002WO-US013135.
 PF
 XX 24-APR-2001; 2001US-0286137P.
 PR
 XX (EPIC-) EPIGENESIS PHARM INC.
 PA
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 PI
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 PS
 XX Disclosure; SEQ ID NO 13151; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiallergic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at fep.wipo.int/pub/published_pct_sequences
 CC
 XX
 SQ Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 1.9%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 722 CCTCTGAGTAGTGGGACT 741
 Db 1 CCTCCGAGTAGTGGGACT 20
 RESULT 777
 AB289861/c
 ID AB289861 standard; DNA; 20 BP.
 XX
 AC AB289861;
 XX
 XX 17-OCT-2003 (first entry)
 DT
 XX Human oligonucleotide sequence.
 DE

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiallergic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX Homo sapiens.
 OS
 XX WO200285308-A2.
 PN
 XX 31-OCT-2002.
 PD
 XX 23-APR-2002; 2002WO-US013135.
 PF
 XX 24-APR-2001; 2001US-0286137P.
 PR
 XX (EPIC-) EPIGENESIS PHARM INC.
 PA
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 PI
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 PS
 XX Disclosure; SEQ ID NO 5103; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiallergic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at fep.wipo.int/pub/published_pct_sequences
 CC
 XX
 SQ Sequence 20 BP; 4 A; 4 C; 9 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 1.9%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 970 TCGGCTCAGTGCACCTCTG 989
 Db 20 TCGGCTCAGTGCACCTCTG 1
 RESULT 778
 AB297902
 ID AB297902 standard; DNA; 20 BP.
 XX
 AC AB297902;
 XX
 XX 17-OCT-2003 (first entry)
 DT
 XX Human RANTES oligonucleotide sequence.
 DE

```
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIC-) EPIGENESIS PHARM INC.
XX
XX Nyce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(e) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Disclosure; SEQ ID NO 13144; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 4 A; 5 C; 8 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 868 GGATTACAGCGTGGAGCCAC 887
XX |||||
XX 1 GGATTACAGCGTGGAGCCAC 20
XX
XX RESULT 779
XX AB292724
XX ID AB292724 standard; DNA; 20 BP.
XX
XX AB292724;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human oligonucleotide sequence.
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XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIC-) EPIGENESIS PHARM INC.
XX
XX Nyce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(e) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Disclosure; SEQ ID NO 7966; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 4 A; 0 C; 4 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 768 TTTTGTATTTTGTAGTA 787
XX |||||
XX 1 TTTTGTATTTTGTAGTA 20
XX
XX RESULT 780
XX AB298012
XX ID AB298012 standard; DNA; 20 BP.
XX
XX AB298012;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human RANRES oligonucleotide sequence.
```

XX	Human; antisense; lung dysfunction; nasal airway dysfunction;
KM	antiinflammatory steroid; ubiquinone; immunosuppressive; antiinflammatory; antiallergic;
KM	antiaesthetic; hypotensive; immunosuppressive; cytosolic; gene therapy;
KM	antisense gene therapy; respiratory; lung; adenosine sensitivity;
KM	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KM	lung inflammation; respiratory disease; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200285308-A2.
XX	
PD	31-OCT-2002.
XX	
PF	23-APR-2002; 2002WO-US013135.
XX	
PR	24-APR-2001; 2001US-0286137P.
XX	
PA	(EPIC-) EPIGENESIS PHARM INC.
XX	
PI	Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI	Miller S, Tang L, Shahabuddin S;
XX	
DR	WPI; 2003-229219/22.
XX	
PT	Pharmaceutical composition for treating ailments associated with impaired
PT	respiration, has oligo(s) antisense to specific gene(s) or its
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT	ubiquinone.
XX	
PS	Disclosure; SEQ ID NO 13254; 872bp; English.
XX	
CC	The invention relates to a novel pharmaceutical composition, which has a
CC	first active agent comprising an oligonucleotide antisense to the
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC	junctions of genes encoding a polypeptide associated with lung and/or
CC	nasal airway dysfunction and a second active agent comprising an
CC	antiinflammatory steroid and ubiquinone. A composition of the invention
CC	has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC	immunosuppressive, and cytosolic activity. The composition may have a
CC	use in antisense gene therapy. The composition is useful for treating or
CC	preventing a respiratory, lung or malignant disease or condition, also
CC	for enhancing the prophylactic or therapeutic respiratory effect of an
CC	antiinflammatory steroid in a subject, for reducing or depleting levels
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC	lung inflammation, lung allergies, or a respiratory disease or condition.
CC	Note: The sequence data for this patent is not represented in the printed
CC	specification, but was obtained in electronic format directly from WIFO
CC	at ftp.wifo.int/pub/published_pot_sequences
XX	
SQ	Sequence 20 BP; 2 A; 6 C; 7 G; 5 T; 0 U; 0 Other;
XX	
QY	636 TCTGTCACCCAGCTCGAGT 655
DB	1 TCTGTCGCCAGCTCGAGT 20
XX	
RESULT 781	
ID	ABZ98015
XX	ABZ98015 standard; DNA; 20 BP.
XX	ABZ98015;
AC	
XX	
DT	17-OCT-2003 (first entry)
XX	
DE	Human RANTES oligonucleotide sequence.

XX	Human; antisense; lung dysfunction; nasal airway dysfunction;
XX	antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW	antihistaminic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW	antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW	lung inflammation; respiratory disease; ds.
OS	Homo sapiens.
XX	
FN	WO200285308-A2.
PD	31-OCT-2002.
XX	
PE	23-APR-2002; 2002WO-US013135.
XX	
PR	24-APR-2001; 2001US-0286137P.
XX	
PA	(EPIG-) EPIGENESIS PHARM INC.
PI	Nyee JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI	Miller S, Tang L, Shahabuddin S;
DR	WPI; 2003-229219/22.
XX	
PT	Pharmaceutical composition for treating ailments associated with impaired
PT	respiration, has oligo(s) antisense to specific gene(s) or its
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT	ubiquinone.
PS	Disclosure; SEQ ID NO 13257; 872pp; English.
XX	
XX	The invention relates to a novel pharmaceutical composition, which has a
CC	first active agent comprising an oligonucleotide antisense to the
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC	junctions of genes encoding a polypeptide associated with lung and/or
CC	nasal airway dysfunction and a second active agent comprising an
CC	antiinflammatory steroid and ubiquinone. A composition of the invention
CC	has antiinflammatory, antiallergic, antihistaminic, hypotensive,
CC	immunosuppressive, and cytostatic activity. The composition may have a
CC	use in antisense gene therapy. The composition is useful for treating or
CC	preventing a respiratory, lung or malignant disease or condition, also
CC	for enhancing the prophylactic or therapeutic respiratory effect of an
CC	antiinflammatory steroid in a subject, for reducing or depleting levels
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC	lung inflammation, lung allergies, or a respiratory disease or condition.
CC	Note: The sequence data for this patent is not represented in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences
XX	
SEQ	Sequence 20 BP; 3 A; 4 C; 9 G; 4 T; 0 U; 0 Other;
XX	
Query Match	1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity	95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	651 GGAGTGCAGTGGCGCAATCT 670
DB	1 GGAGTGCAGTGGCGCAATCT 20
RESULT 782	
ABZ97908	
ID	ABZ97908 standard; DNA; 20 BP.
XX	
AC	ABZ97908;
XX	
DT	17-OCT-2003 (first entry)
XX	
DE	Human RANTES oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiaslarmic; hypotensive; immunosuppressive; cyclostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX MO200285308-A2.
XX
XX PD 31-OCT-2002.
XX
XX PF 23-APR-2002; 2002WO-US013135.
XX
XX PR 24-APR-2001; 2001US-0286137P.
XX
XX PA (EP1G-) EPIGENESIS PHARM INC.
XX
XX PI Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX DR WPI; 2003-229219/22.
XX
XX PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX PS Disclosure; SEQ ID NO 13150; 872pp; English.
XX
XX CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiaslarmic, hypotensive,
CC immunosuppressive, and cyclostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 20 BP; 3 A; 8 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 542 CTCAGCTCCCAAGTAGCTG 561
DB 1 CTCAGCTCCCAAGTAGCTG 20

RESULT 783
AB298003
ID AB298003 standard; DNA; 20 BP.
XX
XX AC AB298003;
XX
XX AC
XX
XX DT 17-OCT-2003 (first entry)
XX
XX DE Human RANTES oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiaslarmic; hypotensive; immunosuppressive; cyclostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX MO200285308-A2.
XX
XX PD 31-OCT-2002.
XX
XX PF 23-APR-2002; 2002WO-US013135.
XX
XX PR 24-APR-2001; 2001US-0286137P.
XX
XX PA (EP1G-) EPIGENESIS PHARM INC.
XX
XX PI Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX DR WPI; 2003-229219/22.
XX
XX PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX PS Disclosure; SEQ ID NO 13245; 872pp; English.
XX
XX CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiaslarmic, hypotensive,
CC immunosuppressive, and cyclostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 642 ACCCAGCTCGAGTAGCTG 661
DB 1 ACCCAGCTCGAGTAGCTG 20

RESULT 784
AB297903
ID AB297903 standard; DNA; 20 BP.
XX
XX AC AB297903;
XX
XX AC
XX
XX DT 17-OCT-2003 (first entry)
XX
XX DE Human RANTES oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiallergic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX Homo sapiens.
XX MO200285308-A2.
XX 31-OCT-2002.
XX 23-APR-2002; 2002WO-US013135.
XX 24-APR-2001; 2001US-0286137P.
XX (EPIC-) EPIGENESIS PHARM INC.
XX NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
DR WPI; 2003-229219/22.
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX Disclosure; SEQ ID NO 13145; 872bp; English.
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end, genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiallergic, hypotensive,
CC immunosuppressive, and cyrostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 20 BP; 4 A; 8 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 873 ACAGCGCTGAGCCACACGCG 892
DB 1 ACAGCGCTGAGCCACACGCG 20
RESULT 785
ABZ99062
ID ABZ99062 standard; DNA; 20 BP.
XX AC ABZ99062;
XX 17-OCT-2003 (first entry)
DT Human PDB4C oligonucleotide sequence.
DE

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiallergic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX Homo sapiens.
XX MO200285308-A2.
XX 31-OCT-2002.
XX 23-APR-2002; 2002WO-US013135.
XX 24-APR-2001; 2001US-0286137P.
XX (EPIC-) EPIGENESIS PHARM INC.
XX NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
DR WPI; 2003-229219/22.
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX Disclosure; SEQ ID NO 14304; 872bp; English.
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end, genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiallergic, hypotensive,
CC immunosuppressive, and cyrostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 20 BP; 3 A; 10 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 538 CTGCTCAGCTCCCAAGTA 557
DB 1 CTGCTCAGCTCCCAAGTA 20
RESULT 786
ABZ99105
ID ABZ99105 standard; DNA; 20 BP.
XX AC ABZ99105;
XX 17-OCT-2003 (first entry)
DT Human PDB4C oligonucleotide sequence.
DE

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 14347; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1115 CTGGTCTCAAACTCTGACC 1134
DB 1 CTGGTCTCAAACTCTGACC 20

RESULT 787
AB298013
ID AB298013 standard; DNA; 20 BP.
XX
XX
AC AB298013;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human RANTES oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 13255; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 3 A; 6 C; 8 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 641 CAGCCAGGCTGAGTGACGT 660
DB 1 CAGCCAGGCTGAGTGACGT 20

RESULT 788
AB299071
ID AB299071 standard; DNA; 20 BP.
XX
XX
AC AB299071;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human PDE4C oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX Homo sapiens.
XX WO200285308-A2.
XX 31-OCT-2002.
XX 23-APR-2002; 2002WO-US013135.
XX 24-APR-2001; 2001US-0286137P.
XX (EPIC-) EPIGENESIS PHARM INC.
XX Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX Disclosure; SEQ ID NO 14313; 872bp; English.
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or
CC receptor, producing bronchodilation, increasing levels of adenosine or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 20 BP; 2 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 199 ATGTTGTCAGCGTGTCTC 218
DB 1 ATGTTGTCAGCGTGTCTC 20
RESULT 789
AB289844/c standard; DNA; 20 BP.
XX
XX AB289844;
XX
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX Homo sapiens.
XX WO200285308-A2.
XX 31-OCT-2002.
XX 23-APR-2002; 2002WO-US013135.
XX 24-APR-2001; 2001US-0286137P.
XX (EPIC-) EPIGENESIS PHARM INC.
XX Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX Disclosure; SEQ ID NO 5086; 872bp; English.
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or
CC receptor, producing bronchodilation, increasing levels of adenosine or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 20 BP; 13 A; 2 C; 0 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 766 ATTTTGTGATTTTAACTA 785
DB 20 AATTTTGTGATTTTAACTA 1
RESULT 790
AB292736 standard; DNA; 20 BP.
XX
XX AB292736;
XX
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.

```
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KM antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KM antisense gene therapy; respiratory; lung; adenosine sensitivity;
KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KM lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIC-) EPIGENESIS PHARM INC.
XX
XX NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 7978; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 4 A; 10 C; 2 G; 4 T; 0 U; 0 Other;
XX
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 367 AGTCACCTGCTCAGCCTC 386
DB 1 AATCCACCTGCTCAGCCTC 20
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RESULT 791
AB299077
ID AB299077 standard; DNA; 20 BP.
XX
XX AB299077;
AC
XX 17-OCT-2003 (first entry)
DT
XX
XX Human PDE4C oligonucleotide sequence.
DE
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```
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KM antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KM antisense gene therapy; respiratory; lung; adenosine sensitivity;
KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KM lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIC-) EPIGENESIS PHARM INC.
XX
XX NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 14319; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 6 A; 2 C; 7 G; 5 T; 0 U; 0 Other;
XX
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 389 AAAGTGCTGGATTATACGC 408
DB 1 AAAGTGCTGGATTATACGC 20
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RESULT 792
ACA88928/C
ID ACA88928 standard; DNA; 20 BP.
XX
XX ACA88928;
AC
XX 08-JUL-2003 (first entry)
DT
XX
XX Selection and amplification of genetic markers PCR related primer #39.
DE
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